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*************************************************
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  __  __ ____   ___   ____   ___ _   _
 |  \/  |  _ \ / __| |  _ \ / __| | | |
 | |\/| | |_) |\__ \ | |_) | |  | |_| |
 | |  | |  __/ |___/ |  _ <| |__|  _  |
 |_|  |_|_|   |____| |_| \_\\___|_| |_|   (TM)
*************************************************
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      Release 2.1D John F. Collins, Biocomputing Research Unit.
      Copyright (c) 1993, 1994, 1995 University of Edinburgh, D.K.
            Distribution rights by IntelliGenetics, Inc.
*************************************************

MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:             Tue Apr 7 22:01:29 1998;  MasPar time 14.40 Seconds
                                              568.190 Million cell updates/sec
Tabular output not generated.

Title:          >US-08-190-411A-1
Description:    (57-219) from 5541104.seq
Perfect Score:  163
N.A. Sequence:  57 ACCCATCCAAACATCTTCAC..........TCGGTCTGAGGGGCGGCTTG 219
                   TGGGTAGGTTGTAGAAGTG.........AGCCAGACTCCCGCCGAAC
        Comp:

Scoring table:   TABLE default
                 Gap 6

Nmatch  STD :    Dbase 0: Query 0

Searched:        96465 seqs, 25105746 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        n-issued
                 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                 10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics:      Mean 6.962;  Variance 3.685;  scale 1.889

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.		Score	% Query Match	Query Length	DB	ID	Description	Pred. No.
1		163	100.0	5674	7	US-08-299-	Sequence 8, Applicatio	9.26e-108
2		163	100.0	5674	6	US-08-190-	Sequence 1, Applicatio	9.26e-108
3		163	100.0	5674	4	US-07-807-	Sequence 8, Applicatio	9.26e-108
4		71	43.6	4157	4	US-07-807-	Sequence 9, Applicatio	1.21e-36
5		71	43.6	4157	7	US-08-299-	Sequence 9, Applicatio	1.21e-36
6		70	42.9	662	7	US-08-299-	Sequence 10, Applicatio	6.74e-36
7		70	42.9	662	4	US-07-807-	Sequence 10, Applicatio	6.74e-36
8	c	32	19.6	215	6	US-08-238-	Sequence 5, Applicatio	8.46e-09
9		28	17.2	215	6	US-08-238-	Sequence 5, Applicatio	3.31e-06
10	c	22	13.5	75	14	PCT-US95-1	Sequence 99, Applicati	1.60e-02
11	c	22	13.5	82	14	PCT-US95-1	Sequence 97, Applicati	1.60e-02
12	c	22	13.5	105	5	US-07-865-	Sequence 13, Applicati	1.60e-02
13		22	13.5	448	7	US-08-702-	Sequence 7, Applicati	1.60e-02
14		21	12.9	7218	7	US-08-232-	Sequence 14, Applicati	6.11e-02
15	c	20	12.3	69	7	US-08-471-	Sequence 142, Applicat	2.28e-01
16		20	12.3	81	14	PCT-US95-1	Sequence 98, Applicati	2.28e-01
17		20	12.3	1205	8	US-08-518-	Sequence 36, Applicati	2.28e-01
18	c	20	12.3	7218	7	US-08-232-	Sequence 14, Applicati	2.28e-01
19	c	19	11.7	66	7	US-08-471-	Sequence 144, Applicat	8.27e-01
20	c	19	11.7	74	14	PCT-US95-1	Sequence 100, Applicat	8.27e-01
21	c	19	11.7	74	14	PCT-US95-1	Sequence 94, Applicati	8.27e-01
22		19	11.7	81	14	PCT-US95-1	Sequence 92, Applicati	8.27e-01
23		19	11.7	3157	7	US-08-336-	Sequence 5, Applicatio	8.27e-01
24	c	19	11.7	3157	7	US-08-336-	Sequence 6, Applicatio	8.27e-01
25	c	19	11.7	4944	7	US-08-623-	Sequence 8, Applicatio	8.27e-01
26	c	19	11.7	5055	7	US-08-623-	Sequence 88, Applicati	8.27e-01
27		18	11.0	56	14	PCT-US95-1	Sequence 145, Applicat	2.91e+00
28		18	11.0	65	7	US-08-471-	Sequence 143, Applicat	2.91e+00
29	c	18	11.0	68	7	US-08-471-	Sequence 143, Applicat	2.91e+00
30		18	11.0	68	7	US-08-471-	Sequence 92, Applicati	2.91e+00
31		18	11.0	75	14	PCT-US95-1	Sequence 99, Applicati	2.91e+00
32	c	18	11.0	81	14	PCT-US95-1	Sequence 98, Applicati	2.91e+00
33		18	11.0	82	14	PCT-US95-1	Sequence 97, Applicati	2.91e+00
34	c	18	11.0	879	6	US-08-243-	Sequence 1, Applicatio	2.91e+00
35		18	11.0	879	13	PCT-US94-0	Sequence 1, Applicatio	2.91e+00
36		18	11.0	898	6	US-08-726-	Sequence 3, Applicatio	2.91e+00
37	c	18	11.0	898	6	US-08-419-	Sequence 3, Applicatio	2.91e+00
38	c	18	11.0	1322	6	US-08-419-	Sequence 1, Applicatio	2.91e+00
39	c	18	11.0	1322	6	US-08-726-	Sequence 1, Applicatio	2.91e+00
40		18	11.0	2959	7	US-08-408-	Sequence 4, Applicatio	2.91e+00
41		18	11.0	2959	7	US-08-408-	Sequence 1, Applicatio	2.91e+00
42		18	11.0	2959	7	US-08-408-	Sequence 1, Applicatio	2.91e+00
43	c	18	11.0	6639	7	US-08-727-	Sequence 1, Applicatio	2.91e+00
44	c	18	11.0	6961	7	US-08-727-	Sequence 2, Applicatio	2.91e+00

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                              ALIGNMENTS

RESULT  1
ID   US-08-299-849B-8 STANDARD; DNA; UNC; 5674 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 8, Application US/08299849B.
CC   Sequence 8, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC      APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
CC      APPLICANT:  Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC      APPLICANT:  Chomez, Patrick
CC      TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
CC      TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precurso
CC      NUMBER OF SEQUENCES:  48
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Felfe & Lynch
CC         STREET:  805 Third Avenue
CC         CITY:  New York City
CC         STATE:  New York
CC         ZIP:  10022
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC         COMPUTER:  IBM
CC         OPERATING SYSTEM:  PC-DOS
CC         SOFTWARE:  Wordperfect
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/299,849B
CC         FILING DATE:  1-SEPTEMBER-1994
CC         CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/037,230
CC         FILING DATE:  26-MARCH-1993
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  PCT/US92/04354
CC         FILING DATE:  22-MAY-1992
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/807,043
CC         FILING DATE:  12-DECEMBER-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/764,364
CC         FILING DATE:  23-SEPTEMBER-1991
CC      PRIOR APPLICATION DATA:
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CC       APPLICATION NUMBER:    07/728,838
CC       APPLICATION NUMBER:    9-JULY-1991
CC    PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:    07/705,702
CC       FILING DATE:    23-May-1991
CC    ATTORNEY/AGENT INFORMATION:
CC       NAME:  Hanson, No. 5612201man D.
CC       REGISTRATION NUMBER:  30,946
CC       REFERENCE/DOCKET NUMBER:  LUD 5355
CC    TELECOMMUNICATION INFORMATION:
CC       TELEPHONE:  (212) 688-9200
CC       TELEFAX:  (212) 838-3884
CC       NAME/KEY:  MAGE-1 gene
CC    INFORMATION FOR SEQ ID NO:  8:
CC    SEQUENCE CHARACTERISTICS:
CC       LENGTH:  5674 base pairs
CC       TYPE:  nucleic acid
CC       STRANDEDNESS:  single
CC       TOPOLOGY:  linear
CC    MOLECULE TYPE:  genomic DNA
CC    FEATURE:
CC       NAME/KEY:  MAGE-1 gene
SQ    Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match    100.0%;   Score 163;   DB 7;   Length 5674;
Best Local Similarity 100.0%;   Pred. No. 9.26e-108;
Matches  163;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Db     57 ACCATCCAAACATCTTCACGTCACCCCCAGCCCAGCGCAGCAGAATCCGGTTCCACC 116
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Qy     57 ACCATCCAAACATCTTCACGTCACCCCCAGCCCAGCGCAGCAGAATCCGGTTCCACC 116

Db    117 CCTGCTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCCACTGACTTGAGCATTA 176
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Qy    117 CCTGCTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCCACTGACTTGAGCATTA 176

Db    177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219
          ||||||||||||||||||||||||||||||||||||||||||
Qy    177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219

RESULT  2
ID    US-08-190-411A-1 STANDARD; DNA; UNC; 5674 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 1, Application US/08190411A.
DE    Sequence 1, Application US/08190411A
CC    Patent No. 5541104
CC    GENERAL INFORMATION:
CC       APPLICANT:  Chen, Yao-Tseng; Stockert, Elisabeth;
CC       APPLICANT:  Chen, Yachi: Garin-Chesa,  Pilar; Rettig, Wolfgang J.;
CC       APPLICANT:  van der Bruggen, Pierre;  Boon-Falleur, Thierry;
CC       APPLICANT:  Old, Lloyd J.
CC    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES WHICH BIND TO
CC    TITLE OF INVENTION:  TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBIN
ANT MAGE-1,
CC    TITLE OF INVENTION:  AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
CC    NUMBER OF SEQUENCES:  4
CC    CORRESPONDENCE ADDRESS:
CC       ADDRESSEE:  Felfe & Lynch
CC       STREET:  805 Third Avenue
CC       CITY:  New York City
CC       STATE:  New York
CC       ZIP:  10022
CC    COMPUTER READABLE FORM:
CC       MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC       COMPUTER:  IBM
CC       OPERATING SYSTEM:  PC-DOS
CC       SOFTWARE:  Wordperfect
CC    CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER:  US/08/190,411A
CC       FILING DATE:  01-FEBRUARY-1994
CC       CLASSIFICATION:  436
CC    PRIOR APPLICATION DATA:
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CC       APPLICATION NUMBER:    037,230
CC       FILING DATE:    26-MARCH-1993
CC    PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:    PCT/US92/04354
CC       FILING DATE:    22-MAY-1992
CC    PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:    07/807,043
CC       FILING DATE:    12-DECEMBER-1991
CC    PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:    07/764,364
CC       FILING DATE:    23-SEPTEMBER-1991
CC    PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:    07/728,838
CC       FILING DATE:    9-JULY-1991
CC    PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:    07/705,702
CC       FILING DATE:    23-MAY-1991
CC    ATTORNEY/AGENT INFORMATION:
CC       NAME:  Hanson, No. 5541104man D.
CC       REGISTRATION NUMBER:  30,946
CC       REFERENCE/DOCKET NUMBER:  LUD 5354
CC    TELECOMMUNICATION INFORMATION:
CC       TELEPHONE:  (212) 688-9200
CC       TELEFAX:  (212) 838-3884
CC    INFORMATION FOR SEQ ID NO:  1:
CC    SEQUENCE CHARACTERISTICS:
CC       LENGTH:  5674 base pairs
CC       TYPE:  nucleic acid
CC       STRANDEDNESS:  single
CC       TOPOLOGY:  linear
CC    MOLECULE TYPE:  genomic DNA
CC    FEATURE:
CC       NAME/KEY:  MAGE-1 gene
SQ    Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match    100.0%;   Score 163;   DB 6;   Length 5674;
Best Local Similarity 100.0%;   Pred. No. 9.26e-108;
Matches  163;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

Db     57 ACCATCCAAACATCTTCACGTCACCCCCAGCCCAGCGCAGCAGAATCCGGTTCCACC 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     57 ACCATCCAAACATCTTCACGTCACCCCCAGCCCAGCGCAGCAGAATCCGGTTCCACC 116

Db    117 CCTGCTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCCACTGACTTGAGCATTA 176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    117 CCTGCTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCCACTGACTTGAGCATTA 176

Db    177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219
          ||||||||||||||||||||||||||||||||||||||||||
Qy    177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219

RESULT  3
ID    US-07-807-043B-8 STANDARD; DNA; UNC; 5674 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 8, Application US/07807043B.
DE    Sequence 8, Application US/07807043B
CC    Patent No. 5342774
CC    GENERAL INFORMATION:
CC       APPLICANT:  Boon, Thierry, Van den Eynde, Beno t
CC    TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
CC    TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
CC    NUMBER OF SEQUENCES:  16
CC    CORRESPONDENCE ADDRESS:
CC       ADDRESSEE:  Felfe & Lynch
CC       STREET:  805 Third Avenue
CC       CITY:  New York City
CC       STATE:  New York
CC       ZIP:  10022
CC    COMPUTER READABLE FORM:
CC       MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC       COMPUTER:  IBM
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CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/807,043B
CC   FILING DATE: 19911212
CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5342774man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 253.3
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 8:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 5674 base pairs
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: singular
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-1 gene
SQ   Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match    100.0%;  Score 163;  DB 4;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 9.26e-108;
Matches 163;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db   57 ACCCATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCCAGGCAGAATCCGGTTCCACC 116
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Qy   57 ACCCATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCCAGGCAGAATCCGGTTCCACC 116

Db  117 CCTGCTCTCAACCCAGGGAAGCCCAGTGCCCAGATGTGACGCCACTGACTTGAGCATTA 176
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  117 CCTGCTCTCAACCCAGGGAAGCCCAGTGCCCAGATGTGACGCCACTGACTTGAGCATTA 176

Db  177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219
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Qy  177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219

RESULT 4
ID   US-07-807-043B-9 STANDARD; DNA; UNC; 4157 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 9, Application US/07807043B.
DE   Sequence 9, Application US/07807043B
CC   Patent No. 5342774
CC   GENERAL INFORMATION:
CC   APPLICANT: Boon, Thierry, Van den Eynde, Beno t
CC   TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
CC   TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CC   NUMBER OF SEQUENCES: 16
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
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CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/807,043B
CC   FILING DATE: 19911212
CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5342774man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 253.3
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 9:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 4157 base pairs
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: singular
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-2 gene
SQ   Sequence 4157 BP; 953 A; 1134 C; 1185 G; 885 T; 0 other;

Query Match    43.6%;  Score 71;  DB 4;  Length 4157;
Best Local Similarity 77.1%;  Pred. No. 1.21e-36;
Matches 31;  Conservative 0;  Mismatches 31;  Indels 1;  Gaps 1;

Db    3 CATCCAGATCCCATCCGGCAGAATCCGGTTCACCCTTGCCGTGAACCCAGGGAAGTC 62
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Qy   80 CACCCCCAGCCCAAGCCCAGGCAGAATCCGGTTCCACCCCGTCTCAACCCAGGGAAGCC 139

Db   63 ACGG-GCCCGGATGTGACGCCACTGACTTGCACATTGGAGGTCAGAGGACAGCGAGATTC 121
          || || |||||||||||||||||||||| || ||||  ||||  |||| ||||||||| ||
Qy  140 CAGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGGAGGTTT 199

Db  122 TCGCCCTGAGCAACGGCCTG 141
          ||| ||||| |||| ||
Qy  200 TCGGTCTGAGGGGCGGCTTG 219

RESULT 5
ID   US-08-299-849B-9 STANDARD; DNA; UNC; 4157 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 9, Application US/08299849B.
DE   Sequence 9, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
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CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 561220Iman D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 10:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 662 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-21 gene
SQ   Sequence 662 BP; 155 A; 244 C; 176 G; 87 T; 0 other;

Query Match   42.9%;   Score 70;   DB 7;   Length 662;
Best Local Similarity   80.0%;   Pred. No. 6.74e-36;
Matches   100;   Conservative   0;   Mismatches   24;   Indels   1;   Gaps   1;

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Qy    95  CCAGGCAGAATCCGGTTCCACCCCTCAACCCCTGCTCCAACCCAGGGAAGCCCCAGAGTGT  154

Db    74  GACGGCCACTGACTTGCGCGTTGGAGGTCAGAGGACAGGAACAGCGAGATTCTCGCCCTGAGCAACG  133
          |||||||||||||||| |  ||| || ||| |||| |||| || |||||||| || ||||| ||
Qy   155  GACGCCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGAAGCGAGGTTTTCGGTCTGAGGGGGCG  214

Db   134  GCCTG  138
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Qy   215  GCTTG  219
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RESULT 7
ID   US-07-807-043B-10 STANDARD; DNA; UNC; 662 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 10, Application US/0780 7043B.

CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 561220Iman D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 9:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 4157 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-2 gene
SQ   Sequence 4157 BP; 953 A; 1134 C; 1185 G; 885 T; 0 other;

Query Match   43.6%;   Score 71;   DB 7;   Length 4157;
Best Local Similarity   77.1%;   Pred. No. 1.21e-36;
Matches   108;   Conservative   0;   Mismatches   31;   Indels   1;   Gaps   1;

```
Db     3  CATCCAGATCCCCATCCGGGCAGAATCCGGTTCCACCCTTGCCGTGAACCCAGGGAAGTC  62
          || | || | ||| || |||||||||||||||||||| | ||||||||||||||||||
Qy    80  CACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTGCTCCAACCCAGGGAAGCC  139

Db    63  ACGG-GCCCGGATGTGACGCCACTGACTTGCACATTGGAGGTCAGAGGACAGCGAGATTC  121
          ||||  |||||||||||||||| ||||||||  |||| |||| ||||| ||| |||||||
Qy   140  CAGGTGCCCAGGATGTGACGCCCACTGACTTGACGCATTAGTGGTTAGAGAAGAAGCGAGGTTT  199

Db   122  TCGCCCTGAGCAACGGCCTG  141
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Qy   200  TCGGTCTGAGGGGCGGCTTG  219
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RESULT 6
ID   US-08-299-849B-10 STANDARD; DNA; UNC; 662 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 10, Application US/08299849B.
CC   Sequence 10, Application US/08299849B.
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   NUMBER OF SEQUENCES: 48

Thu Apr. 9 07:08:16 1998

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CC   Sequence 10, Application US/07807043B
CC   Patent No. 5342774
CC   GENERAL INFORMATION:
CC     APPLICANT: Boon, Thierry, Van den Eynde, Beno t
CC     TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
CC     TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CC     NUMBER OF SEQUENCES: 16
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Felfe & Lynch
CC       STREET: 805 Third Avenue
CC       CITY: New York City
CC       STATE: New York
CC       ZIP: 10022
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC       COMPUTER: IBM
CC       OPERATING SYSTEM: PC-DOS
CC       SOFTWARE: Wordperfect
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/07/807,043B
CC       FILING DATE: 19911212
CC       CLASSIFICATION: 424
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/764,364
CC       FILING DATE: 23-SEPTEMBER-1991
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/728,838
CC       FILING DATE: 9-JULY-1991
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/705,702
CC       FILING DATE: 23-May-1991
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Hanson, No. 5342774man D.
CC       REGISTRATION NUMBER: 30,946
CC       REFERENCE/DOCKET NUMBER: LUD 253.3
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (212) 688-9200
CC       TELEFAX: (212) 838-3884
CC     INFORMATION FOR SEQ ID NO: 10:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH: 662 base pairs
CC         TYPE: NUCLEIC ACID
CC         STRANDEDNESS: singular
CC         TOPOLOGY: linear
CC       MOLECULE TYPE: genomic DNA
CC       FEATURE:
CC         NAME/KEY: MAGE-21 gene
SQ   Sequence 662 BP; 155 A; 244 C; 176 G; 87 T; 0 other;

Query Match       42.9%;  Score 70;  DB 4;  Length 662;
Best Local Similarity 80.0%;  Pred. No. 6.74e-36;
Matches  100;  Conservative  0;  Mismatches 24;  Indels  1;  Gaps  1;

Db   15 CCAGGAAGAATCCAGTTCCACCCCTGCTGTGAACCCAGGGAAGTCACGGGCCG-GATGT 73
         ||||| |||||||| ||||||||||||  |||||||| | |||||||||||||  |||||
Qy   95 CCAGGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGT 154

Db   74 GACGCCCACTGACTTGCCGCGTTGGAGGTCAGGAGAACAGCCAGAATTCTCCGCCCTGAGCAACG 133
         |||||||||| |||| | ||| ||||| ||||| |||||||| ||||||  |||| |||| ||
Qy  155 GACGCCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGCCG 214

Db  134 GCCTG 138
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Qy  215 GCCTG 219

RESULT 8
ID   US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 5, Application US/08238163.
CC   Sequence 5, Application US/08238163
CC   Patent No. 5569830
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CC   GENERAL INFORMATION:
CC     APPLICANT: BENNETT, Alan
CC     APPLICANT: LABAVITCH, John M.
CC     APPLICANT: POWELL, Ann
CC     APPLICANT: STOTZ, Henrik
CC     TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC     TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
CC     DISEASE
CC     NUMBER OF SEQUENCES: 24
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Townsend and Townsend Khourie and Crew
CC       STREET: Steuart Street Tower, One Market Plaza
CC       CITY: San Francisco
CC       STATE: California
CC       COUNTRY: US
CC       ZIP: 94105-1493
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Floppy disk
CC       COMPUTER: IBM PC compatible
CC       OPERATING SYSTEM: PC-DOS/MS-DOS
CC       SOFTWARE: PatentIn Release #1.0, Version #1.25
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/08/238,163
CC       FILING DATE: 03-MAY-1994
CC       CLASSIFICATION: 800
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Bastian, Kevin L,
CC       REGISTRATION NUMBER: 34,774
CC       REFERENCE/DOCKET NUMBER: 2307E-540
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (415) 543-9600
CC       TELEFAX: (415) 543-5043
CC     INFORMATION FOR SEQ ID NO: 5:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH: 215 base pairs
CC         TYPE: nucleic acid
CC         STRANDEDNESS: single
CC         TOPOLOGY: unknown
CC       MOLECULE TYPE: protein
CC       FEATURE:
CC         NAME/KEY: misc_feature
CC         LOCATION: 1..215
CC         OTHER INFORMATION: /standard_name= "Deduced amino acid
CC         OTHER INFORMATION: sequence of PGIP from bean."
SQ   Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;

Query Match       19.6%;  Score 32;  DB 6;  Length 215;
Best Local Similarity 17.6%;  Pred. No. 8.46e-09;
Matches   15;  Conservative 37;  Mismatches 33;  Indels  0;  Gaps  0;

Db   96 DSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDK 155
         :::  :||::   |:|    ||:|    |:|::  :||:|:::  |:!:!:::
Cp  163 AGTGGCGTCACATCTGGGCACCTGGGCTTCCCTGGGTTGAGAGCAGGGGTGGAACCGGAT 104

Db  156 NTKKHAKNSADGKVGSKNNGDRNNR 180
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Cp  103 TCTGCCTGGCTTGGGCTTGGGGGTGA 79

RESULT 9
ID   US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 5, Application US/08238163.
CC   Sequence 5, Application US/08238163
CC   Patent No. 5569830
CC   GENERAL INFORMATION:
CC     APPLICANT: BENNETT, Alan
CC     APPLICANT: LABAVITCH, John M.
CC     APPLICANT: POWELL, Ann
CC     APPLICANT: STOTZ, Henrik
CC     TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC     TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL
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DISEASE
CC   NUMBER OF SEQUENCES: 24
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Townsend and Townsend Khourie and Crew
CC     STREET: Steuart Street Tower, One Market Plaza
CC     CITY: San Francisco
CC     STATE: California
CC     COUNTRY: US
CC     ZIP: 94105-1493
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/238,163
CC     FILING DATE: 03-MAY-1994
CC     CLASSIFICATION: 800
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Bastian, Kevin L.
CC     REGISTRATION NUMBER: 34,774
CC     REFERENCE/DOCKET NUMBER: 2307E-540
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (415) 543-9600
CC     TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 215 base pairs
CC     TYPE: nucleic acid
CC     STRANDEDNESS: single
CC     TOPOLOGY: unknown
CC   MOLECULE TYPE: protein
CC   FEATURE:
CC     NAME/KEY: misc_feature
CC     LOCATION: 1..215
CC     OTHER INFORMATION: /standard_name= "Deduced amino acid
CC     OTHER INFORMATION: sequence of PGIP from bean."
SQ  Sequence 215 BP; 15 A; 8 C; 25 G; 26 T; 141 other;

Query Match     17.2%;  Score 28;  DB 6;  Length 215;
Best Local Similarity  13.7%;  Pred. No. 3.31e-06;
Matches  13;  Conservative  46;  Mismatches  35;  Indels  1;  Gaps  1;

Db    79  HYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGA-DSYGSSKTAMTSRNRTGKTA 137
          :::|: :: |:::. :: ..:: ::: |:. ::::|  ::| :|| : :|  :
Qy   121  CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGGCCACTGACTTGAGCATTAGTGG 180

Db   138  NNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSK 172
          |:::. ::.: ::|:::|: :  :|:::. ::
Qy   181  TTAGAGAAGCCGAGGTTTTCGGTCTCGAGGGGCGG 215

RESULT 10
ID  PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
AC  xxxxxx
DT  01-JAN-1900
DE  Sequence 99, Application PC/TUS9511934.
DE  Sequence 99, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC   APPLICANT: Cytogen Corporation
CC   TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
CC   TITLE OF INVENTION: Peptide Libraries
CC   NUMBER OF SEQUENCES: 103
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Pennie & Edmonds
CC     STREET: 1155 Avenue of the Americas
CC     CITY: New York
CC     STATE: New York
CC     COUNTRY: USA
CC     ZIP: 10036
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: PCT/US95/11934
CC     FILING DATE: 20-SEP-1995
CC     CLASSIFICATION:
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Misrock, S. Leslie
CC     REGISTRATION NUMBER: 18,872
CC     REFERENCE/DOCKET NUMBER: 1101-196-228
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (212) 790-9090
CC     TELEFAX: (212) 869-9741/8864
CC     TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 99:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 75 base pairs
CC     TYPE: nucleic acid
CC     STRANDEDNESS: single
CC     TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
SQ  Sequence 75 BP; 1 A; 1 C; 7 G; 5 T; 61 other;

Query Match     13.5%;  Score 22;  DB 14;  Length 75;
Best Local Similarity  9.1%;  Pred. No. 1.60e-02;
Matches  6;  Conservative  19;  Mismatches  41;  Indels  0;  Gaps  0;

Db    9  BNNBNBNBNBNNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNNBNNBNNBGG 68
         : :.: .:: . :::. :.: . : ::: ::. :: . : :: ::: :|
Cp  148  GGGCACCTGGCGTTCCCTGGGTTGAGAGCAGGGTGGAACCGGATTCTGCCTGGCTTGGG 89

Db   69  TTGTGG 74
         | | ||
Cp   88  CTGGGG 83

RESULT 11
ID  PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
AC  xxxxxx
DT  01-JAN-1900
DE  Sequence 97, Application PC/TUS9511934.
DE  Sequence 97, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC   APPLICANT: Cytogen Corporation
CC   TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
CC   TITLE OF INVENTION: Peptide Libraries
CC   NUMBER OF SEQUENCES: 103
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Pennie & Edmonds
CC     STREET: 1155 Avenue of the Americas
CC     CITY: New York
CC     STATE: New York
CC     COUNTRY: USA
CC     ZIP: 10036
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Floppy disk
CC     COMPUTER: IBM PC compatible
CC     OPERATING SYSTEM: PC-DOS/MS-DOS
CC     SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: PCT/US95/11934
CC     FILING DATE: 20-SEP-1995
CC     CLASSIFICATION:
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Misrock, S. Leslie
CC     REGISTRATION NUMBER: 18,872
CC     REFERENCE/DOCKET NUMBER: 1101-196-228
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (212) 790-9090
CC     TELEFAX: (212) 869-9741/8864
CC     TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 97:
CC   SEQUENCE CHARACTERISTICS:
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CC   LENGTH: 82 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: DNA (genomic)
SQ   Sequence 82 BP; 1 A; 2 C; 10 G; 8 T; 61 other;

Query Match   13.5%;  Score 22; DB 14; Length 82;
Best Local Similarity   9.1%;  Pred. No. 1.60e-02;
Matches   6; Conservative  19; Mismatches 41; Indels  0; Gaps  0;

Db   16 BNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBGG 75

Cp  148 GGGCACCTGGCTTCCCTGGGTGAGAGCAGGCAGGGGTGGAACCGGATTCTGCCTGGCTTGGG 89

Db   76 TTGTGG 81
         | ||
Cp   88 CTGGGG 83

RESULT  12
ID   US-07-865-662F-13 STANDARD; DNA; UNC; 105 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 13, Application US/07865662F.
CC   Sequence 13, Application US/07865662F
CC   Patent No. 5451670
CC   GENERAL INFORMATION:
CC   APPLICANT: Marcia M. Miller
CC   TITLE OF INVENTION: Restriction Fragment Length
CC   TITLE OF INVENTION: Polymorphism Test For Haplotyping Domesticated Fow
CC   NUMBER OF SEQUENCES: 14
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: City of Hope
CC   STREET: 1500 East Duarte Road
CC   CITY: Duarte
CC   STATE: California
CC   COUNTRY: United States of America
CC   ZIP: 91010-0269
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: 3M Double Density 5 1/4" diskette
CC   COMPUTER: Wang PC
CC   OPERATING SYSTEM: MS DOS Version 3.20
CC   SOFTWARE: Microsoft
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/865,662F
CC   FILING DATE: 07 April, 1992
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/688,326
CC   FILING DATE: 22 April 1991
CC   APPLICATION NUMBER: 07/588,922
CC   FILING DATE: 27 September 1990
CC   APPLICATION NUMBER: 07/210,405
CC   FILING DATE: 23 June 1988
CC   APPLICATION NUMBER: US 07/130,529
CC   FILING DATE: 9 December 1987
CC   APPLICATION NUMBER: US 07/068,176
CC   FILING DATE: 30 June 1987
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Irons, Edward S.
CC   REGISTRATION NUMBER: 16,541
CC   REFERENCE/DOCKET NUMBER: No. 5451670e
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (202) 783-6040
CC   TELEFAX: (202) 783-6031
CC   TELEX: NO. 5451670e
CC   INFORMATION FOR SEQ ID NO: 13:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 105
CC   TYPE: Nucleic Acid
CC   STRANDEDNESS: Double
CC   TOPOLOGY: Linear
CC   MOLECULE TYPE: DNA
CC   ORIGINAL SOURCE: Synthetically Prepared
CC   IMMEDIATE SOURCE: Synthetically Prepared
SQ   Sequence 105 BP; 15 A; 0 C; 8 G; 1 T; 81 other;

Query Match   13.5%;  Score 22; DB 5; Length 105;
Best Local Similarity  11.6%;  Pred. No. 1.60e-02;
Matches   8; Conservative  24; Mismatches 37; Indels  0; Gaps  0;

Db   28 KNSGKNKSANAVNNGNNAKNSNNNKSNNMGTRDNKNNRAAKNNNSGVADNKNNASNNYD 87
          :   :    :|    |           |:|::   :| ::      ::|    ::
Cp  127 TTGAGAGCAGGGTGAACCGGATTCTGCCTGGCTTGGGCTGGGGGTGAGCGTGAAGATG 68

Db   88 NGSGVADNK 96
          |:|: |
Cp   67 TTTGGATGG 59

RESULT  13
ID   US-08-702-080-7 STANDARD; DNA; UNC; 448 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 7, Application US/08702080.
CC   Sequence 7, Application US/08702080
CC   Patent No. 5654173
CC   GENERAL INFORMATION:
CC   APPLICANT: Jacobs, Kenneth
CC   APPLICANT: McCoy, John
CC   APPLICANT: LaValie, Edward
CC   APPLICANT: Racie, Lisa
CC   APPLICANT: Merberg, David
CC   APPLICANT: Treacy, Maurice
CC   APPLICANT: Spaulding, Vikki
CC   TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
CC   TITLE OF INVENTION: ENCODING THEM
CC   NUMBER OF SEQUENCES: 11
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Genetics Institute, Inc.
CC   STREET: 87 CambridgePark Drive
CC   CITY: Cambridge
CC   STATE: Massachusetts
CC   COUNTRY: U.S.A.
CC   ZIP: 02140
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.30
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/702,080
CC   FILING DATE:
CC   CLASSIFICATION: 514
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Brown, Scott A.
CC   REGISTRATION NUMBER: 32,724
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (617) 498-8224
CC   TELEFAX: (617) 876-5851
CC   INFORMATION FOR SEQ ID NO: 7:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 448 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: double
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA
SQ   Sequence 448 BP; 121 A; 103 C; 120 G; 78 T; 26 other;

Query Match   13.5%;  Score 22; DB 7; Length 448;
Best Local Similarity  27.8%;  Pred. No. 1.60e-02;
Matches  10; Conservative  19; Mismatches 19; Indels  7; Gaps  0;

Db   76 RGAKYATRRYGYGRKKTYRYYSKGKKWKSMGGSTT 111
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Qy      183 AGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTT 218
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RESULT 14
ID   US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 14, Application US/08232463.
CC   Sequence 14, Application US/08232463
CC   Patent No. 5670367
CC   GENERAL INFORMATION:
CC   APPLICANT: DORNER, F.
CC   APPLICANT: SCHEIFLINGER, F.
CC   APPLICANT: FALKNER, F. G.
CC   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC   NUMBER OF SEQUENCES: 52
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Foley & Lardner
CC   STREET: 1800 Diagonal Road, Suite 500
CC   CITY: Alexandria
CC   STATE: VA
CC   COUNTRY: USA
CC   ZIP: 22313-0299
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/232,463
CC   FILING DATE:
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/935,313
CC   FILING DATE:
CC   APPLICATION NUMBER: EP 91 114 300.6
CC   FILING DATE: 26-AUG-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: BENT, Stephen A.
CC   REGISTRATION NUMBER: 29,768
CC   REFERENCE/DOCKET NUMBER: 30472/114 IMMU
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (703)836-9300
CC   TELEFAX: (703)683-4109
CC   TELEX: 899149
CC   INFORMATION FOR SEQ ID NO: 14:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 7218 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   IMMEDIATE SOURCE:
CC   CLONE: pTZgpt-F1s
SQ   Sequence 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 other;

Query Match   12.9%; Score 21; DB 7; Length 7218;
Best Local Similarity   0.0%; Pred. No. 6.11e-02;
Matches   0; Conservative   47; Mismatches   26; Indels   0; Gaps   0;

```
Db 1067 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1126
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Qy   58 CCCATCCAAACATCTTCACGCTCACCCCCCAGCCCAGCGCCCAAGCCCAGGCGAGAATCCGGTTCCACCC 117

Db 1127 YYYYYYYYYYYYY 1139
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Qy  118 CTGCTCTCAACCC 130
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RESULT 15
ID   US-08-471-052A-142 STANDARD; DNA; UNC; 69 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 142, Application US/08471052A.
CC   Sequence 142, Application US/08471052A
CC   Patent No. 5625033
CC   GENERAL INFORMATION:
CC   APPLICANT: Kay, B. K.
CC   APPLICANT: Fowlkes, D. M.
CC   TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CC   NUMBER OF SEQUENCES: 166
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Pennie & Edmonds
CC   STREET: 1155 Avenue of the Americas
CC   CITY: New York
CC   STATE: New York
CC   COUNTRY: U.S.A.
CC   ZIP: 10036-2711
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Floppy disk
CC   COMPUTER: IBM PC compatible
CC   OPERATING SYSTEM: PC-DOS/MS-DOS
CC   SOFTWARE: PatentIn Release #1.0, Version #1.25
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/471,052A
CC   FILING DATE: 06-JUNE-1995
CC   CLASSIFICATION: 530
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Misrock, S. Leslie
CC   REGISTRATION NUMBER: 18,872
CC   REFERENCE/DOCKET NUMBER: 1101-179
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: 212 790-9090
CC   TELEFAX: 212 869-8864/9741
CC   TELEX: 66141 PENNIE
CC   INFORMATION FOR SEQ ID NO: 142:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 69 bases
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: unknown
CC   MOLECULE TYPE: DNA
SQ   Sequence 69 BP; 2 A; 4 C; 6 G; 2 T; 55 other;

Query Match   12.3%; Score 20; DB 7; Length 69;
Best Local Similarity   10.2%; Pred. No. 2.28e-01;
Matches   6; Conservative   16; Mismatches   37; Indels   0; Gaps   0;

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Db    2 GCTCGAGNNNBNBNBNNBNNBNBNBNNBNNBNBNNBNNBNNBNNBNNBNNBNNBNNB 60
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Cp  172 GCTCAAGTCAGTGGCGTCACATCTGGCGACCTGGGCTTCCCTGGGTTGAGAGCAGCAGGGGT 114
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Search completed: Tue Apr 7 22:01:47 1998
Job time : 18 secs.

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**  ****
* W I S C O N S I N *
**  ****
**********  (TM)
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Release 2.1D John F. Collins, 1995, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 19:19:01 1998; MasPar time 4445.43 Seconds
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Tabular output not generated.

Title: >US-08-190-411A-1
Description: (1-5674) from 5541104.seq
Perfect Score: 5674
N.A. Sequence: 1 CCCGGGGCACCACTGGCATC.........TAATGATCTTGGGTGGATCC 5674
Comp: GGGCCCCGTGGTGACCGTAG.........ATTACTAGAACCCACCTAGG

complete sequence

Scoring table: TABLE default
                Gap 6

Nmatch   STD :
Dbase 0: Query 0

Searched: 354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 08
                 Listing first 45 summaries

Database: embl53
            1:em_in   2:em_or   3:em_om   4:em_ov   5:em_pl   6:em_htg
            7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
            13:em_pat
Database: genbank105
            14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
            20:b_st   21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
            26:gb_htg

Statistics: Mean 12.559; Variance 6.482; scale 1.937

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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### SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 5674 | 100.0 | 5674 | 25 | I24013 | Sequence 1 from patent | 0.00e+00 |
| 2 | 5674 | 100.0 | 5674 | 25 | I36923 | Sequence 8 from patent | 0.00e+00 |
| 3 | 2419 | 42.6 | 2419 | 25 | I36922 | Sequence 7 from patent | 0.00e+00 |
| 4 | 1483 | 26.1 | 4157 | 25 | I36924 | Sequence 9 from patent | 0.00e+00 |
| 5 | 1399 | 24.7 | 2531 | 25 | I36928 | Sequence 13 from paten | 0.00e+00 |
| 6 | 1399 | 24.7 | 2531 | 25 | I36929 | Sequence 14 from paten | 0.00e+00 |
| 7 | 1225 | 21.6 | 2305 | 25 | I36932 | Sequence 17 from paten | 0.00e+00 |
| 8 | 943 | 16.6 | 2226 | 25 | I36931 | Sequence 16 from paten | 0.00e+00 |
| 9 | 811 | 14.3 | 1640 | 25 | I36926 | Sequence 11 from paten | 0.00e+00 |
| 10 | 683 | 12.1 | 1068 | 25 | I36930 | Sequence 15 from paten | 0.00e+00 |
| 11 | 645 | 11.4 | 1412 | 25 | I36936 | Sequence 21 from paten | 0.00e+00 |
| 12 | 611 | 10.8 | 1947 | 25 | I36934 | Sequence 19 from paten | 0.00e+00 |
| 13 | 562 | 9.9 | 1810 | 25 | I36935 | Sequence 20 from paten | 0.00e+00 |
| 14 | 392 | 6.9 | 1107 | 25 | I36938 | Sequence 23 from paten | 2.39e-280 |
| 15 | 350 | 6.2 | 943 | 25 | I36927 | Sequence 12 from paten | 3.71e-246 |
| 16 | 207 | 3.6 | 1866 | 25 | I32295 | Sequence 1 from patent | 3.77e-131 |
| 17 | 199 | 3.5 | 920 | 25 | I36937 | Sequence 22 from paten | 8.12e-125 |
| 18 | 149 | 2.6 | 225 | 25 | I36933 | Sequence 18 from paten | 1.14e-85 |
| 19 | 138 | 2.4 | 1609 | 14 | MMU19033 | Mus musculus Smage-3 p | 3.45e-77 |
| 20 | 136 | 2.4 | 2099 | 25 | I36940 | Sequence 25 from paten | 1.18e-75 |
| 21 | 137 | 2.4 | 2150 | 25 | I36939 | Sequence 24 from paten | 2.02e-76 |
| 22 | 137 | 2.4 | 3809 | 14 | MMU19031 | Mus musculus Smage-1 p | 2.02e-76 |
| 23 | 136 | 2.3 | 7428 | 14 | MMU19032 | Mus musculus Smage-2 p | 1.18e-75 |
| 24 | 130 | 2.3 | 662 | 25 | I36925 | Sequence 10 from paten | 4.64e-71 |
| 25 | 127 | 2.2 | 7218 | 25 | I66494 | Sequence 14 from paten | 9.01e-69 |
| 26 c | 123 | 2.2 | 288886 | 25 | AC002406 | Mus musculus; HTGS pha | 9.94e-66 |
| 27 | 87 | 1.5 | 687 | 25 | I32298 | Sequence 4 from patent | 6.29e-39 |
| 28 c | 78 | 1.4 | 7218 | 25 | I66494 | Sequence 14 from paten | 1.87e-32 |
| 29 | 62 | 1.1 | 461 | 25 | I32296 | Sequence 2 from patent | 2.69e-21 |
| 30 | 59 | 1.0 | 1585 | 14 | MUSNECDIN | M.musculus necdin mRNA | 2.86e-19 |
| 31 | 59 | 1.0 | 3899 | 14 | MUSNCP | Mouse gene for necdin, | 2.86e-19 |
| 32 | 53 | 0.9 | 476 | 25 | I32297 | Sequence 3 from patent | 2.69e-15 |
| 33 | 51 | 0.9 | 174877 | 26 | AC002060 | *** SEQUENCING IN PROG | 5.34e-14 |
| 34 c | 53 | 0.9 | 238000 | 26 | HSAC000134 | Homo sapiens clone 137 | 1.69e-15 |
| 35 | 47 | 0.8 | 215 | 25 | I28278 | Paramecium primaurelia | 1.89e-11 |
| 36 | 43 | 0.8 | 543 | 17 | PPTELO2 | Paramecium primaurelia | 5.69e-09 |
| 37 | 43 | 0.8 | 1475 | 19 | AB001836 | Lactobacillus aviarius | 5.69e-09 |
| 38 c | 44 | 0.8 | 238582 | 26 | AC003059 | *** SEQUENCING IN PROG | 5.69e-09 |
| 39 c | 41 | 0.7 | 215 | 25 | I28278 | Sequence 5 from patent | 9.18e-08 |
| 40 c | 42 | 0.7 | 1577 | 17 | TETMIC4A2D | Tetrahymena thermophil | 2.30e-08 |
| 41 | 41 | 0.7 | 7820 | 21 | XXEVCG | Encephalomyocarditis ( | 3.62e-08 |
| 42 | 40 | 0.7 | 7829 | 21 | EMCDCG | Encephalomyocarditis ( | 3.62e-08 |
| 43 | 41 | 0.7 | 7835 | 21 | EMCPOLYP | Encephalomyocarditis v | 9.18e-08 |
| 44 | 41 | 0.7 | 7861 | 21 | EVCGAA | Encephalomyocarditis v | 9.18e-08 |
| 45 c | 40 | 0.7 | 160000 | 26 | AC004062 | *** SEQUENCING IN PROG | 3.62e-07 |

### ALIGNMENTS

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RESULT  1
LOCUS       I24013          5674 bp    DNA                       PAT    14-AUG-1996
DEFINITION  Sequence 1 from patent US 5541104.
ACCESSION   I24013
NID         g1603883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5674)
  AUTHORS   Chen,Y., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J., van der
            Bruggen,P., Boon-Falleur,T. and Old,L.J.
  TITLE     Monoclonal antibodies which bind to tumor rejection antigen
            precursor mage-1
  JOURNAL   Patent: US 5541104-A 1 30-JUL-1996;
FEATURES             Location/Qualifiers
     source          1..5674
                     /organism="unknown"
BASE COUNT     1276 a   1644 c   1569 g   1185 t
ORIGIN

Query Match             100.0%;  Score 5674;  DB 25;  Length 5674;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches 5674;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        1 CCCGGGGCACCACTGGCATCCTCCCCTACCACCCCCAATCCTCCCTTTACGCCACCC 60

Db       61 ATCCAAACATCTTCACGCTCACCCGTTCCACCCCTG 120
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Qy       61 ATCCAAACATCTTCACGCTCACCCGTTCCACCCCTG 120

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Qy      121 CTCTCAACCCAGGAGAAGCCCAGGTGCCACTGACCGCCAGATTGCACGCGCCACTGAGCATTAGTGG 180

Db      181 TTAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTGAGATCGTGGTGGGAGGAAGCGGG 240
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Qy    181  ||||||||||||||||||||||||||||||||||||||||||||
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Db    181  TTAGAGAAGCGAGGTTTCGGTCGAGATCGGTCGTGAGGAGGCGGG    240

Db    241  CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACCCACTTACCCC   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241  CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACCCACTTACCCC   300

Db    301  AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGACCATCTGGTTGGTGGACTTC   360
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Qy    301  AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGACCATCTGGTTGGTGGACTTC   360

Db    361  TCAGGCTGGGCCACCCCAGCCCTGCTTAAACCACTGGGACTCGAAGTCAGAG   420
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Qy    361  TCAGGCTGGGCCACCCCAGCCCTGCTTAAACCACTGGGACTCGAAGTCAGAG   420

Db    421  CTCCGTGTGATCAGGGAGGGCTGCTTAGGAGAGGCAGCGTCCAGGCTCTGCCCAGACAT   480
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Qy    421  CTCCGTGTGATCAGGGAGGGCTGCTTAGGAGAGGCAGCGTCCAGGCTCTGCCCAGACAT   480

Db    481  CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCACTCCCGTGACCCAAC   540
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Db    541  CCCACTCCAATGCTCACTCCGTGACCCAACCCCTCTTCATTGTCAATTCCACCCCCA   600
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Qy    601  CCCACATCCCCACCCCACCCCATCCTGATGCCATTCGGCCAGCCATTCCACCCT   660

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Qy    661  CACCCCACCCCCACCCCACCCCACGCCCACTCCACCAGGCAGGATCCGGTTCCG   720

Db    721  CCAGGAAACATCCGGTGCCGGATGTGACGCGCCACTGCCATTGTGGGCCAGAGA   780
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Db    781  GAAGCGGAGGTTTCCATTCTGAGGGACGGCGGTAGAGTTCGGCCGAAGGAACCTGACCCAGG   840
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Qy    781  GAAGCGGAGGTTTCCATTCTGAGGGACGGCGGTAGAGTTCGGCCGAAGGAACCTGACCCAGG   840

Db    841  CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACCCGCCACTCCCAAATA   900
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Db    901  GAGAGCCCAAATATTCCAGCCGCCCCTTGCTGCCAGGCCTGGGCGGGGAAGA   960
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Qy    901  GAGAGCCCAAATATTCCAGCCGCCCCTTGCTGCCAGGCCTGGGCGGGGAAGA   960

Db    961  CGTCTCAGGCCTGGGCTGCCCCAGACCCCTTGAGAGAGCCTTCAAAAGCCACCAGGTTC  1020
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Qy    961  CGTCTCAGGCCTGGGCTGCCCCAGACCCCTTGAGAGAGCCTTCAAAAGCCACCAGGTTC  1020

Db   1021  TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACACTGTTAGGAGAGG  1080
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Qy   1021  TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACACTGTTAGGAGAGG  1080

Db   1081  GCAGGGCACAGGCTCTGCTCAAGATCAGCACCCCAAGAGGAGGCTGTGTGGGCCC  1140
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Qy   1081  GCAGGGCACAGGCTCTGCTCAAGATCAGCACCCCAAGAGGAGGCTGTGTGGGCCC  1140

Db   1141  CCAAGACTGCACTCCAATCCCACCCCATTCGCATTCCTGCCACTCCCACCCCAACC  1200
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Qy   1141  CCAAGACTGCACTCCAATCCCACCCCATTCGCATTCCTGCCACTCCCACCCCAACC  1200

Db   1201  CCCATCTCCTCAGTACACCTCCACCTCCTACTCCGTCACCTGACCACC  1260
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Qy   1201  CCCATCTCCTCAGTACACCTCCACCTCCTACTCCGTCACCTGACCACC  1260

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Qy   1261  ACCCTTCCAGCCCCAGCACCAGCCCAACCCTTCTGCCACCTCACCCTGCCCCCAAC  1320


Db   1321  CCCACCCTCATCTCTCTCATGTGCCACTCCCATTCTGGCAGAATCC  1380
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Qy   1321  CCCACCCTCATCTCTCTCATGTGCCACTCCCATTCTGGCAGAATCC  1380

Db   1381  GGTTTGCCCTGCTCTCAACCCAGGAAGCCCTGTAGGCCCGATGTGAAACCACTGACT  1440
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Db   1441  TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGGTTCTGAGGGGCGGCTTGAG  1500
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Qy   1441  TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGGTTCTGAGGGGCGGCTTGAG  1500

Db   1501  ATCCACTCAGAGGGGAGTGGTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG  1560
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Qy   1501  ATCCACTCAGAGGGGAGTGGTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG  1560

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Db   1921  TCAACCCACGGAGGCACGGGAATGGCGGCCAGGCACTCGGACTTGACGTCCCATCCA  1980
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Qy   1921  TCAACCCACGGAGGCACGGGAATGGCGGCCAGGCACTCGGACTTGACGTCCCATCCA  1980

Db   1981  GGGTCTGATGGGAGGGAAGGGCTTGAACAGGGCCTCAGGGAGCAGAGGGAGGGGCCCTAC  2040
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Qy   1981  GGGTCTGATGGGAGGGAAGGGCTTGAACAGGGCCTCAGGGAGCAGAGGGAGGGGCCCTAC  2040

Db   2041  TGGGAGATGAGGAGGACCCCAGAGGCCTCAGAGCACACCGCCACCCCTGTCTGAG  2100
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Qy   2101  ACTGAGGCTGCCACTTCTTGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG  2160

Db   2161  GTGGGACCCCAGGCCTGCAAGGCTTACGCGCAGGGCACACCGAGAAGTGGGGACCTT  2220
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Qy   2281  GCCCATATTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC  2340

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Qy  2581  ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT  2640

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Qy  2881  GACCAGAACACTGAGGGAGGACTGCACAGAAATCAGCCCTGCCCCTGTCACCCCAGAG  2940

Db  2941  AGCATGGCTGGGCCGTCGCTGCCGCCAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941  AGCATGGCTGGGCCGTCGCTGCCGCCAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG  3000

Db  3001  ACGGGGAGGCCTTGGTCTGAGAAGGCTGCCTCAGTCAGTGAGGGAGCGTCCCAGGCC  3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001  ACGGGGAGGCCTTGGTCTGAGAAGGCTGCCTCAGTCAGTGAGGGAGCGTCCCAGGCC  3060

Db  3061  CTGCCAGGAGTCAAGGTGAGGACCAGGCCACGCGGCACCGGCACCCACCCAGGACACATTAATTCCAAT  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061  CTGCCAGGAGTCAAGGTGAGGACCAGGCCACGCGGCACCGGCACCCACCCAGGACACATTAATTCCAAT  3120

Db  3121  GAATTTGATATCTCTTGCCTCCATTCCTTATCATGGATGTGAACTCTGATTGGATTTCTCAG  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121  GAATTTGATATCTCTTGCCTCCATTCCTTATCATGGATGTGAACTCTGATTGGATTTCTCAG  3180

Db  3181  GTCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACTCTGATTGGATTTCTCAG  3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181  GTCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACTCTGATTGGATTTCTCAG  3240

Db  3241  ACCAGCAAAAGGGCCAGGAGCCAGGATCCCAGGCCCTGCCAGGAAAAATATAAGGGCACGTGTGCCGTGAGAA  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241  ACCAGCAAAAGGGCCAGGAGCCAGGATCCCAGGCCCTGCCAGGAAAAATATAAGGGCACGTGTGCCGTGAGAA  3300

Db  3301  CAGAGGGGGTCATCCACTGCATGAGAGTGGGATGTCACAGAGTCCAGCTCCACCCTG  3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301  CAGAGGGGGTCATCCACTGCATGAGAGTGGGATGTCACAGAGTCCAGCTCCACCCTG  3360

Db  3361  GTAGCACTGAGAAGCCAGGCCGTGTTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361  GTAGCACTGAGAAGCCAGGCCGTGTTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT  3420

Db  3421  CTTCCTGAGGCTCCAGGAACCAGGCAGCAGTGAGCCCTTGGTCTGAGACAGTATCCTCAGGTC  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421  CTTCCTGAGGCTCCAGGAACCAGGCAGCAGTGAGCCCTTGGTCTGAGACAGTATCCTCAGGTC  3480
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Db  3481  ACAGAGCAGAGGATGCACAGGGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA  3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481  ACAGAGCAGAGGATGCACAGGGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA  3540

Db  3541  GGGCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG  3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541  GGGCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG  3600

Db  3601  TCAGTCCTGTAGAATCGACCTGCTGCTGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601  TCAGTCCTGTAGAATCGACCTGCTGCTGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT  3660

Db  3661  CCTTCAGGTTTCAGGGGACAGGCAACCCAGAGGACAGGATTCCTGGGGCCACAGAG  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661  CCTTCAGGTTTCAGGGGACAGGCAACCCAGAGGACAGGATTCCTGGGGCCACAGAG  3720

Db  3721  GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTGAGTCTCCAAGGTTCAGTTCTC  3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3721  GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTGAGTCTCCAAGGTTCAGTTCTC  3780

Db  3781  AGCTGAGGCCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT  3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781  AGCTGAGGCCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT  3840

Db  3841  CCTGCCCACACTCCTGCTCGCCCTGCCCTGACGAGTCATCATGTCTCTTGAGCAGAGGAG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3841  CCTGCCCACACTCCTGCTCGCCCTGCCCTGACGAGTCATCATGTCTCTTGAGCAGAGGAG  3900

Db  3901  TCTGCACTGCAAGCCTGAGGAGCCCAACCCAGTGAGGGCCCAACAAGAGGCCCTGGTGTG  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3901  TCTGCACTGCAAGCCTGAGGAGCCCAACCCAGTGAGGGCCCAACAAGAGGCCCTGGTGTG  3960

Db  3961  TGTGCAGGCTGCCACCTCCTCCTCGTCCTCGGCAGCGCCTTCCGCCCTTCCCACTAC  4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3961  TGTGCAGGCTGCCACCTCCTCCTCGTCCTCGGCAGCGCCTTCCGCCCTTCCCACTAC  4020

Db  4021  CACTGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGACAGTCATTACTAAGAAGGTGGC  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4021  CACTGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGACAGTCATTACTAAGAAGGTGGC  4080

Db  4081  CATCAACTTCACTCGACGACAGAGGCAACCCAGTGAGGGTTCCAGCACTGTTTCTGAGATCTTCGGCAAAGC  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4081  CATCAACTTCACTCGACGACAGAGGCAACCCAGTGAGGGTTCCAGCACTGTTTCTGAGATCTTCGGCAAAGC  4140

Db  4141  GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGACCAGTAATCACTAAGAAGGTGGC  4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4141  GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGACCAGTAATCACTAAGAAGGTGGC  4200

Db  4201  TGATTTGGTTTCGTCTCCTCAAATATCGAGCCCAGGAGGCCAGTCACAAAGGCAGA  4260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4201  TGATTTGGTTTCGTCTCCTCAAATATCGAGCCCAGGAGGCCAGTCACAAAGGCAGA  4260

Db  4261  AATGCTGGAGAGTGTCATCAAGAACACTGTTTCCTGAGATCTTCGGGTCATGAGGAGGCGG  4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4261  AATGCTGGAGAGTGTCATCAAGAACACTGTTTCCTGAGATCTTCGGGTCATGAGGAGGCGG  4320

Db  4321  CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCA  4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4321  CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCA  4380

Db  4381  CTCCTATGTCCTTGTCACCTGGTCTCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA  4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4381  CTCCTATGTCCTTGTCACCTGGTCTCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA  4440

Db  4441  GATCATGCCAAGACAGGCTTCCTCGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG  4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4441  GATCATGCCAAGACAGGCTTCCTCGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG  4500

Db  4501  CCATGCTCCTGAGGAGGAAATCTGGGAGAGCTGAGTGTGATGGGAG  4560
          ||||||||||||||||||||||||||||||||||||||||||||||
Qy  4501  CCATGCTCCTGAGGAGGAAATCTGGGAGAGCTGAGTGTGATGGGAG  4560

Db  4561  GGAGCACAGTGCCTATGGGGAGCCCAGGAGAGCTGCTCACCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA  4620
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Qy   5641  GGGGGAGCTGATTGTAATGATCTTCGGTGGATCC  5674


RESULT     2
LOCUS      I36923      5674 bp   DNA                PAT    21-APR-1997
DEFINITION Sequence 8 from patent US 5612201.
ACCESSION  I36923
NID        g2084883
KEYWORDS
SOURCE     Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 5674)
  AUTHORS  De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
           Chomez,P.
  TITLE    Isolated nucleic acid molecules useful in determining expression of
           a tumor rejection antigen precursor
  JOURNAL  Patent: US 5612201-A 8 18-MAR-1997;
FEATURES            Location/Qualifiers
     source         1..5674
                    /organism="unknown"
BASE COUNT     1276 a   1644 c   1569 g   1185 t
ORIGIN

Query Match       100.0%;   Score 5674;   DB 25;   Length 5674;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 5674;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db     1  CCCGGGCACCACTGCATCCCTCCCCTACCACCCCAATCCTCCCTTTACGCCACCCC   60
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Qy     1  CCCGGGCACCACTGCATCCCTCCCCTACCACCCCAATCCTCCCTTTACGCCACCCC   60

Db    61  ATCCAAACATCTTCACGCTGCCCAGCTGCCCAGCCAGGCAGGAATCCGGTTCCACCCCTG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61  ATCCAAACATCTTCACGCTGCCCAGCTGCCCAGCCAGGCAGGAATCCGGTTCCACCCCTG  120

Db   121  CTCTCAACCCAGGGAAGCCCAGTGCCCAGATGTGACGCCCACTGAGTGAGCATTAGTGG  180
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Qy   121  CTCTCAACCCAGGGAAGCCCAGTGCCCAGATGTGACGCCCACTGAGTGAGCATTAGTGG  180

Db   181  TTAGAGAAGCGAGGTTTCGGTCGAAGGTGACATGCGAGGGAGGACTGAGGAGGAAGCGGGG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181  TTAGAGAAGCGAGGTTTCGGTCGAAGGTGACATGCGAGGGAGGACTGAGGAGGAAGCGGGG  240

Db   241  CCCAGCTCTGTAAGGAGGCAAGTGACATGCTGGAGGAGGTGCGTCGCTCTGCCAGACAT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241  CCCAGCTCTGTAAGGAGGCAAGTGACATGCTGGAGGAGGTGCGTCGCTCTGCCAGACAT  300

Db   301  AGATAGAGGACCCCAAATAATCCCTTCATGCGAGTCTCGGACATCTGGTGTGGGACTTC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301  AGATAGAGGACCCCAAATAATCCCTTCATGCGAGTCTCGGACATCTGGTGTGGGACTTC  360

Db   361  TCAGGCTGGGCACCCCAGCCCTTGCTGCTTAAACCACTGGGACTCGAAGTCAGAG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361  TCAGGCTGGGCACCCCAGCCCTTGCTGCTTAAACCACTGGGACTCGAAGTCAGAG  420

Db   421  CTCCGTGTGATCAGGAGTCAGGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCGTC  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421  CTCCGTGTGATCAGGAGTCAGGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCGTC  480

Db   481  CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCGTGAGACCCCAC  540
          |||||||||||||||||||||||||||||||||||||||||||||||
Qy   481  CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCGTGAGACCCCAC  540

Db   541  CCCACTCCCAAATGCTCACTCCCGTGACCCAACCCTCTTCATTGTCATTCCAACCCCCA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541  CCCACTCCCAAATGCTCACTCCCGTGACCCAACCCTCTTCATTGTCATTCCAACCCCCA  600

Db   601  CCCACATCCCCACCCCATCCTCAACCCTGATGCCCATCCTGAAGCCATTCCACCCT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601  CCCACATCCCCACCCCATCCTCAACCCTGATGCCCATCCTGAAGCCATTCCACCCT  660

Db   661  CACCCCCACCCCCACGCCCACCACCCCCAGGCAGGATCCGGTTCCCG  720
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Qy   4561  |||||||||||||||||||||||||||||||||||  4620
           GGAGCACAGTGCCTATGGGAGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGT

Db   4621  GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGT  4680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4621  GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGT  4680

Db   4681  CCAAGGGCCCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT  4740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4681  CCAAGGGCCCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT  4740

Db   4741  GCAAGAGTTCGCTTTTTCTTCCCATCCTGCGTGAAGCAGCTTTGAGAGGAGGAAGAG  4800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4741  GCAAGAGTTCGCTTTTTCTTCCCATCCTGCGTGAAGCAGCTTTGAGAGGAGGAAGAG  4800

Db   4801  GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGCCAGTGCACCTT  4860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4801  GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGCCAGTGCACCTT  4860

Db   4861  CCAGGGCCGGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT  4920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4861  CCAGGGCCGGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT  4920

Db   4921  GAAGAGGAGGCAGTGCAGTGTTCCAGTAGTAGTTTCGTTCATTGGGTGACTTGGAGATT  4980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4921  GAAGAGGAGGCAGTGCAGTGTTCCAGTAGTAGTTTCGTTCATTGGGTGACTTGGAGATT  4980

Db   4981  TATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGATGGTTGAATGAAC  5040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4981  TATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGATGGTTGAATGAAC  5040

Db   5041  TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG  5100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5041  TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG  5100

Db   5101  TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT  5160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5101  TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT  5160

Db   5161  AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAATGAGCAGTAAAATAGATGAGATAA  5220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5161  AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAATGAGCAGTAAAATAGATGAGATAA  5220

Db   5221  AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA  5280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5221  AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA  5280

Db   5281  ATTTTAAAGATATATGCATAATCCTGATTCCTTGGCCTTCTTGAGAATGTTAAGAGAAAT  5340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5281  ATTTTAAAGATATATGCATAATCCTGATTCCTTGGCCTTCTTGAGAATGTTAAGAGAAAT  5340

Db   5341  TAAATCTGAATAAAGAATTCTTCCCTGTTCACTGGCCTCTTTTCTCTCCATGCACTGAGCA  5400
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Qy   5341  TAAATCTGAATAAAGAATTCTTCCCTGTTCACTGGCCTCTTTTCTCTCCATGCACTGAGCA  5400

Db   5401  TCTGCCTTTTTGGAAGGCCCTGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC  5460
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Qy   5401  TCTGCCTTTTTGGAAGGCCCTGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC  5460

Db   5461  CCACCCATAGGGTCGTAGAGCTCGAGTCACGTAGAGCTCGCATTTGGGCCTTGGCAAGATGTC  5520
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Qy   5461  CCACCCATAGGGTCGTAGAGCTCGAGTCACGTAGAGCTCGCATTTGGGCCTTGGCAAGATGTC  5520

Db   5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGTGAGGGTGTGGGGTCCGGGTGAGAGTG  5580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGTGAGGGTGTGGGGTCCGGGTGAGAGTG  5580

Db   5581  GTGGAGTGTCAATGCCCTGAGCTGGGCATTTGGGCTTTGGGCATTTGGGAAACTGCAGTTCCTTCT  5640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5581  GTGGAGTGTCAATGCCCTGAGCTGGGCATTTGGGCTTTGGGCATTTGGGAAACTGCAGTTCCTTCT  5640

Db   5641  GGGGGAGCTGATTGTAATGATCTTCGGTGGATCC  5674
           ||||||||||||||||||||||||||||||||||
Qy   5641  GGGGGAGCTGATTGTAATGATCTTCGGTGGATCC  5674
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Thu Apr 9 08:15:24 1998   US-08-190-411A-1.rge

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Qy    661  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CACCCCCACCCCCCACGCCCACTCCCACCCCAGGCAGGCATCCGGTTCCCG  720

Qy    721  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CCAGGAAACATCCGGGTGCCGGATGCGGCCACTGACTTGCGCATTGTGGGGCAGAGA  780

Qy    781  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GAAGCGGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAGGAACCTGACCCAGG  840

Qy    841  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGAGGACTGAGGACCCGCCACTCCCAAATA  900

Qy    901  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  GAGAGCCCCAAATATTCCAGCCCCTGCTGCCAGCCCTGGCCCACCCGCCGGGAAGA  960

Qy    961  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAGCCTTGAGAGACACCAGGTTC  1020

Qy   1021  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGTGACCAGGCAGGACTGGTTAGGAGAGG  1080

Qy   1081  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGACACCCAAGAGGAGGGCTGTGTGGCCC  1140

Qy   1141  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  CCAAGACTGCACTCCAATCCCACTCCCACCCCATTCCCATTCCCCACCCCAACC  1200

Qy   1201  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CCCATCCTCCAGCTACACCTCCACCCCCATCCCCATCCCTACTCCGTCACCTGACCACC  1260

Qy   1261  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ACCCTCCAGCCCCAGACCCCCAACCCTTCTGCCACCTCACCCTTCTGCCCCCAAC  1320

Qy   1321  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCCACCCTCCATCTCTCATGTGCCCCACTCGCCTCCCCCATTCTGGCCAGAATCC  1380

Qy   1381  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  GGTTTGGCCCCTGCTGTCTCAACCCAGGGAAGCCCAGGGGACCCTGGTAGCCCGATGTGTTC  1440

Qy   1441  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGTTCTGAGGCGGCCTTGAG  1500

Qy   1501  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG  1560

Qy   1561  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  ACTGAGGAGGCACACACCCCCTGACCACCCGCCGCCCAAAATGATCCAGTCAGTACCACCCCGCTG  1620

Qy   1621  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CCAGCCCTGGACCACCCGCCAGACACCCGCCCAGGACCACCCGTCCGTCC  1680

Qy   1681  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CACTGCCACTTAACCCAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGT  1740

Qy   1741  ||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GGTCAGGAGAGCAGGGCCCAGGCATCCGCCCGGCATTAGGGTCAGG  1800
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Qy   1741  GGTCAGGAGAGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG  1800
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Db   1801  ACCCTGGAGGGAACTGAGGGTTCCCACCACCTGCTCCTCCATCTCCACCGCCACC  1860
Qy   1801  ACCCTGGAGGGAACTGAGGGTTCCCACCACCTGCTCCTCCATCTCCACCGCCACC  1860

Db   1861  CCACTCACATTCCATACTACCCCCTACCCCCAACCTTGTCAGAATCCTGCTG  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1861  CCACTCACATTCCATACTACCCCCTACCCCCAACCTTGTCAGAATCCTGCTG  1920

Db   1921  TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCATCCA  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1921  TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCATCCA  1980

Db   1981  GGGTCTGATGGAGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGAGGGGCCCTAC  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1981  GGGTCTGATGGAGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGAGGGGCCCTAC  2040

Db   2041  TGCGAGATGAGGGAGGAGGCCTCAGAGGACCCTAGGAACGACACCGCACCCTGTCTGAG  2100
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Qy   2041  TGCGAGATGAGGGAGGAGGCCTCAGAGGACCCTAGGAACGACACCGCACCCTGTCTGAG  2100

Db   2101  ACTGAGGCTGCCACTTCTTGGCTCTCAAGAATCAGGATGGGGACTCAGATTGCATGGGG  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2101  ACTGAGGCTGCCACTTCTTGGCTCTCAAGAATCAGGATGGGGACTCAGATTGCATGGGG  2160

Db   2161  GTGGGACCCCAGGCCTGCAAGGCTTACGGCGGAGAAGGAGGAGGAGGACTCAGGGGACCTT  2220
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Qy   2161  GTGGGACCCCAGGCCTGCAAGGCTTACGGCGGAGAAGGAGGAGGAGGACTCAGGGGACCTT  2220

Db   2221  GGAATCCAGATCAGTGTGGACCCTCGGCCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG  2280
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Qy   2221  GGAATCCAGATCAGTGTGGACCCTCGGCCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG  2280

Db   2281  GCCCATATTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGGGAAGTGGGGCC  2340
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Qy   2281  GCCCATATTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGTCTGAGAAGTGGGGCC  2340

Db   2341  TCAGGTCAACAGAGGAGGAGTTCCAGGATCCATATGGCCCAAGAGTGTGCCCCCTTCATG  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2341  TCAGGTCAACAGAGGAGGAGTTCCAGGATCCATATGGCCCAAGAGTGTGCCCCCTTCATG  2400

Db   2401  AGGACTGGGGATATCCCCGGCTCAGAAAGAAAGGGACTCCACACAGTCTGCTGTCCCCTT  2460
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Qy   2401  AGGACTGGGGATATCCCCGGCTCAGAAAGAAAGGGACTCCACACAGTCTGCTGTCCCCTT  2460

Db   2461  TTAGTAGCTCTAGGGGGACCCAGATCAGGGGATGGCGGTATGTTCCATTCTCACTCTGTACCA  2520
           |||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||||
Qy   2461  TTAGTAGCTCTAGGGGGACCCAGATCAGGGGATGTGGGGTATGTTCCATTCCACTGTGTACCA  2520

Db   2521  CAGGCAGGAAGTTGGGGTGAGGGGCCCTCAGGGAGGTGAGGAAGCGCTGCAGGCGGATGTCT  2580
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Qy   2521  CAGGCAGGAAGTTGGGGTGAGGGGCCCTCAGGGAGGTGAGGAAGCGCTGCAGGCGGATGTCT  2580

Db   2581  ACTCATGTCAGGGAATTGGGGGTTGAGGAGGCAAGGTGAGATGCTGAGGGAGGAATAAAGATGAGT  2640
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Qy   2581  ACTCATGTCAGGGAATTGGGGGTTGAGGAGGCAAGGTGAGATGCTGAGGGAGGAATAAAGATGAGT  2640

Db   2641  GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTTGGACACC  2700
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Qy   2641  GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTTGGACACC  2700

Db   2701  TCACCCAGGATGGTGGCTTCTTTTCACTCGTTTCACTCGTGTTTCCAGATCTGGGGCAGGTGAGGACCT  2760
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Qy   2701  TCACCCAGGATGGTGGCTTCTTTTCACTCGTTTCACTCGTGTTTCCAGATCTGGGGCAGGTGAGGACCT  2760

Db   2761  CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCGTGTCTAAAGACAGAGCG  2820
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Qy   2761  CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCGTGTCTAAAGACAGAGCG  2820

Db   2821  GTCCCAGGATCTGCCATGCGTTCGGTGCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG  2880
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Qy   2821  GTCCCAGGATCTGCCATGCGTTCGGTGCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG  2880
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Db    61 ACTGCATGAGAGTGGGATGTCACAGAGTCCAGCCCACCCTCGGTAGCACTCAGAGAGC 120
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Qy  3316 ACTGCATGAGAGTGGGATGTCACAGAGTCCAGCCCACCCTCGGTAGCACTCAGAGAGC 3375

Db   121 CAGGGCTGTGCTTGCGTCTGCACCCTGAGGGCCGTTGGATTCCTCTTCCTGGAGCTCCA 180
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Qy  3376 CAGGGCTGTGCTTGCGTCTGCACCCTGAGGGCCGTTGGATTCCTCTTCCTGGAGCTCCA 3435

Db   181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGTGCACAGAGCAGGAGGATG 240
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Qy  3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGTGCACAGAGCAGGAGGATG 3495

Db   241 CACAGGGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCACCTGCCA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3496 CACAGGGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCACCTGCCA 3555

Db   301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTCACTTCCTCCTGTCAGTCCTGTAGAAT 360
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Qy  3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTCACTTCCTCCTGTCAGTCCTGTAGAAT 3615

Db   361 CGACCTGCTGGCCGGCTGTACCCTGAGACTACCCTCCTCACTTCCTCCTTCAGGTTTTCAG 420
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Qy  3616 CGACCTGCTGGCCGGCTGTACCCTGAGACTACCCTCCTCACTTCCTCCTTCAGGTTTTCAG 3675

Db   421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGCACCAAGGAGAGA 480
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Qy  3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGCACCAAGGAGAGA 3735

Db   481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTCAGTTCTCAGTCGTCA 540
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Qy  3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTCAGTTCTCAGTCGTC 3795

Db   541 CACACTCCCTCCTGTGGTCTTCATTGCCCAGCTCCTGCCCAGCTCCTGCCACACTCCT 600
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Qy  3796 CACACTCCCTCCTGTGGTCTTCATTGCCCAGCTCCTGCCCAGCTCCTGCCACACTCCT 3855

Db   601 GCCTGCTGCCCTGACGAGTCATCATGTCTCTTGAGCAGGAGTCTGCACTGCAAGCC 660
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Qy  3856 GCCTGCTGCCCTGACGAGTCATCATGTCTCTTGAGCAGGAGTCTGCACTGCAAGCC 3915

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Db   721 CTCCTCCTCCTCCTCCTCCTGGTCCTGGCCACCCTGGGCACACCCTGGGCTGCCCACTGCTCGGTCAAC 780
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Qy  4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCAGTAATCACTAAGAAGTGGCTGGATTTGGTGGTTT 4155

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Qy  4156 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGTGGCTGGATTCTTCGGCAAGCCTTGAGTCCTTGCA 4215

Db   961 TCTGCTCCTCAAATATCGAGCCAGGAGGTTCACAAAGGCCAGAAATGCTGGAGAGTGT 1020
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Qy  4216 TCTGCTCCTCAAATATCGAGCCAGGAGGTTCACAAAGGCCAGAAATGCTGGAGAGTGT 4275

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Qy  4276 CATCAAAAATTACAAGCACTGTTTCTGGAGATCTTCGGCAAAGCCTTCGAGTCCTTGCA 4335

Db  1081 GCTGGTCTTTGCATTGACGTGAAGGAAGCAGAGAACAGAGGGGGTCATCC 1140
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Qy  4336 GCTGGTCTTTGCATTGACGTGAAGGAAGCAGAGAACAGAGGGGGTCATCC 4395

Db  1141 CACCTGCCTAGGTCTCCTCCTATGATGGCCCGTGGTGGTGATAATCAGATCATGCCCAAGAC 1200
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Qy  3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGACCCCTGCGAGAACAGAGGGGGTCATCC 3315
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Qy  5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100
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Db  5101 TAAGAGTTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
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Qy  5101 TAAGAGTTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Db  5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATA 5220
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Qy  5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATA 5220

Db  5221 AGAACTAAAGAAATTAAGAGAGATAGTCAATTCTGCCTATACCTCAGTCTATTCTGTAA 5280
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Qy  5221 AGAACTAAAGAAATTAAGAGAGATAGTCAATTCTTGCCTATACCTCAGTCTATTCTGTAA 5280

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Qy  5281 ATTTTAAAGATATATGCATACCTGGATTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

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Qy  5341 TAAATCTGAATAAAAGAATTCTTCCTGTCACTGGCTGCTCTTTTCTTCTCCTCATGCACTGAGCA 5400

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Qy  5401 TCTGCTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAAGACTCATAC 5460

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Qy  5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGAGAGTCACGTCAGTCGCAGTGGCAAGATGTC 5520

Db  5521 CTCTAAAGATGTGAGGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
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Qy  5581 GTGGAGTGTCAATGCCCTGAGCTCAGGAGTCTAGGAGCTGAGACTCACGTAGCCATTTGGGCTTTGGGGAAACTGCAGTTCCTTCT 5640

Db  5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Qy  5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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Qy  5476  TAGAGTCTTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCAAAGATGTAGG  5535
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Db  2281  GAAAAGTGAGAGAGGGTGAGGGTGTGGGCTCCGGGTGAGAGTGTGGAGTGTGCAATGC  2340
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Qy  5536  GAAAAGTGAGAGAGGGTGAGGGTGTGGGCTCCGGGTGAGAGTGTGGAGTGTGCAATGC  5595

Db  2341  CCTGAGCTGGGGCATTTTGGGCTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT  2400
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Qy  5596  CCTGAGCTGGGGCATTTTGGGCTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT  5655

Db  2401  AATGATCTTGGGTGGATCC  2419
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Qy  5656  AATGATCTTGGGTGGATCC  5674


RESULT  4

LOCUS           I36924                 4157 bp    DNA                  PAT       21-APR-1997
DEFINITION      Sequence 9 from patent US 5612201.
ACCESSION       I36924
NID             g2084884
KEYWORDS        .
SOURCE          Unknown.
  ORGANISM      Unknown.
                Unclassified.
REFERENCE       1  (bases 1 to 4157)
  AUTHORS       De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
                Chomez,P.
  TITLE         Isolated nucleic acid molecules useful in determining expression of
                a tumor rejection antigen precursor
  JOURNAL       Patent: US 5612201-A 9 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1..4157
                     /organism="unknown"
BASE COUNT      953 a     1134 c     1185 g     885 t
ORIGIN

Query Match             26.1%;  Score 1483;  DB 25;  Length 4157;
Best Local Similarity   78.7%;  Pred. No. 0.00e+00;
Matches 2615;  Conservative    0;  Mismatches 622;  Indels 85;  Gaps 51;

Db   858  CAGGGGGTTGGGGCCCAGCCTGCGAGAGTCAAGGGAGGAAGAAGAGGGAGGGAGGACTGAGG  917
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Qy  2154  CATGGGGGTGGGACCCAGCCCTGCGCAAGGCTTACCGGAGGAAGGGAGGGAGGGACTCAGG  2213

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Qy  2214  GGACCTTGGAATCCAGATCAGTGTGGACCCTCGCGCCCTCGAGAGGTGCACGGTGGCC  2273

Db   977  GAATGTGCCCGTGCTCATTGCACCTTCAGGGTGACAGAGAGTGAGGGCTGTGTCTGA  1036
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Qy  2274  ACATATGCCCATATTTCCTGCATCTTTGAGGTGACAG-GACA-GAG--CTGTGTCTGA  2329

Db  1037  GGGCTGGGACTTCAGGTCAGCAGAGGGAGGAATCCCAGGATCTGCCGACCCAAGGTGTG  1096
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Qy  2330  GAGTGGGGCCCTCAGGTCAACAGAGGAGGAGTTCCAGGATCCCATATGGCCCAAGAGTGTG  2389

Db  1097  CCCCCTTCATGAGGACTCCCCATACCCCGGTCGGGGACTTGGGACTCCGATGATGCCACAGTCTG  1156
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Qy  2390  CCCCCTTCATGAGGACTCCCAGGTCAACAGGGGAGATCCCCGGTCAGAGAAGAAGGGACTCCACAGTCTG  2449

Db  1157  GAAGTAAATTGTTCTTAGCTCTGGGGAGAACCTGATCAGGGATGGCCCTAAGTGACAATCT  1216
               || | | | |||||||||  ||||| || | |||| |||| |  ||||||| | ||||
Qy  2450  GCTGTCCCCTTTTAGTAGCTCTAGGGGGACCTAGGGGATGGGACCCAGATCAGGGTATGTTCCATTCT  2509

Db  1217  CATTTGTACCACAGGCAGGAGGTTGGGAACCTCAGGGAGATAAGGTGTTGGTGTAAAG  1276
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Qy  2510  CACTTGTACCAGGCAGGAAGTTGGGGGCGTTGGGGGCTGTGGGTAAAG  2569

Db  1277  AGGAGCTGTCGCTCATTGAGGTGGGGTTCCGGGGGTTCAGGGAAAGGGCAGTCCCTGGCAGGAG  1336
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Qy  2570  GGGGATGGTCTACTCACTGGGGAATTGGGGTTCAGGGAATTGGGGTTGAGGAAGCACAGCCGCTGGCAGGAA  2629

Db  1337  TAAAGATGAGTAACCCACAGGAGGCCATCATAACGTTCACCCTAGAACCAAAGGGGTCAG  1396
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Left column:

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Qy  4396  CACCTGCCTAGGTCTCTCCTATGATGGGCCTGCTCGGTGATAATCAGATCATGCCCAAGAC  4455
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Db  1201  AGGCTTCCTGATAATTGTCCTGGTCATGATTGAAGCGGCCATGCTCCTGAGGA  1260
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Qy  4456  AGGCTTCCTGATAATTGTCCTGGTCATGATTGAAGCGGCCATGCTCCTGAGGA  4515

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Qy  4516  GGAAATCTGGAGGAGCTGTAGTGTGATGAGGTGTATGATTGGGAGGGAGCCACAGTGCCTA  4575

Db  1321  TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTAGTCGGAGTACGG  1380
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Qy  4576  TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTAGTCGGAGTACGG  4635

Db  1381  CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCT  1440
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Qy  4636  CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCT  4695

Db  1441  GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT  1500
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Qy  4696  GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT  4755

Db  1501  TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAGGGAGTCTGAGCATGA  1560
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Qy  4756  TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAGGGAGTCTGAGCATGA  4815

Db  1561  GTTGCAGCCAAGGCCAGTGGAGGGGGACTGGCCCAGTGCACCTTCCAGGCCGCGGTCCA  1620
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Qy  4816  GTTGCAGCCAAGGCCAGTGGGGGGGACTGGGCCCAGTGCACCTTCCAGGCCGCGGTCCA  4875

Db  1621  GCAGCTTCCCCTGCGTGTGCACATGAGGCCCATTCTTCACTCTGAAGAGAGGGGTCAG  1680
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Qy  4876  GCAGCTTCCCCTGCGTGTGCACATGAGGCCCATTCTTCACTCTGAAGAGAGGGGTCAG  4935

Db  1681  TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTCTATTGGGTGACTTGGAGATTTATCTTGTGTTCTCTT  1740
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Qy  4936  TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTGTGTTCTCTT  4995

Db  1741  TTGGAATTGTTCAAATGTTTTTTTTTTTTTTTAAGGATGTTGAATGAACTTCAGCATCCAAGTT  1800
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Qy  4996  TTGGAATTGTTCAAATGTTTTTTTTTTTTTTTTTAAGGATGTTGAATGAACTTCAGCATCCAAGTT  5055

Db  1801  TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGTGAAGTCTTGTGTT  1860
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Qy  5056  TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGTGAAGTCTTGTGTT  5115

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Qy  5116  TTATTCAGATTGGGAAATCCATTCTATTTGTGATAATAACAGCAGTGGAATA  5175

Db  1921  AGTACTTAGAAATGAAAAATGAGCAGTAAAATAGATAGAGATAAAGAACTAAAGAAATT  1980
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Qy  5176  AGTACTTAGAAATGAAAAATGAGCAGTAAAATAGATAGAGATAAAGAACTAAAGAAATT  5235

Db  1981  AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA  2040
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Qy  5236  AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTTAAAGATATA  5295

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Qy  5296  TGCATAACCTGGATTTCCTTGGCTTCTTTCTTCTCCATGGAATGTAAGAGAAATCTGAATAAAG  5355

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Qy  5356  AATTCTTCCTGTTCACTGGCTCTTTCTTCCTCATGCACTGACCATCTGCTTTTTTGGAAG  5415

Db  2161  GCCCTGGGTTAGTAGTGGGAGATGCTAAGTAAGCCAGACTCATACCCACCCATAGGGTCG  2220
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5416  GCCCTGGGTTAGTAGTGGGAGATGCGTAAGTAAGCCAGACTCATACCCACCCATAGGGTCG  5475

Db  2221  TAGAGTCTTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCAAAGATGTAGG  2280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3689  CCAGAGGACAGGATTCCCTGGAGGCACCAGAGGAGCACCAAGGAGAGATCTGTAAGTAG  3748
          ||||||||||||||| || ||||||||||||||| | |||  ||||||||||||||||
Db  2468  TCAGAGGCTCCAAGTTCA--GTTCAGTTCTCACCTAAGGCCTCACACGCTCCTCTC      2525

Qy  3749  GCCTTTGTTAGAGTCTCCAAGTTCAGTTCTCAGCTCCTGCCGGCCTTCCACCACTCCCTCTC  3808
          ||||| |||||||||||||  |||||  |  |||||||||||||||||| ||||||||||||
Db  2526  CCTGGACCACCTCCACCCAGGACGATGT----CTTTTTCACTCCTGTTTCCCAGATC      2585

Qy  3809  TCCCCAGGCCTGTGGGTCTTCATTGCCCAGTTCCTGCCGGCCTGCCGCCACTCCTGCTGCCCTG  3868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2586  TCAGGGAGTTGATGACCTTGTTTCAGAAGGTGACTCAG-TCAACACAGGGGCCCC--TC     2645

Qy  3869  ACGAGAGTCATCATGTCTCTTGAGCAGAGGCTGCACTGCGCAAGCCTGAGGAGCCCTT  3928
          || | |||||||||||||||||||||||||||||| | |||
Db  2646  TGGTCGACAGATGCAGTTGTCTCTAGGACATCCCAAGCATCCAGGTGCAGAGAGCTGAGGTA  2705

Qy  3929  ACGAGAGTCATCATGTCTCTTGAGCAGAGGCTGCACTGCGCAAGCCTGAGGAGCCAG  3978
          |||||||||||||||||  ||| |||||||||||||||  || ||||
Db  2706  TGGTCTAAAGACAGAGAGCGGTCCGCCATGCCGTTCGGGTGAGGAACATGAGGGA    2765

...

Qy  4747  GTTCGGTTTTCTTCCGTCGGTGGGCCATCCCGTGCGGTGGTGAAGCAGCAGCAGTTTGAGAGGAGAGGAGTC  4806
          || | ||  |||  || |  |||||| || || ||
Db  3486  CCTCACATTTCCTACCACCCCTGCATGAACGGGCTTTGAAGGAGGAGAAGAGTGAGTC        3545
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[Page consists of a dense nucleotide sequence alignment (Query "Qy" vs Database "Db") with flanking position numbers; left-column pairs run Db 2630–3688 / Qy 2689–3571 and right-column pairs run Qy 3689–4806 / Db 2468–3545.]

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Db   3256 GGATCCAGGCCCTGCCAGCAGAAAATATAAGGGCCCTGCTGAGAACAGAGAGGGGTCATCC 3315
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Qy     61 ACTCCATGAGAGTGGGACCTCCAGCTCCAGCTCCAGCTCCTCTTGATGCATGCTGAGGGAC 120

Db   3316 ACTCCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCTCCTGGTAGCCACTGAGAAGC 3375
          |||||||||||||||||||||  |||||||||||||||||| |  ||||||||||||||||
Qy    121 CGGGGCTGTGCTACAGTCGCGGTCGTGGTCGTGCTCCTGAGGGCCCATGGAGCTCCA 180

Db   3376 CCGCGTCCAGCAGCTTCCCCTGCTCGTGTGACATGAGCGCCATTCTTCACTCT--GAAG 3435
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Qy    181 CAGGGCTGTGCTCGCGTCGTGGTCGTGCTCCTGAGGGACACAGTGTCTCCAGGTTACAGACAGAGGATG 240

Db   3436 GGAACAAGGCAGTGAGGCCTTGGTCTGTTGTCTGTGGGATGACTTTGAGATTTATC 3495
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Qy    241 GGAACCAGCAGTGAGGCCTTGGTCTGACAGTCATCCCAGGTCACAGGGCCCCACTGCCA 300

Db   3496 CACAGGCTGTGCCAGCAGTGAATGTTGCCCAGCAGTGAATGCACACCAAGGGCCCACTGCCA 3555
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 CAAGACACATAGGACTCCAAAGAGTCTGCCTCACCTCCTCCTCCTCAGGTTCTGA 360

Db   3556 CAGGGGTGTGCCAGCAGTGAATGTTTGCCCAGCAGTGAATGCACACCAAGGGCCCACTGCCA 3615
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Qy    361 CGACCTCTGCTGCCGGCTATACCCTGAGGTGTGTCTCTCACTTCCTCCTCCTCAGGTTTTCA 420

Db   3616 CGACCTCTGCTGCCGGCTGTACCCTGAG-TACCCTCTCAGTTCCTCCTCCTCAGGTTTCA 3674
          |||||||||||||||||| |  ||||||   ||||||||||||||||||||||||||| ||
Qy    421 GCAGACAGGCCAACCG-GAG-ACAGGATTCCCTGGAGGCCACAGAGGACCACCAAGGAGA 478

Db   3675 GGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 3734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    479 AGATCGTAAGTAAGCCTTTGTTAGAGCTCAAGATTGGTTCTCAGCGTGAGGCTCTC 538

Db   3735 AGATCGTAAGTAAGCCTTTGTTAGAGTCCAAGGTTCAGTTCTCAGCGTGAGGCCCTCTC 3794
          ||||||||||||||||||||||| |  |||||||||||||||||||||||||| |||||
Qy    539 ACATGCTCCCTCTCTGTGGGCTGTGGGCTGCCCATTGCCCATGCTTTTGCCTGCCACTCT 598

Db   3795 ACACTCCCTCTCTCCCCGGCCGTGTGGGTCTTCATTGCCCAGCTGGCTGTCATGCTGCCACTCC 3854
          ||||| |||||||  ||||||||||||||||||||  ||||||||  |||| ||||||||||||
Qy    599 TGCCTGCTGCCCTGCCCTGACCAGAGTCATCATGTCTTCTGACGAGTAGTCAGCACTGCAAGC 658

Db   3855 TGCCTGCTGCCCTGCCCTGACGAGAGTCATCATGTCTTCTGAGCAGTCTGCACTGCAAGC 3914
          ||||||||||||||||||||| ||||||||||||  ||||||||| || ||||||||||||
Qy    659 CTGAGGAAGGCGTTGAGGCCCAAGAAGAGAGCCCTGGGCCTTGGTGGTGCACAGGCCCTA 718

Db   3915 CTGAGGAAGGCCCTTGAGGCCCACAAGAGAGGCCCTGGGCCTTGGTGTGTGCAGGCTGC-- 3972
          ||||||||||||| |   | ||  |||||||||||||  |||||||||||||| ||||||
Qy    719 CTACTGAGGAGGCAGGAGGCGTGCTGTGTCTCCTCGTGTCTCCTCGTTGGCACCCTGG 778

Db   3973 --------------||------CA-------C---CTCCTCCTCCTGTCTCGTGCCCACCCTGG 4010
                        ||      ||      |   |||||||||||| |||| || |||||||||||
Qy    779 AGGAAGGCCTGCTGCGTGCTGAGTCAGCAGTCTCCCCAGAGTCCTCCCCAGAGGCCTCTGCCT 838

Db   4011 AGGAGGGCCTGCTGCGTGCTGAGTCAGCAGTCTCCGAGTCCTCCCCAGAGCCTCCCCAGGGCCT 4070
          ||||||||||||| |||| ||||||  |||||||||||||||| | ||||||| |||||||||||
Qy    839 TACCCACTACCATCACAGCTTCACTTGCTGAGGCAACCCAATGAGGGTTCCAGCAGCCAAG 898

Db   4071 TTCCACTACCATCAACTTCACTCACTGCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTG 4130
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Qy    899 AAGAGGAGGGGCCAAGCACCTGCCTGCACGGCAGAGTCGTTGTTCCGAGAAGCACTCAGTA 958

Db   4131 AAGAGGAGGGGGCCAAGCACCTGCCTGCACGGCAGAGTCCTGGAGTCCTTTCCGAGCAGTAATCACTA 4190
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Qy    959 ACAAGGTGGATGAGTTGGCTGCATCCGAGCATATCGAGCCAGGATCCGCAGCGCCAAG 1018

Db   4191 AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCCTCAAATATCGAGCCAGTAGCCAGTCA 4250
          |||||||||||  || ||   |||||||||| |||||||||||||||||||||||||| ||||
Qy   1019 CAAAGGCAGAAATGCTGGAGAGAGTCATCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCT 1078

Db   4251 CAAAGGCAGAAATGTCATCAAAAATTACAACTGTTTTCCTGAGATCT 4310
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Qy   1079 TCGGCAAAGCCCTGCTGAGTCCTGAGTGAACACAGTGGGATCATCC 1138

Db   4311 TCGGCAAAGCCCTGCTGAGTCCTGAGTCTTTGCATTGAGATGACAGTGGACC 4370
          ||||||||||||||| ||||||||||||  |||||||||||||||||||||||
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Db   3546 TCAGCACAATGTTCAGCCAGCCAGGCGAGGGGTCTGGGCCAGTGACACCTTCCAGGG 3605
          |  |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4807 TGAGCATGAGTTGCAGCCAGCCAGGCCAGGGGGAGGGGGACTGGGCCAGTGACACCTTCCAGGG 4866

Db   3606 CCCCATCCATTAGCTTCCACTGCCTCGTGTGATAATGAGCCCATTCCTGCCTCCTTGAAG 3665
          |  | ||| |||||| |||||| || ||||||||||||||||||||||||||||  ||||
Qy   4867 CCGCGTCCAGCAGCTTCCCCTGCTCGTGTCGTGTGACATGAGCGCCATTCTTCACTCT--GAAG 4924

Db   3666 AGAGCAGTCAGCATTCTTAGCAGTGAGTTTCTGTTCTGTGGGATGACTTTGAGATTTATC 3725
          |||||| |||||||||  |||| || |  ||  |||||||||||| || |||||||||||
Qy   4925 AGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATC 4984

Db   3726 TTTCTTCCTGTGGAATGTTCAAAAGTTCCTTTT-AACAAATGGTTGGATGAACTTCA 3784
          || || |||| ||| || |||||| ||| ||||  |||| |||||||| ||||||| |
Qy   4985 TTTGTTCTTTTGGAATGTTCAAAAGTTTTTTTTTTTAAGGGATGGTTGGATGTTTGAATGAACTTCA 5044

Db   3785 GCATCCAAGTTATGAATGACAGTAGTCACACATAGTGCTTGTTTATATAGTTAGGGGTA 3844
          ||||||||||| ||||| ||| |||||||| ||  |||||||| |||| |||||| ||||
Qy   5045 GCATCCAAGTTATGAATGACAGCAGTCACCACA-GTTCTGTGTATATAGTTTTAAGGGTA 5102

Db   3845 AGAGTCCTGTTTTTTTATTCAGATTGGGAAATCCATTTCCATTTGTGAGTTGTCACATAAT 3904
          |||||| |||||||||||||||| |||| |||| ||||||||||||||| || | |
Qy   5103 AGAGTCTTGTTTTTTATTCAGATTGGGAAATCCATTTCTATTTGTGAGTTGAATTGGGA--TAAT 5160

Db   3905 AACAGCAGTGGAATATGTATTTGCCTATATTGTGAACGAGTTAGCAGTAGAAT-ACATGA 3963
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Qy   5161 AACAGCAGTGGAATAAGTACTTAGAAATGGACAGTAAAAATAGAGCAGTAAAATAGATGAGATAA 5220

Db   3964 T--AC-AAGGAACTCAAAAGATAGTAATTCTTGCCTTATACCTCAGTTATTATTGTAAA 4020
          |  || ||||||  || ||| ||||||  |||| |||||||| | |  | |||| |||||
Qy   5221 AGAACTAAGAAGATTAAGAGATAGTGCAATTCTTGCCTTATACCTCCAGTTATTTATTTGTAAA 5280

Db   4021 ATTA--AAA-ATATGTG--TA--TG-CTTCTTGAGAATGCAAAAGAAAT 4068
          ||||   ||  || ||||  ||  ||   || || ||||  || | ||||
Qy   5281 ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTGGAAGTGAAGAGAAAT 5340

Db   4069 TAAATCTGAATAAA---TTCTTCCTGTTCACTGGCTCATTTCTTTACCATTTCACTTCAGCA 4125
          |||||||||| |||   || ||||| |||||||||| |||  ||| ||||  ||||||||||
Qy   5341 TAAATCTGAATAAAGAATTCTTCCTGTTTTCTTCTTCCTTTTTTCTTCCCATGCACTGAGCA 5400
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Db   4126 TCTGCTCTGTGGGAGGCCCTGG 4147
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Qy   5401 TCTGCTTTTTGGAGGGCCCTGG 5422
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Query Match         24.78;    Score 1399;   DB 25;    Length 2531;
Best Local Similarity  84.38;  Pred. No. 0.00e+00;
Matches  2068;   Conservative  0;  Mismatches 327;  Indels 57;  Gaps 27;

Db.      1 GGATCCAGGCCCTGCCTGAGAAAATGTGAGGGCCCTGAGTGAACACAGTGGGATCATCC 60
           ||||||||||||||||| ||| | ||||  | ||||| |  ||||||||||| |||||||
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Db   2203  GTAAGCCAGCACACACCTACCGATAGGGTATTAAGAGTCTAGGAGC-GCGGTCATATAA  2261
           ||||||||||| ||  ||| ||||||  ||||||||||||| || |||||||  ||||||
Qy   5444  GTAAGCCAGCACTACCCACCCACCCATAGGGTCGTA-GAGTCTAGGAGCTCGAGTCACGTAA  5502

Db   2262  TTAAGGTGACAAGATGTCTCTAA-GATGTAGGGGAAAA-GT-A-ACGAGTGTGGGTATG  2317
           ||||||  |||||||||||| |||  ||||| ||||| ||  || |  ||||||| ||||
Qy   5503  TCGAGGTGCAAGATGTCCTTCTAAAGATGTAGGGAAAAGTGAGGAAAGTGAGAGGGGTGTG  5562

Db   2318  GGGCTCCAGTGCAGTGAGAGTGCGGGATGGCTGTAAATTCCCTGTG-TGGGGCCTTTTGGGCTTTGG  2376
           ||||||||||||||||||||  ||  || |||||||||||| ||| ||||||||||||||||
Qy   5563  GGGCTCCGGTGCAGTGCTGGAGTGGCTGGATGCTGTCAATGCCCTGAGCTGGGCATTTTGGGCTTTG  5622

Db   2377  GAAACTGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTCA  2428
           ||||||||||| || |  ||| ||| || |||||||||||||| |
Qy   5623  GAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGATCC  5674

RESULT   6

LOCUS        I36929     2531 bp   DNA              PAT        21-APR-1997
DEFINITION   Sequence 14 from patent US 5612201.
ACCESSION    I36929
NID          g2084889
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 2531)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 14 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1..2531
                     /organism="unknown"
BASE COUNT      607 a    593 c    701 g    630 t
ORIGIN

Query Match   24.7%;  Best Local Similarity  84.3%;     Score 1399;  DB 25;   Length 2531;
Matches 2068;  Conservative   0;  Mismatches 327;  Indels  57;  Gaps  27;     Pred. No. 0.00e+00;

Db      1  GGATCCAGCCCTGCCTGCCTGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGATCATCC    60
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Qy   3256  GGATCCAGCCCTGCCTGCCTGAGAAAATATAGGGCCCTGAGAGCAGAGGGGGTCATCC   3315

Db     61  ACTCCATGAGAGTGGGACCTCACAGAGTGCAGTGGCCATGGCCTGATGCGTCAGGGAC   120
           ||| |||||| ||||| || ||| |||||| |||| ||||||||||| | |||||||||
Qy   3316  ACTGCATGAGAGTGGGGATGTCACAGAGTGCAGTGGCCACCCACCCGTGTAGCACTGGAGAAGC   3375

Db    121  CGGGGCTGTGCTTACAGTGCTGCACCTAGGGCCCATGGCCTCCTAGGAGTCCTCCA   180
           |||||| |||||||||||| |||||||||||||||||||| ||||||||||||||||
Qy   3376  CAGGGCTGTGCTTGCGGTCGCTGCACCCTGAGGGGCCCGTGGGATCCCTGAGGAGCTCCA   3435

Db    181  GGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCCTGGTTTACAGACAGAGGATG   240
           |||||| |||||| |||||||||||||||||||| |  ||||| |||||| |||||||
Qy   3436  GGAAGCACCAGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTGGTCACAGAGCAGAGGATG   3495

Db    241  CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGACAGTCTCCTTATACC   300
           ||||||| |||||||||||||||| |||||  |||| |||| ||||||
Qy   3496  CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGACAGTCTCCTTACCACC   3555

Db    301  CAAGACACATAGGACTCCAAAGAGTCTAGTTAACGTATATTGCTG-   360
           || ||| ||||||||||||| | ||||| ||| |||||| |||||
Qy   3556  CAGGACACATAGGACTCCACAGAGTCTGGGATTTCACTCCGATTTCTTT   3615

Db    361  CGACCTGCTGCCGGCTAACTGGTGAGGTGCTATACCGAGGTTCTGA   420
           |||||||||||||||||  || |||||| || || |||| |||| |
Qy   3616  CGACCCTGCTGCCGGCTGCCGTGCTGCCTGAG-TACCCTCTCACTTCCTCTCTCAGGTTTCA   3674

Db    421  GCAGACAGGCCAACCG-GAG-ACAGATTCCCTGGAGGCCACCAAGGAGA   478
           |||||||| |||||  |||  ||||||||||| ||||| || ||||||||
Qy   3675  GGGGACAGGCCAACCCCAGGATTCCCTGGAGGCCACCAAGGAGA   3734
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... (additional alignment blocks, left column, continued)

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Db   1139  CCGGCCAGCAACACCTACACCCTTGTCACCTGCCTGGCCTTCTCCTATGATGGCCTGCTGG  1198
Qy   4371  CCACCGGCCACTCCTATGCCTGTCACCTGCCTAGGTCTCCTATGATGGCCTGCTGG  4430

Db   1199  GTAATAATCAGATCTTCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAA  1258
Qy   4431  GTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAA  4490

Db   1259  TGGAGGGGACAGCGCCCTCTGAGGAGCAAATCTGGGAGGACTGGGTGTGATGGGGGTGT  1318
Qy   4491  TGGAGGGGCGGCCATGCTCCTGAGGAGCAAATCTGGAGGAGCTGAGTGTGATGGAGGTGT  4550

Db   1319  ATGATGGGGAGGGAGCACACTGTCTATGGGAGGCCAGGAAACTGCTCACCCAAGATTGGG  1378
Qy   4551  ATGATGGGGAGGGAGCACAGTGCCTATGGGGAGCCAGCAGTGCTGCTCACCCAAGATTTGG  4610

Db   1379  TGCAGGAAAACTACCTGGAGTACCGGCCAGCAGTGAATAATCCTGCCGCCTATGAGT  1438
Qy   4611  TGCAGGAAAAGTACCTGGAGTAC-GGCAGGTGCCCGGACCAGTGATCCCGCACGCTATGAGT  4669

Db   1439  TCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGG  1498
Qy   4670  TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA  4729

Db   1499  TCAGGGTCAATGCAAGAGAGTTGCCATTGCCTACCACCATCCCTGCGTGAAGCAGCTTTGTTAG  1558
Qy   4730  TCAAGGTCAGTGCAGGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG  4789

Db   1559  AGGAGGAAGAGGGAGGTCTGAGCATGAGTGAGGGAAGGGGCCAGGGCT  1618
Qy   4790  AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGGC  4849

Db   1619  GGGCCAGTGCATCTAACGACCGTGTGCGAGCAGCTTCCTCTGTGTAACATGAGGCC  1678
Qy   4850  CAGTGCAC-CTTCCAGG-GCCGGCGTCCAGCAGCTTCCCTGCCGTGCTGCATGAGGGCC  4907

Db   1679  CATTCTTCACTCTGTTTGAAGAAAATAGTCAGTGGTTCTTAGTAGTGGTTTCTATTTTGT  1738
Qy   4908  CATTCTTCACTCTG----AAGAGACGGTCAGTGTTTCTCAGTAGTAGTTTCTGTTCTAT  4963

Db   1739  TGGATGACTTGGAGATTTATCTCGTTTACCTTTTACAATTGTTGAAATGTTCCTTTT-AA  1797
Qy   4964  TGGGTGACTTGGAGATTTATCTTGTTTCTTGTTCTTTTGGAATTGTTCAAATGTTTTTTTTAA  5023

Db   1798  TGGATGGTTGAATTAACTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTG  1857
Qy   5024  GGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATCGTAGTTATGAATCAGCAGTTCTG  5083

Db   1858  TTAATATAGTTTAGGAGTAAGAGTCTTGTTTTATTCAGATTGGGAAATCCGTTCTATT  1917
Qy   5084  TGTATATAGTTTAAGGTAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATT  5143

Db   1918  TTGTGAATTGGGACATAATAACAGCAGTGGA-GTA---AGTATT-T-AGAAGTGTGAAT  1971
Qy   5144  TTGTGAATTGGGATAATAACAGCAGTGGAATAAGTAGACTTAGAAATGTGAAAATGAGCAG  5203

Db   1972  TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATAGTCTTAATTCCCGCCTTATGCC  2025
Qy   5204  TAAAATAGATGAGATAAAGAATAAGAATTAAGAGATTAGTCAATTCTTTGCCTTATACC  5263

Db   2026  TCAGTCTATTCTGTAAAATTTAAAAATTTAAAGATTATATGCATAAATATATGCCTTCGT-  2084
Qy   5264  TCAGTCTATTCTGTAAAATTTTTAAAGATTATATGCATAAATATGCGATTTTCCTTGGCTTCTTT  5323

Db   2085  --GAATGTAAGAGAAATTAAATCTGAATAAAATACTGTTAACTGGCTCATTTCT  2142
Qy   5324  GAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCACTGCCTCTTTTCT  5383

Db   2143  TCTCTATGCATGAGCACTCGTCTGTGTGGAATCATGCCTGCTGTCTCTTGTCTCTGTTCT  2202
Qy   5384  TCTCCATGCGACTGAGCCATCGTCGTTGTTTTGGAAGGCCCTGGGTTAGTGAGTGAATGCTAAG  5443
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Db   479  AGATCTGTAAGTAAGCCTTTGTTGTTAGAGCCTCTAAGATTTGGTTCTTCAGCTGAGGTCTCTC  538
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Qy  3735  AGATCTGTAAGTAAGCCTTTGTTTAGAGTCTTCAGTTCTTCAGCTTCAGCTGAGGCCCTCTC   3794

Db   539  ACATGCTCCCTCTCCGTAGGCCTGTGGGTCCCATTGCCCAGCTTTGCCTGCACTCT        598
          ||||   || || |||||||||||||||||  ||| |||||  ||| ||||
Qy  3795  ACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTCATTGCCCAGCTCCTCCCACACTCC     3854

Db   599  TGCCTGCTGCCCTGAGCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGC     658
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Qy  3855  TGCCTGCTGCCCTGACGACGAGTCATCATGTCTCCTGAGCAGAGGAGTCTGCACTGCAAGC    3914

Db   659  CTGAGGAAGGCGTTGAGCGCCAAGAAGAGGCCCTGGGCCTGGTGGTGCCGCAGGCTCCTA     718
          |||||||||||||||||||   |||||||||||| || |||||||||||||||| ||||
Qy  3915  CTGAGGAAGGCCCTTGAGCGCCAACAAGAGGCCCTGGGCCTGGTGTGTGCGAGCCTGC--    3972

Db   719  CTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCCTGTCCCTGCACCCTGG         778
          ||            |  ||  || ||||||||||||||||  ||||||||||||
Qy  3973  --------CA---------CA---CTCCTCCTCCTCCTGTCCCTGGGCACCCTGG      4010

Db   779  AGGAGTGCCTGCTGCTGAGTCAGCAGGTCCTCTCCCCAGAGTCCTCAGGGAGCCTCTGCCT    838
          || |||||||||||||| |||| |||||| ||||  ||||||||||||||||||||| |||
Qy  4011  AGGAGTGCCACTGCTGGGTCAACAGATCCTCTCCCCCAGAGTCCCCAGGGAGCCTCCCCCT    4070

Db   839  TACCCACTACCATCAGCTTCACTTGCTGAGGCAACCCATGAGGGTTCCAGCAGCCAAG      898
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Qy  4071  TTCCCACTACCATCAACTTCACTTCACTGCGACAGAGCAACCCCAGTGAGGGTTCCAGCCGTG   4130

Db   899  AAGGAGGAGGGCCAAGCACTCGCCTGACGAGTCCTTGTTCCGAGAAGCAGCACTCAGTA    958
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Qy  4131  AAGGAGGAGGGCCAAGCACTCTGTATCCTGGAGTCCTGTGGAGTTCCGAGGAGCCAGTCA   4190

Db   959  ACAAGGTGGATGAGTTGGCTCATTTTCGCTCCGCAAGTATCGAGCAGGAGCTGTGTCA    1018
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Qy  4191  AGAAGGTGGCTGATTTGGCTGTTTTTCTGGTTCTCCAAATATCGAGCCAGGAGCCAGTCA   4250

Db  1019  CAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGCCGCTGCTTCCTGTGATCT   1078
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Qy  4251  CAAAGGCAGAAATGCTGGAGAGAGTGTCATCAAAATTACAAGCACTGTTTTCCTGAGATCT   4310

Db  1079  TCGGCAAAGCCCTCCGAGTCCTCCGAGTCCTCCGAGATCTTTGGCATTGACGTGAAGGAAGTGACC  1138
          |||||||||||||||   ||  | ||||| || ||||  |  ||||||||||||||||
Qy  4311  TCGGCAAAGCCCTCTGAGTCCTGGAGTCCTGGAGCATTGACGTCCTTGGCATTGACGTGAAGGAAGCAGACC  4370

Db  1139  CCACCAGCAACACCTTACACCCTTGTCACCTGCCTTTCCTATGATGCCCTGCTGG    1198
          |||| ||  | | |||   ||||| ||||||| |||||||||  |||||||||||
Qy  4371  CCACCGGCCCCACTCCTATGTCCTCCTAGGTCTCCCATGATGCCCTGCTGG      4430

Db  1199  GTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATCGTCTGGGCACAATTGCAA   1258
          ||||||||| || ||| |||| || || ||||| |||||  || ||  ||||||  ||
Qy  4431  GTGATAATCAGATCATGCCCAAGACAGGCCTTCCTGATAATTGTCCTTGGTGATGATTGCAA   4490

Db  1259  TGGAGGGGCGACACGTCCCTGGGGAGACTCGGGAAATCGGGGAGGTGTGATGGGGTGT   1318
          |||||||| ||| | ||||||||  |||| ||||| |||| || ||||||||||||||
Qy  4491  TGGAGGGGCCGGTCCGGTCCCTGGGGAGTCGTGGGGTCATTTTGGGCTTTTGG       4550

Db  1319  ATGATGGAGGGGAGCACACTGCTATGGGAGGGCCCAGGAAACTGCTCACCCAAGATTGGG    1378
          ||||||||||||||||||||||||||||||||||| || ||||  |||||||||||||||
Qy  4551  ATGATGGAGGGGAGCACAGTGCCTATGGGGAGGGCCCAGGAAGCTGCTCACCCAAGATTTGG   4610

Db  1379  TGCAGGAAAACTACCTGGAGTACCGGCAGCTACCCGGCAGTAATCCTGCGCCGCTATGAGT   1438
          |||||||||||||||| || ||||| ||| |||||||| || ||| |||||||| ||||
Qy  4611  TGCAGGAAAAGTACCTGGAGTAC--GGCGCAGTGATCCCGGACCGCTATGAGT       4669

Db  1439  TCCTGTGGGGTCCAAGGGCCTCTGGCTGAAAACCAGCTATGTGAAAGTCCTGGACATGTGG   1498
          |||||||||||||||||| ||| ||||||||||||||||| ||||||||||| ||||||||
Qy  4670  TCCTGTGGGGTCCAAGGGCCCTCTGGAAACCAGCTATGTGAAAGTCCTTGGGAAAGTCGTGA  4729

Db  1499  TCAGGTCAATGCAAGAGTTGCGCTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAG     1558
          ||| ||  |||| || |||||||  | ||  |||  ||  |||||||||||||||| |
Qy  4730  TCAAGGTCAGTGCAAGAGTTCGCTTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG   4789
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Db  1559  AGGAGGAAGAGAGGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGCGGGAAGGGGCAGGGCT  1618
          ||||||||||||| ||||||||||||||||||   ||  ||||  ||||||||||||||
Qy  4790  AGGAGGAAGGAGGAGGGGAGTCTGAGCATGAGTTGCAGCCAAGGGCCAAGGCCAGTGGGAC     4849

Db  1619  GGGCCAGTGCATCTAACAGCCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAACATGAGGCC  1678
          |    ||||| || |  ||   ||  ||  ||||||||||  | ||||| ||||||||||
Qy  4850  CAGTGCAC-CTTCCAGG-GCCGGCGTCAGCAGCTTCCCTCGTGTGACATGAGGCC      4907

Db  1679  CATTCTTCACTCGTTTGAGAAGAAAATAGTCAGTGTTCTTGTTTCTATTTTGT       1738
          |||||||||||||   |||||   |||  ||||||  |||||||   |||||
Qy  4908  CATTCTTCACTCTG----AAGAGGACGGTCAGTGTTCTCAGTAGTAGGTTTCTGTGTCTAT    4963

Db  1739  TGGATGACTTGGAGATTATCTCGTTCCTTTACAATTGTGAAATGTTCCTTTT-AA  1797
          ||| |||  ||||||| || |  |||| |||   | ||| |||| || |||| ||
Qy  4964  TGGGTGACTTGGAGATTATCTTCGTCCTTTTGGAATTGTTCAAATGTTTTTTTTTAA     5023

Db  1798  TGGATGGTTGAATTAACTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTG   1857
          |||| || | ||| |||| ||| || |||| |  |||| ||||  |||| || ||  |||
Qy  5024  GGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATTGGAAATCCATTCTATT       5083

Db  1858  TTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTCAGATTGGGAAATCCGTTCTATT    1917
          | |||||||||| | |||||||||| | ||||| ||| || || |||||||  |||||
Qy  5084  TGTATATAGTTTAAGGGTAAGAGTCTTGTTTTTTATTCAGATTGGGAAATCCATTCTATT     5143

Db  1918  TTGTGAATTTGGGACATAATAACACAGCAGTGA-GTA---AGTATT-T-AGAAGTGTGAAT  1971
          ||||||||||| ||| | |||||||| || ||  |||    |   ||  | ||| ||||||
Qy  5144  TTGTGAATTGGGATAATAACAGCAGTAAGTACTTAGAAATGTGAAAATGAGCAG     5203

Db  1972  TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATACTTAATTCCCGCCTATGCC   2025
          || ||   | ||||||| ||   ||||||||||||||  ||  || |||| |||||||||
Qy  5204  TAAAATAGTAGATTAAAGAACTAAGAAGATAGTCAATTCTTGGCCTTATACC     5263

Db  2026  TCAGTCTATTCTGTAAAATTCTGTAAAATTTAAAATATATATGCATACCTGGATTTCCGT-  2084
          ||||||||||||||||||||| ||||||||| |  |||||||||||||||||||||||||
Qy  5264  TCCAGTCTATTCTGTAAAAATTTTAAAGATATTGTTTAAGATATGCATACCTGGATTTCCTTT   5323

Db  2085  --GAATGTAAGAGAAATTAAATCTGATAAATAATAATTCTTTCGTTAACTGGCTCATTTCT  2142
            | ||||||||||| ||||||||||||| || ||  ||| | || ||||||| || ||||
Qy  5324  GAGAATGTAAGAGAAATTAAATCTGATAAATCTGAATAGAAGAATTCTTCCTGTTCACTGGCTCCTTTTCT  5383

Db  2143  TCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCCAGGATTAGTAGTGGAGATACTAGG  2202
          |||| |||||||||||||| ||||  | ||||||   |||| || | |||||||||| |||
Qy  5384  TCTCCATGCACTGAGCATCTGCTTTTGTTGGAGGCCCCTTGGGTTAGTAGTGGAGATGCTAAG   5443

Db  2203  GTAAGCCAGACAACACACCACACCTACCGGTATTAAGAGTCTAGGAGC-GCGGTCATATAA  2261
          |||||||||||||||||||| ||||| || ||| ||||||| |||||| ||||||  |||
Qy  5444  GTAAGCCAGAACTCATACCCCACCCATAGGGTCGTA-GAGTCTAGGAGCTGCAGTCCACGTAA    5502

Db  2262  TTAAGGTGACAAGATGTCCTCTAA-GATGTAGGGGAAAA-GT-A-ACGAGTGTGGGTATG   2317
          |  ||||| |||| |||||||| || |||||||||||| | || | |||||||| ||||
Qy  5503  TCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGGAAAAGTAGGGGTGAGGGGTGTG      5562

Db  2318  GGGCTCCAGTGAGAGTGGTGTCGGGTTGTAAATTCCCTGTG-TGGGGGCCTTTGGCTTTGG  2376
          |||||| ||||| ||||| |||||||| |||||||||||| ||||||||||||||||||||
Qy  5563  GGGTCCCGGGTGAGAGTGGTCAATGCCGTCAATGCCCTGTGAGCTCCGGTGGGGCCATTTTGGGCTTTGG   5622

Db  2377  GAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATCTAATGAAGCTTGGGGTATG      2428
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Qy  5623  GAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGGTGGATCC       5674
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RESULT      7
LOCUS       I36932                 2305 bp    DNA                 PAT       21-APR-1997
DEFINITION  Sequence 17 from patent US 5612201.
ACCESSION   I36932
NID         g2084892
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2305)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
            Chomez,P.
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TITLE   Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
JOURNAL   Patent: US 5612201-A 17 18-MAR-1997;
FEATURES   Location/Qualifiers
  source   1..2305
            /organism="unknown"
BASE COUNT   549 a   568 c   611 g   577 t
ORIGIN

Query Match   21.6%;   Score 1225;   DB 25;   Length 2305;
Best Local Similarity   84.1%;   Pred. No. 0.00e+00;
Matches 1956;   Conservative   0;   Mismatches 299;   Indels   72;   Gaps   32;

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Db      1 GGATCCAGGCCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTC 60
          |||||||||||||||| |||      ||||||| |||  |||      |   |||||
Qy   3256 GGATCCAGGCCTGCCAGGAAAAATATAAGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315

Db     61 ACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCTACCTCCTTGTTAGCACTGGGGGCC 120
          || |||| |||| ||||| ||| ||||||| ||||||| ||||||| | |||||| |
Qy   3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCACCCACCCTGGTAGCACTGAGAAGC 3375

Db    121 TGAGGCTGTGTTCGTTGCACCTGAGGGCCCATGCATTCCTCTTCCAGGAGTCCA 180
          ||||||||||||| ||||||||| ||||||||| || |||||||| ||||||||
Qy   3376 CAGGGCTGTGTCTGCTTGCCGGTCTGCACCCTGGGCCCGTGGAGTCCTTCCTGGAGCTCCA 3435

Db    181 GGAAACAGACACTGAGGCCTTGGTCTGAGGCCGTGCCCTCAGGTCACAGAGCAGAGGAGA 240
          ||||| ||||| |||||||||||||||||||||  |||      ||||||||||||
Qy   3436 GGAACCAGGCCAGTGAGGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGA-- 3493

Db    241 TGCGAGACGTTCAGTGCCAGCAGTCCTTGCCTTGAATGCACACTAATGGCCCCCCATC 300
          |||| | ||||| | |||| ||||||||| ||||| ||||| |||| | |||||||
Qy   3494 TGCACAGGG-T-GTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGGCCCCACCT 3551

Db    301 GCCCCAGACATATGGGACTCCAGAGACTCCAGCACCTGGCCTCACCCTCTCTACTGTCCTGC 360
          |||| | |||| || ||||||||||| |||| || |||||||||| || ||| |||||||
Qy   3552 GCCCACAGACCACATAGGACTCCACAGAGTCTGGGCCTCACC-TCCCTACTGTCAGTCCTGT 3610

Db    361 AGATCAGCCTCTGCTTCCTG-TGTACCCTGAGGTGCCCTCTCCACTTTTCCTTCCAGGT 419
          ||||| | ||||||||| || ||| | || | ||||||||  |||      |||||||
Qy   3611 AGAATGACCTCTGCTGGCCGGCTGTACCCTGAG-TACCCTCACTTCCTTCCTTCCAGGT 3669

Db    420 TCTCAGGGACAGAGCCTGACCAGGAGCTCACCAGGAAGCTCCAGGAGGATCCCAGAGGAGGCCCT 479
          |||||| || |  | | ||| ||||| |||| |||||||||||||| ||||| |||||||
Qy   3670 TTTCAGGGGACAGGC----CA--A-C-CCAG--AGGAC--AGGATTCCCTGGAGGCCACC 3716

Db    480 AGAGGAGCACCAAAGGAGGAGATCTGTAAGTAAGCCTTTGTTAGAGCTTGTTAGAGCCTTGAGC 539
          |||||||||||||||||||||||||||| || ||| |||||||||||| |||||||| |||
Qy   3717 AGAGGAGCACCAA--GGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAG 3775

Db    540 TTTTTAGTGAGGCTTCTCACACTGCCTCCCTCTCTCTCTCTCCAGGCCAGTGGGTCTCCATTGCC 599
          |||||||||||| ||||||  || |||||||| |||| | |||| ||||| ||| |||||||
Qy   3776 TTCTCAGCTGAGGCCTTCTCACACACTACCTCCTCTCCCCAGGCCTGTGGGTCTTCATTGCC 3835

Db    600 CAGTCCTCGTGCCCCACACTCCTGCCTCCTGGGTGACCAGGAAGCCTTGACACCCAAGAGAG--CCCTGGGCCTG 659
          |||||| | |||| |||||| |||| |||||||||| |||||||| |||||| ||||||||
Qy   3836 CAGTCCTCTGCCCCACACTCCTGCCTCCTGGGTGACGAGGAAGCCCTGGGCCTG 3895

Db    660 AAGAGTCAGCACTGCAAGCCTGCGAGGAAAGGCCTGAGGAGAGACACCCAAGAAGAC--CCTGGGCCTG 718
          | ||||||| |||| |||||| ||||| ||| |||||| || |||||||||||
Qy   3896 AGGAGTCTGCACTGCAAGCCTGCGAGGAGGAAGCCCTGAGGAGAGACACCCAAGAAGAGCCCTGGGCCTG 3955

Db    719 GTGGGTGTCGCAGCTGCGGCTGCCACTACTGAGGAGCGTGTCCCTCTCTCCTGG 778
          || |||||||||||| ||||||| ||| | |          ||||| ||||||| |
Qy   3956 GTGTGTGTCGCAGGCTGCCAC------------------CT-----CCTCCCTCCTCTCTG 3994

Db    779 GTCCTCCAGGCCACCCTGGGGGAGGTGCCTGCTCGGTCTCGGTCAACAGATCCTCCCCAGAGTCCT 838
          |||||||||| |||||| |||||||||| | |||||||||||| ||| ||||| |||||||||
Qy   3995 GTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGGTCTCGGTCAACAGATCCTCCCAGAGTCCT 4054

Db    839 CAGGGAGGCCTCCGCCATCCCAGCCATCGATTCACTCTATGCAGGCAATCCATTAAG 898
          ||||||||||||||||  | ||||| ||| | |||||||||||| ||||||||
Qy   4055 CAGGGAGGCCTCCGCCTTTCACTCACCACCATCACTTCACTCGACAGAGCAGCCAGTGAG 4114
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Db    899 GGCTCCAGCAACCAAGAGAGAGGAGGGGCCAAGCACTCCCTGACCCAGAGTCTGTGTTC 958
          || ||||| || | |||||||||||||||||||||||||||||| |  |||| |||||||
Qy   4115 GGTTCCAGCAGCCAGCAGGAGGGGCCAAGCACCTCTGTATCCTGAGTCCTGTTC 4174

Db    959 CGAGCAGCACTCAGTAGAAGGTGGCTGACTTGATTCATTTTCTGCTCCTCAAGTATTAA 1018
          |||||||| | |||  || ||||  |||| ||| |  ||  | |||||||||||||
Qy   4175 CGGACAGTAATCACTCAAGAAGGTGGCTGATTTGTTGGTTTGGTTCTGCTCCTCAAATATGA 4234

Db   1019 GTCAAGGAGCCGGTCACAAAGCAGAAATGCTGGAGAGCGTCATCAGAAAATTACAAGCGC 1078
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Qy   4235 GCCAGGGAGCCAGTCACAAAGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCAC 4294

Db   1079 TGCTTCCTGAGATCTTCGGCAAGCCTCCGAGTCCTTGCAGCTGGTCTTTGGCATTGAC 1138
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Qy   4295 TGTTTCCTGAGATCTTCGGCAAGCCTCCGAGTCCTTGCAGCTGGTCTTTGGCATTGAC 4354

Db   1139 GTGAAGGAAGCCGACCCCACCAGCAACACCTACCACCCTTGTCACCTGCCTGGGACTC--C 1196
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Qy   4355 GTGAAGGAAGCAGCACCCCACCGGCCACTCCTATGTCCTGTCACCTAGGTCTCC 4414

Db   1197 TATGATGGCCTGGTGGTT--TAATCAGATCATGCCCAAGACACGGGCCTCCTGATAAATCGTC 1254
          |||||||||||||||| ||   ||||||||||||||||| || ||||||||||| |||||| |
Qy   4415 TATGATGGCCTGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAATTGTC 4474

Db   1255 TTGGGCATGATTGCAATGGAGGCAAATCGTCCTGAGGAGAAAATCTGGGAGGAGCTG 1314
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Qy   4475 CTGGTCATGATTGCAATGGAGTGGCCATGCTCCTGAGGAGGAGGAAATCGGGAGGAGCTG 4534

Db   1315 GGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGAGCCAGGAAGCTG 1374
          |||||||| |||||||||| ||||||||| |||| || |||| ||| |||||||||||||
Qy   4535 AGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGTGCTATGGGAGCCCAGGAAGCTG 4594

Db   1375 CTCACCCAAGATTTGGTGCAGGAAAATACCTGGAGTACCGGACCGCCAGTGCCCAGTGATC 1434
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Qy   4595 CTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGACCGCCAGTGCCCAGTGATC 4654

Db   1435 CCATATGCTATGAGTTACTGTGGGTCCAAGGGCACTCCTG------CT---TGAAAG 1484
          ||  | |||| ||  ||| |||| |||||||||| | |||      ||   |||||
Qy   4655 CCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCCTGAAACCAGTATGTGAAAG 4714

Db   1485 TACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTCATTCCTACCCATCCCTGCATG 1544
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Qy   4715 TCCTTGAGTATGTGATCAAGGTCAGTGCCAGAGTTGTCAGAAGTTCCCATCCCTGCGTG 4774

Db   1545 AAGCAGCTTGAGAGAGAGGGAGAGGAGGAGTCTGAGCATGAGGCCCAGGGCCACTG 1604
          |||||||||||||||||||||||||||| |||||||| ||||||| |||||||||||
Qy   4775 AAGCAGCTTGAGAGGAGGGAGAGGAGGAGTCTGAGCATGAGGCCCAGGGCCACTG 4834

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          |||||| ||| | ||||||||| | |||||||| | |||| |||||||| || |||||
Qy   4835 GGAGGGGGACTGGGCCAGTGACGCACCTTCCAGGGTCGTCCCAGCGTCCCCTGCCTCG- 4893

Db   1665 TGTGACATGAGGCCCATTCTTCTCTTTGAGGAGCAGCAGCAACATTCTTAGTAGTGGG 1724
          ||||||||||||||||||||| ||| | | | |   |||||||||| | |||||||||
Qy   4894 TGTGACATGAGGCCCATTCTTCTCACTCT--GAGAGAGCCGGTCAGTGTTCAGTAGTAGG 4951

Db   1725 TTTCTGTTCTATTGGATGAGATTTGTCTTTGTTCCTTTTGGAATTGTTCAAAT 1784
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Qy   4952 TTTCTGTTCTATTGGGTGACTTGGGGATTTATTCTTTTGTTCTCTTTTGGAATTGTTCAAAT 5011

Db   1785 GTTCCTTTAATGGG-TGGTTGAATGAAGACTTCAGACTTCAAATTTATGAAGTGACAGTAGT 1843
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Qy   5012 GTTTTTTTTTAAGGGATGGTTGAATGGAGACATCCAAGTTTATGAATGAACAGCAGT 5071

Db   1844 CACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTGTTTTTTATTCAGATTGGG 1903
          ||||||  | | |||    || ||| ||||| ||||| | ||   ||||||||||||
Qy   5072 CACACA--GTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTTATTCAGATTGGG 5129

Db   1904 AAATCCATTCATTTTGTGAATTGGACA-TAGTTACAGCAGTGGAA-TAAGTATTCATT 1961
          ||| |||||| |||||||| |||| || |||||| ||||| | | | |||||| |  |
Qy   5130 AAATCCATTCATTTTGTGAATTGGATAATAACAGCAGTGGAATAAGTACTTAGAAATG 5189

Db   1962 T-AGAAATGTGAA-TGAGC-AGTAAAACTGATGAGATAAAGAAAATTAAAAGATATTAAT 2018
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Qy   5190  ||  ||||| |||   || |   | ||  |   || |   |||||||||||| |||||| |||| |||
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Db   2019  TCTTGCCTTATAC-TCAGTCTATTCGGTAAAATTTTTTTAAAAATGCATACCTGGA  2077
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Qy   5250  TCTTGCCTTATACCTCAGTCTATTCGGTAAAATTTTAA--AGATATGCATACCTGGA  5307

Db   2078  TTTCCTTGGCTTCTTTGAGAAGTGTAAGACAAATTAAATCTGAATAAATCATTCTCCCTGT  2137
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Qy   5308  TTTCCTTGGCTTCTTTGAGAAGTGTAAGAGAATTAAATCTGAATAAAGAATTCTTCCTGT  5367

Db   2138  TCACTGGCTCATTATTCTCTATGCACTGAGCATTTGCTCTGTGGAAGGCCCTGGGTTAA  2197
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Qy   5368  TCACTGGCTCCTTTTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTTAG  5427

Db   2198  TAGTGAGATGCTAAGGTAAGCCAGACTCACCCTACCCACGGGTAGTAAAGTCTAGGA  2257
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Qy   5428  TAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGA  5487

Db   2258  GCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCTAA-GATGTAG  2303
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Qy   5488  GCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGAGATGTAG  5534
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RESULT   8
LOCUS   I36931   2226 bp   DNA   PAT   21-APR-1997
DEFINITION Sequence 16 from patent US 5612201.
ACCESSION I36931
NID   g2084891
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 2226)
  AUTHORS De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
           Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
           a tumor rejection antigen precursor
  JOURNAL Patent: US 5612201-A 16 18-MAR-1997;
FEATURES   Location/Qualifiers
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BASE COUNT   539 a   542 c   582 g   563 t
ORIGIN

Query Match   16.6%; Score 943; DB 25; Length 2226;
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Matches 1320; Conservative 0; Mismatches 209; Indels 28; Gaps 17;

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Qy   3987  CTCCCTCTGGTCCGGAGCACCTGGGGAGGTGCCTGCTGGTCAACAGATCCTCCCC  4046

Db    747  AGAGTCCTCAGGGAGGCTCCGGCTCCCGCCATCCCGCCATCGATTTCACTCTATGGAGGCAAT  806
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Qy   4047  AGAGTCCTCAGGGAGGCTCCGGCTCCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAAC  4106

Db    807  CCATTAAGGCGTCCAGCAACCAAGAGAGAGGAGGGGCCAAGCACCTCCCCTGACCCAGAGT  866
           ||| || |||||||||||| |||| ||||||||||||||||||||||| | ||  |||||
Qy   4107  CCAGTGAGGGTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGT  4166

Db    867  CTGTGTTCCGAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCATTTCTGCTCCTCA  926
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Qy   4167  CCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCA  4226

Db    927  AGTATTAAGTCAAGGAGCTGGTCACAAGGCAGAAATGCTGAGAGCGTCATCAAAATT  986
           ||||||||||||||||||||||||||||||||| |||||||||| | |||||||||||
Qy   4227  AATATCGAGGCAGGGAGCCAGGAGCCAGCCAGAAATGCTCACAAAGGCAGAAATGTCATCAAAAAT  4286

Db    987  ACAAGCCGCTGCTTTCCTGAGATCTTCGGCAAAGCCTTCGAGTCCTTG  1046
           |||||| ||| ||||||||||||||||||||||||||||||||||||||
Qy   4287  ACAAGCCACTGTTTTCCTGAGATCTTCGGCAAAGCCTTCGAGTCCTTG  4346
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Db   1047  GCATTGACTGAAGGAGCGGACCCCACCGGCAACACCTACACCCTTGTCACCTGCCTGG  1106
           ||||||||||||||||||||||| ||||||||||||| || |||   ||| ||||||||
Qy   4347  GCATTGACGTGAAGGAAGCAGACGCCCACTCCTGTCCCTGTCCTAG  4406

Db   1107  GACTCCTATGATGGCCTCTGGTGATATAATCAGATCATGCCCAAGACGGGGCTCCTG  1166
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Qy   4407  GTCTCTCCT-ATGATGGGCCTGCTGCGTGATAATCAGATCATGCCCAAGACAGGCTTCCTG  4465

Db   1167  ATAATCGTCTTGGGCATGATGCAATGGAGGGCAAATGCGTCCTCCAGAGAAAAATCTGG  1226
           |||||  ||||||||||||||||||||||   |||| |||| ||||| |||||||||||
Qy   4466  ATAATTGTCCTGGTCATGATTGCAATGGAGGGCCGGCCCATGCTCCTGAGAGGAAATCTGG  4525

Db   1227  GAGAGCTGAGTGTGATGAAGGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCC  1286
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Qy   4526  GAGGAGCTGAGTGTGATGAAGGTGTATGATGGGGAGGAGCACAGTGTGCCTATGGGGGAGCCC  4585

Db   1287  AGGAAGCTGCTCACCCAGATTTGGTGGAGGAAAACTACCTGGAGTACCGGCAGGTGCCC  1346
           ||||||||||||||||||| | |||| ||||||||||| |||||||||||||| ||||||
Qy   4586  AGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAGTACCTGGGATGAC-GGCAGGTGCCG  4644

Db   1347  AGCAGTGATCCCATATGCTATGAGTTACTGTGGGTGGGGTCCAAGGGCACTGCTG------C  1399
           |||||||||||||||| ||||| |  |   ||||||||||  ||||| |  ||
Qy   4645  GACAGTGATCCCACGCTATGAGTTCCTGTGGGTCGGGTCCAAGGGCCCTGCTCGCTGAAACCAGC  4704

Db   1400  T---TGAAAGTACTGGACACGTGTCAGGTCAATGCAAGAGTTCTCATTTCCTACCCA  1456
           |   ||| | || || |||| ||| ||||||||||||||||||| |||| ||||||||
Qy   4705  TATGTGAAAGTCCTTGAGTATGTGACATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTCCCA  4764

Db   1457  TCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAGGGGAGTCTGAGCATGAGCTCGCAGCC  1516
           ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Qy   4765  TCCCTGCGTGAAGCAGCGTTTGAGAGAGGAGGAGGGGAGTCTGAGCATGCAGTCAGTGCCG  4824

Db   1517  AGGGCCACTGCGAGGGGGGCTGGGCTGGCCCAGGGCTCACCTTCCAGGGCTCCGTCCAGTAGTTCC  1576
           ||||||| |   |  ||| || ||||| ||||| ||||||||||||| | ||||||||||||||
Qy   4825  AAGGCCAGTGGGAGGGGGACTGGGCCAGGTGGGCCCGTCCAGCAGCTTCC  4884

Db   1577  CCTGCCTTAATGTGACATGAGGCCCATTCTCTCTTTGAAGAGAGCAGTCAACATTCT  1636
           |||||  |  ||||||||||| |||||||| | ||  || |||||||| ||||||||||
Qy   4885  CCTGCCTCG-TGTGACATGAGGCCCATTCTCACTCT--GAAGAGAGGGTCAGTGTTCT  4941

Db   1637  TAGTAGTGGTTCTGTTCTATTGGATGACTTTGTCTATTGTTTTCCTTTTGAA  1696
           |||| || |||||||||||||||||||  | || || |||||| |||| ||||
Qy   4942  CAGTAGTAGTTTGTTCTGTTGGACTTGGAGATTTATCTTTGTTTGTTTTGGAA  5001

Db   1697  TTGTTCAAATGTTTCTTTTAATGGG-TGGTTGAATGAACTTCAGCATTCAAATTTATGAA  1755
           ||||||||||||||||| ||| ||| |||||||| |||||||||||| | ||| |||||||
Qy   5002  TTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAA  5061

Db   1756  TGACAGTAGTCAACATAGTGCTGTCTTTATATAGTTGGATAACTCTTGTTTTGTTTTAT  1815
           |||| ||  ||||| || ||||| | |||| |||||  |||| | |||| |||| |||||
Qy   5062  TGACAGCAGTCACACA--GTTCTGTGTATATAGTTGGTAAGAGTCTTGTGTTTTAT  5119

Db   1816  TCAGATTGGGAAATCCATTCCATTCAGATTTCAGTCTATGGAGGCACA-TAGTTACAGCAGTGAA-TA  1873
           |||||||||||||||||||| ||||| ||||| ||  | || ||||  |||| ||  ||||
Qy   5120  TCAGATTGGGAAATCCATTCCATTCTATTTGTGAATTGGGATAATAACAGCAGTGGAATAAGTA  5179

Db   1874  AGTATTCATTT-AGAAAGTGAA-TGAGC-AGTAAAAACTGATGACATAAAACTAAAA  1930
           | || ||||    | ||||||| |||| |||| ||||| |||||||| |  |||||||
Qy   5180  CTTAGAAAATGTGAAAAATGAGCAGTAAAAATGAGATAAAATAGAACTAAAGAATTAAGA  5239

Db   1931  GATATTTAATTCTTGC-TTATAC-TCAGTCTATTCGGTAAAATTTTTTTAAAAAATGTG  1988
           |||| || ||||   |  |||| ||||||| || | |||||||||| |||  |||||||
Qy   5240  GATAGTCAATTCTTGCCTTATACCTCAGTCTATTCGTAAAATTTTTA--AAGATATATG  5297

Db   1989  CATACCTGGATTTCCTTGGCTTCTTGGTGAGAAATGCTGAGAAGCGCATCAAAATT  2048
           ||||||||||||||||||||||||  |||||||||| ||||||| |||||||||||
Qy   5298  CATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAATGTAAGAAATTAAATCTGAAT  5357

Db   2049  TTCTCCCTGTTCCCTTTTCATTTATTCTTATTGTCTGTGGAAGGC  2108
           ||| |||||||||| ||| || ||| |||||||||||||||||||
Qy   5358  TTCTTCCTGTTCACTGGCTCCTTTTCCATGCACTGAGCATCTGCTTTTTGGAAGGC  5417

Db   2109  CCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTACCCACCAGGGTAGTA  2168
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Qy   5418  ||||||||  |||||||  ||||||||                        ||  ||||||||  ||||||| ||||  |||
           CCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTA 5477
Db   2169  AAGTCTAGGAGGAGCCAGCAGTCATATAATTAAGGTGGAGAAGATGCCCTCTAA-GATGTAG 2224
           |||||||||| ||||||  ||||||| |||| ||||||  ||||||| |||||||  ||||||
Qy   5478  GAGTCTAGGAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534

RESULT   9
LOCUS        I36926        1640 bp    DNA              PAT    21-APR-1997
DEFINITION   Sequence 11 from patent US 5612201.
ACCESSION    I36926
NID          g2084886
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 1640)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 11 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1..1640
                     /organism="unkown"
BASE COUNT    380 a    402 c    457 g    401 t
ORIGIN

Query Match             14.3%;    Score 811; DB 25; Length 1640;
Best Local Similarity   81.7%;    Pred. No. 0.00e+00;
Matches 1257;  Conservative    0;  Mismatches 248;  Indels  33;  Gaps  15;

Db    107  GCCAGTGGGTCTCCATTGCCAGTCCTCGCCACACTCCCGCCGTGTGCCTTGCCCTGACCAGAG 166
           |||  ||||||||  |||||||||||||||||||  |||||| |||||  |||||||| ||||
Qy   3816  GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875

Db    167  TCATCATGCCTCTTGAGCAGAGAGTCAGCACTGCAAGCTGCAAGAGCCTGAGGCC 226
           ||||| |||| |||||||||||||||||||||||||||  |||||  ||||||||
Qy   3876  TCATCATGTCTCTTGAGCAGAGAGAGTCTGCACTGCCAAGCTCCAAGCTCCTGAGGGCCTC 3935

Db    227  GAGGAGAGGCCCTGGGGCCCTGGTGGGTGCGGCCAGGCTCCTGCTACTGAGGAGCAGGAGGCTG 286
           |  ||||||||||||||||||| |||||| || ||||||  ||  ||     |  |   |
Qy   3936  AACAAGAGGCAACCCAGTGAGGGTTCCAGCGGTGTGCAGGCT---GC--C-----A-C------CT- 3977

Db    287  CCTCCTCCTTCTACTCAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCCAGTCAC 346
           ||||||||| -||||| | |||||||||||||||||||   |||||||| |||| |||
Qy   3978  CCTCCTCCTCT-C--CCTCTGGTCCTCGGGAGCACTCGGAGGAGGTGCCCACTGCCTGGGGTCAA 4034

Db    347  CAGATCCTCCCCAGAGTCCTTCAGGGAGGCCTCCAGCCTCCCAGCCATTGAACTACCCTC 406
           ||||||||| ||||||||||||||  ||||| || ||||||||||||  ||||||||||||
Qy   4035  CAGATCCTCCCCAGAGTCCTTCAGGGAGGCCTCCGCCTTCCAAGCCATCAACTTCAACTC 4094

Db    407  TCTGGAGCCAATCCTATGAGGAGGTCCAGCAGGACTCCAGCAACCAAGAGAGGAGGGCCAAGCACCTTCC 466
           |||  || ||  ||||||| | |||||| |||||| |  ||||||||||||||||| |||  |||||||
Qy   4095  GACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCAGTGCAGAGGAGGAGGGCCAAGCACCCTCT 4154

Db    467  CTGACCTGGAGTCCGAGTCCAAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTCATT 526
           | ||||||||||| | ||||||||||||||  ||  ||||||||| |||||| ||||||||
Qy   4155  GTATCCTGGAGTCTTGTTCCGAGCAGTAATCACTAAGAGGTGGCTGATTTGGTTGGTT 4214

Db    527  TTCTGCTCCAAGTAGTCGAGTATCGAGCGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG 586
           ||| |||||  ||  ||||  |||||||||||  |||||||||||||||||||||||||||||
Qy   4215  TTCTGCTCCCTCAATATCGAGCGAGCCAGCCAGTGCACAAAGGCAGAAATGCTGGAGAGTG 4274

Db    587  TCGTCGGAAATGGCAGTATTTCTTTCCTGTGATCTTTCCAGCAACGCTTCCAGTTCCTTGC 646
           ||| | |  ||  |||  ||||  |||||||  ||   ||||| |||||| |||||||||||
Qy   4275  TCATCAAAAATTACAAGCACGTGTTTTCCTGAGATCTTCGGCCAAAGCCCTCGAGTCCTTGC 4334

Db    647  AGCTGGTCTTTGGCATCGATGGAAGTGGACCCCATCCAGCGGACCACTTGTACATCTTTG 706
           |||||||  ||| ||||||  ||  |||  |  ||||||||  ||||||  |  |||||||
Qy   4335  AGCTGGTCTTTGCCATTGACGTGAAGGAGCAGCAGCACCCCGCACCCCCACTCCTAGTCCTTG 4394
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Db    707  CCACCTGCCTGGCCTCCTCCTACGATGGCCTGCTGGGTGTCACAATCAGATCATGCCCAAGG 766
           ||||||||  |||  |||||||||||   |||||||||| ||||| |||||||||||||||
Qy   4395  TCACCTGCCTAGGTCTCTCCTATGATGCCGTGCTGCTCGGTGTATAATCAGATCATGCCCAAGA 4454

Db    767  CAGGCCCTCCTGGTGATAATCGTCCTGGCCCATAATCGCAAGACTGTGCCCCTGAGG 826
           |||||||| |||||||  ||| ||||| |||||| |||| |||||||||||||||||
Qy   4455  CAGGCCTCCTGGTGATAATCGTCCTGTCCCATGATGGCCCATGTCATGCTCCTGAGG- 4514

Db    827  AGAAAATCTGGAGGAGCTGAGTGTGTTGAGAGCTGTTTGAGGGAGGAAGACAGTATGT 886
           ||  |||||||||||||||| ||||||||| |||||||||||||||||||||||||||
Qy   4515  AGGAAATCTGGAGGAGCTGAGTGTGATGGTGAGCAGTGTATGTGGTCTTCCTGGTGCCT 4574

Db    887  TGGGGGATCCCAAGAAGTGCTCACCCACCACTACTGGAGTAGCCT 946
           ||  |||  |||||||||||| ||||||||||  |||||||||| -
Qy   4575  ATGGGAGCCACCAAGAAGTGCTCACCCACCACTACTGGAGTAGC- 4633

Db    947  GGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAATTCCTGTGTGGGGTCCCAAGGGCCCTCG 1006
           ||||||||||||||||||| |||||||| ||||| ||||||||||||||||||||||||||||
Qy   4634  GGCAGGGTCCGGACAGTGATCCCGCACCTATGAGTTCCTGTGTGGGGTCCCAAGGGCCCTCG 4693

Db   1007  TTGAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCACA 1066
           ||||||||||||||||  |||||||| ||||||||||||||| ||| |||   |  |||||
Qy   4694  CTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCT 4753

Db   1067  TTTCCTACCACCCTGCATGAGTGGGTTTGAGAGAGGGGGAAGAGTGAGTCTGAGACAC 1126
           ||  ||  ||| ||  ||  |||  ||  | | |||||||| | ||||||||| ||||||
Qy   4754  TTTTCTTCCATCCCTGCGTGAAGCAGCTTGACGGAGAGGAGCAGCAGGAGGAGTCTGAGCAT 4813

Db   1127  GAGTTGCAGCCAGGCCAGTGGGAGGGGTCTGGGCCAGTGCACCTTCCGGGCCGCCATC 1186
           |||||||||||||||||||  ||||||| |||||||||||||||||||||| |||| |
Qy   4814  GAGTTGCAGCCAGGCCAAGGCCCAGTGGGGAGGGGACTGGGCCACCTTCCAGGCCGCGTC 4873

Db   1187  CCTTAGTTCCACTGCCTCTGCACGTGAGGCCCATTCTCCACTCTTGAAGCGAGCAG 1246
           || ||||  |||| |||| ||||  |||  |||  |||||||||| --||||||||||
Qy   4874  CAGCAGCTTCCCCTGCCTCGTGTGTGACATGAGCCCATTCCTCTTCACTCT--GGAAGAGCGG 4931

Db   1247  TCAGCATTCTTAGTAGTGGTTTCTGTTCTGTTTGAGACTTTGAGATTATTCTTTGTTT 1306
           |||| | ||||  ||||||  || || | |||  ||||  |||||  ||  |||||||||
Qy   4932  TCAGTGTTCTCAGTAGTAGGTTTTCTGTTCTTGGTTGGTGACTTGGAGATTTTATCTTTGTTC 4991

Db   1307  CCTGTTGGAGTTGTTCAAAATGTTCCTTTT-AACGGATGGTTGAATGAGCGTCAGCATCCA 1365
           ||| | ||||||| || |  ||||  ||||  | |  ||  |||||| ||||  |||||||
Qy   4992  TCTTTTGGAATTGTTCAAATGTTTTTTTTTTTAAGGGATGGTTGAATGAGTTTCAGCATCCA 5051

Db   1366  GGTTTATGAATGACAGTAGTCACACATAGTGCTTGTTTATATAGTTTAGGGTAAGAAGTCT 1425
           ||||||||||||||||||| ||||||  |||| || ||||||| ||  |||||||| |||||
Qy   5052  AGTTTATGAATGAACAGTCAGTCACACA--GTTCGTGTATATAGTTTTAAGGGTAAGAGTCT 5109

Db   1426  TGTTTTTTACTCAAATTGGAAATCCATTCCATTTGTGACATAATAATAGCA 1485
           |||| ||||  | |||||||||| ||  |||  | |||||| |||||||| |
Qy   5110  TGTGTTTTATTCAGATTGGGAAATCCAGTTCTATTTTGTGAATTGGGA--TAATAACAGCA 5167

Db   1486  GTGGTAAAAGTATTGCTTAAAATTGTGAGCCGAATTAGCAATAAACATACAGATAACT 1545
           |||  | ||||  || ||| |   | ||||||||  | || |  ||||  ||||| |||||
Qy   5168  GTGGAATAAGTACTTAGA-AATGTGAAAAATGAACAGTAGAAAAATAGATGAGATAAAGAACT 5226

Db   1546  CAAGAAATCAAAAGATAGTTGATTCTTGCCTTGTCACTCAATCTATTCTGTAAAAATT--- 1602
           | |||  |||| ||| |  |||  ||  |||  |  ||| |||  || ||||| ||||| 
Qy   5227  AAAGAAATTAAGAGATAGTTCAATTCTTGCCTTTATACCTCCAGTCTATTCTGTAAAAATTTTT 5286

Db   1603  AAACAAATATGCAAACCAGGATTTCCTTGACTTCTTTG 1640
           |||| || | |||| ||||||| || ||||||||||||
Qy   5287  AAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG 5324

RESULT  10
LOCUS        I36930        1068 bp    DNA              PAT    21-APR-1997
DEFINITION   Sequence 15 from patent US 5612201.
ACCESSION    I36930
NID          g2084890
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
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Thu Apr 9 08:15:24 1998

US-08-190-411A-1.rge

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Db  841  CTTGGAGATTTATTCTCTGTTCCTTTACAATTGTTGAAATGTTCCTTTT-AATGGATGG  899
              IIII IIIIIIIII IIII  IIII  IIII IIIIIIIIIIIIIIIIIIII  IIIIII
Qy  4971 CTTGGAGATTTATTCTTGTTCCTTTGTTCCTTTGGAATTGTTCAAAATGTTTTTTTTTTAAGGGATGG  5030

Db  900  TTGAATTAACTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATGCTGTTAATAT  959
              IIIIIIIIIIIIII IIIIIIIIIIIII IIIIIII IIIIIIIII IIIIIIIIIIIIII
Qy  5031 TTGAATGAACTTCAGCATCCAAGTTTATGAATCGTAGTTAATGACAGCAGTCACACAGTTCTGTGTATAT  5090

Db  960  AGTTTAGGAGTAAGAGTCTTGTTGTTTTTATTCAGATTGGGAAAATCCGTTCTATTTGTGAA  1019
              IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  5091 AGTTTAAGGGTAAGAGTCTTGTGTTTTATTCAGATTGGGAAAATCCATTCTATTTTGTGAA  5150

Db  1020 TTTTGGACATAATAACAGCAGTGGAGTAAGTATTAGAAGTGTGAA  1065
              II  IIII  IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  5151 TT-GGGA--TAATAACAGCAGTGGAATAAGTAACTAGAAATGTGAA  5193
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RESULT 11
LOCUS   I36936   1412 bp   DNA   PAT
DEFINITION   Sequence 21 from patent US 5612201.   21-APR-1997
ACCESSION   I36936
NID   g2084896
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
             1 (bases 1 to 1412)
REFERENCE   1 (bases 1 to 1412)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 21 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..1412
                     /organism="unknown"
BASE COUNT   324 a   402 c   393 g   293 t
ORIGIN

Query Match   11.4%;   Score 645;   DB 25;   Length 1412;
Best Local Similarity 78.7%;   Pred. No. 0.00e+00;
Matches 1103;   Conservative   0; Mismatches 266;   Indels 32; Gaps 18;

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Db  1    TCTGAGACAGTGTCCTCAGTCGCGAGACGAGGAGACCCAGGCAGTGTCAGCAGTGAAG  60
              IIIIIIIIIII IIIIIIIIIIIIIII IIIIIII I IIII IIIII IIIIIIIIIIIIIII
Qy  3459 TCTGAGACAGTATCCTCAGTCACAGAGCAGGGGATGCAACCTGCCCCAGCACACATGGGACC  3517

Db  61   GTGAAGTGTTCACCCTGAATGTGCACCAAGGGCACCAAGGGCCCACCCACCGCCACCATAGGACT  120
              IIIIIIIIIIIIIIIIIII  I II IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  3518 -TG--T--TTG-CCCTGAATGCACACACCCACCCACCCACCCACCGCCACCATAGGACT  3571

Db  121  CCATAGCACCTGGCCCCCCATTCCCCTACTGTCATCAGAGCCTTGATCTCTGCAGGCT  180
              III IIII IIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  3572 CCACAGAGTCTGGCCTCAC-CTCCCTACTGTCAGTTCCTGTAGAATCGACCTCTGCTGGCC  3630

Db  181  AGCTGCACCCTGAGTAGCCCCTGCACTTCCTCCCTCCTTCAGGTTCTC--GGGACAGGCTAACC  238
              IIIIIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIII II IIIIIIIIIIIIIIIII
Qy  3631 GGCTGTACCCTGAGTA-CCCTCTCACTTCCTCCCTCCTTCAGGTTTTCAGGGGACAGGCCAACC  3689

Db  239  AGAGGACAGGAGCCCCAGAGAGGCCCCAGGCCACCACTGACGA--AGAACCTGTAAGTCAG  296
              IIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIII
Qy  3690 CAGAGGACAGGAGGATTCCCTGGCCCGAGGCCACAGAGCACCAAGGAGAAGATCGTAAGTAGG  3749

Db  297  CCTTTGTTAGAACCTGCAAGGTTCGTTCCTGTCCATGCTGAAGTCTCTCACACTCCCTCT  356
              IIIIIIIIIIIIIIIIIIIIIII IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  3750 CCTTTGTTAGAGTCCAAGGTTCAGTCGCCTCCGGTCTCCAGCGCCTCCACCACTCCCTCTCT  3809

Db  357  CCCCAGGCCTGTGGGTCTCCATCGGCCAGCTCCTGCCAGCCTCCTGCCCCTGA  416
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  3810 CCCCAGGCCTGTGGGTCTTCATTGCCCACTGGAGTCGCCTCTGCCTGCTGCCCTGA  3869

Db  417  CCAGAGTCATCATGTCTCTGAGCAGAGAGAGTCCCACTGCAAGCCTGATGAAGACCTTG  476
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  3870 CGAGAGTCATCATGTCTCTGAGCAGAGAGAGTCGCACTGCAAGCCTGAGGAAGAGCCTTG  3929
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REFERENCE   1
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 15 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..1068
                     /organism="unknown"
BASE COUNT   258 a   222 c   302 g   286 t
ORIGIN

Query Match   12.0%;   Score 683;   DB 25;   Length 1068;
Best Local Similarity 84.6%;   Pred. No. 0.00e+00;
Matches 902;   Conservative   0; Mismatches 153;   Indels 11; Gaps 7;

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Db  1    GGGGCCAAGCACCTGCCCTGCAGCGAGTCCTTGTTCCGAAGCACTCAGTAACAAGGT  60
              IIIIIIIIIIII  I  I IIIIIIIIIII I  IIIIIIIIIIII II IIIIIIIIIII
Qy  4138 GGGGCCAAGCACCTCCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGT  4197

Db  61   GGATGAGTTGGCTCATTTCTGCTCCGCAAGTATCGAGTCACTATCGAGCCAAAAGGC  120
              II  IIII I IIII  IIIIII IIIIIII IIIIIIIIIII II II IIIIIIII
Qy  4198 GGCTGATTTGGTTGGTTTCTGCTCCTCCTCAAATAATCGAGCCCAAAATCCACAAAAGGC  4257

Db  121  AGAAATGCTGGAGAGAGTCATCAAAAAATTACAAGGCTGCTTTCCTTGTGATCTTCGGCAA  180
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4258 AGAAATGCTGGAGAGAGTGTCATCAAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAA  4317

Db  181  AGCCTCCGAGTCCGGATGATCTTTGGCATTGACGTGAAGAGGATGGACCCCCGCCAG  240
              IIIIIIIIIIIII IIII  II IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4318 AGCCCTGAGTCCTGCAGCTGGTCTTTGCAGTGGTTGACGTGAAGGAAGCAGACCCCACCGG  4377

Db  241  CAACACTACACCCTTGTCACCTGGCCTTTCCTATGATGGCCTGCTGCTGGGTAATAA  300
              II II IIIII IIIIIIIIIIIII II IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4378 CCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTAGGTCTCCTGGGTGGGTGATAA  4437

Db  301  TCAGATCTTTCCCAAGACACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGG  360
              IIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4438 TCAGAATCATGCCCAAGACACAGGCTTCCTGATATAATTGTCCTGGTCATGATTGCAATGGAGGG  4497

Db  361  CGACACGCCCTGCGGAGGAGAAATCGGGAGGAGCTGGGTGCGATGGGTGTATGATGG  420
              IIIIIIIIIIII II IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4498 CGGCCATGCGCTCCTGGAGGAGAAATCGGGAGGAGCTGGGTGCGATGGGTGTATGATGG  4557

Db  421  GAGGGAGCACACTGTCTATGGGAGGCCAGGAAACTCCTCACCCAAGAGTTGGGTGCAGGA  480
              IIIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4558 GAGGGAGCACAGTGCCTATGGGAGGCCAGCCAAGGCCTGGGGGACTGGGCCAGTGCA  4617

Db  481  AAACTACCTGGAGTACCGGCAGGTACCCGGCGTAATCCTGCGCGCCTATGAGTTCCTGTG  540
              IIII IIII IIII  II IIIIII IIII  IIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4618 AAAGTACCTGGAGTAC-GCGCCAGTGCCGGACAGTGGGAGTTCCCTATGAGTTCCCTGTG  4676

Db  541  GGGTCCAAGGGCTCCTGCGTCGGAAACCAGCTATGTGAAAGTCGGAGCTTCCTGGACAGT  600
              IIIIIIIIIIIIIIIII IIIIIIII III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4677 GGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTGAATGTCTTGAGTGTGATCAAGGT  4736

Db  601  CAATGCAAGAGTTCGCATTGCCGATACCACCCATCCCAAGGCTTGTGGGAAGGGAGGAGGA  660
              IIII  II  IIIIIIIII II  IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4737 CAGTGCAAGAGTTCGCAGAGTTGCAGCCAAGGCCTTGAAGCAGCTTGAGAGGAGGAGGA  4796

Db  661  AGAGGGAGGTCTGAGCATGACATTGCAGCCAGCAGTTCCCTGCCTCGTGTAACATGAGGCCCATTCTT  720
              IIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4797 AGAGGGAGGTCTGAGCATGAGTGCAGCCAGCAGTGCCCTGGGCCACTGGGCCAGTGCA  4856

Db  721  TGCATCTAAACAGCCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAACATGAGGCCCATTCTT  780
              IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy  4857 C-CTTCCAGG-GCGCGCCTCCAGCAGCTTCCCTTGCCTCGTGTGACATGAGGGCCCATTCTT  4914

Db  781  CACTCCTGTTGAAGAAAATAGTCAGTTGTTCTTAGTAGTGGGTTTCTATTTTGTTGGATGA  840
              IIIIII  I  IIIIII  IIII IIIIIIIIIIIIIII II IIIIIIIIIIIIIIII
Qy  4915 CACTCTG---AAGAGAGCGGTCAGTGTTCTTCAGTAGTAGGGTTTCTTCATTGTTGGGTGA  4970
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ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1947)
AUTHORS     De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
            Chomez,P.
TITLE       Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
JOURNAL     Patent: US 5612201-A 19 18-MAR-1997;
FEATURES    Location/Qualifiers
    source  1..1947
            /organism="unknown"
BASE COUNT  457 a     499 c     538 g     453 t
ORIGIN

Query Match        10.8%;    Score 611;   DB 25;    Length 1947;
Best Local Similarity  79.9%;     Pred. No. 0.0e+00;
Matches 1070;   Conservative   0;   Mismatches 231;   Indels 38;   Gaps  19;
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Db      1  TGAATGGACACAAGGGCCCCACACTCCCAGAACACAAGGGACTCCAGAGAGCCCAGCC    60
           |||||| ||| ||||||||||||||  || ||  ||| |||| |||||||  ||||| |
Qy   3527  TGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGCC  3586

Db     61  TCACCTTCCTACTGTCAGTCCTGCAGCCTCAGCCTCGCTGGCCGGCTGTACCCTGAGG   120
           ||||||||  | ||||||||||||| || ||||| |||  |||  | || |||||||| 
Qy   3587  TCACCT-CCCTACTGTCAGTCCTGTAGAATCGACCTCGCTGCTGCCGTGTACCCTGAG-  3644

Db    121  TGCCCTCTCCACTTCCTTCCTTCAGGTTCTCAGCCGACAGGCCCGGCCAGGAGTCAGAGCC   180
           |||||| | |||||| ||||||||||||||| | ||||||||||||| || || ||| |
Qy   3645  TACCCTCTCCACTTCCTTCCTTCAGGTTTCAGGGCACAGGCCAACCCAGAGACAGAGATTC  3704

Db    181  CCAGGAGGCCCCAGAGGAGCACCGAAGGAGAGAATCGTAAGTAGGCTTTGTTAGGGCC   240
           || ||||||||| |||||||||||| ||||||||||||||||||||||||||||| |
Qy   3705  CCTGAGGGCCACAGAGGAGCACC-AAGGAGAGAATCGTAAGTAGGCCTTTGTTAGAGTC  3763

Db    241  TCCAGGGCGTGGTTCACAAATGAGGCCCCCACAAGCTCCTCTCTCTCCCAGATCGTGG   300
           || |||||| | ||||||||||||||| ||||||| ||||||||||||||||||||
Qy   3764  TCCAAGGTTCAGTTCTGCAGGCTGAGGCCTCGCAGCCTGCCTGCCTGCCTGACGAGAGTCAT  3823

Db    301  GTTCCCCCATCCCAGTCGTGCTGCCCAGCTGCTGACCAGAGTCAT   360
           ||| | || | |||||||| ||||| |||| ||||| |||||||
Qy   3824  GT--CTTC--ATTGCCCAGCTCCTCCCACACTCCTGCCTGCTGCCTGCTGACGAGAGTCAT  3879

Db    361  CATGTCTTCTGAGCAGAGGAGTCAGCACTGCAAGCCTGAGGCCCAAGGA   420
           ||||||| | |||||||||||| ||| ||| | || |||||||| || |
Qy   3880  CATGTGTCTCTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAGCCTTGAGGGCCCCA--A  3937

Db    421  CAGGAGGCTTGGGCCTGGTTGGGTGCGCCAGCGTCCCGGAGCACGAGGCTGCC   480
           || |||||||| || || |||| | | || ||| ||| |||||||| |||
Qy   3938  CAAGAGGCCCTGGGCCTGGTGTGTGGCAGGCT---GCCACCT-----C----CT-CC  3982

Db    481  TCCTCCTCACTCTGATTGAAGGCACCCTGGAGGTGCCTGCTGGGTCCCCCAGT   540
           |||||| | |||| || ||||| ||||||||||||||| || ||| | |||||
Qy   3983  TCCTC--TC-CTCTGGTCCTGGGCACCCTGGAGGTGCCTGCCACTGCTGGGTCCACAGAT  4039

Db    541  CCTCCCGAGTC-TCAGGGTTCCTCTTTTCCTGAGCCATCAGCAACACTCTATGG   599
           ||| | ||||| | | |||||| | || ||| ||||| |||| || ||| ||
Qy   4040  CCTCCCAGAGTCCTCAGGGAGCCTCGGCCTTCCAGCAGCGGCCAAGAGGGAGGAGGAGTTC  4099

Db    600  AGCCAATCAGTGAGGGCACCAGCAGGGCCACCACCTAGACACAC   659
           | || |||||||||| || ||||| |||| || || ||||||| |
Qy   4100  AGGCAACCCAGTGAGGGTTCCAGCACCCGTGAAGAGGAGGAGGGCCAAGCACCTCTTGTATC  4159

Db    660  CCCGCTCACCTGG--CGTCCTTGTTCCAATGGAAGGTGGCTGAGTTGGTTCGCTTCCTG   717
           ||| | |||||||  ||| |||||| | | || ||||||| || || ||| || | |||
Qy   4160  CTGGAGTCCTTGTTCCGACAGTAATCACTAAGAGAGTGGCTGATTTGGTTGGTTTTCTG  4219

Db    718  CTGCACAAGTATCGAGTCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGACAGTGTCATC   777
           || ||  || ||| |||||||||| || ||| || ||||||||||||||||||||| ||
Qy   4220  CTCCTCAAATATCGAGCCAGGAGCCAGGCACAAAGGCAGAAATGCTGGAGAGTGTCATC  4279

Db    778  AAAAATTACAAGCACTAGTTTCCTTGTGATCATGCAAAGCCTCATATGGCAAAGTGCATGCAGGT   837
           |||||||||||||||||||||||| ||||  || || ||||||||||| |||| || || |
Qy   4280  AAAAATTACAAGCACTGTTTTCCT-GAGATCTTCGGCAAAGCCTCTGAGTCCTTGCGCACT  4338
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Db    477  AAGCCCAAGGAGGAGGACTTGGGCCTGATGGGTGCACAGGAGAACCCAGAGGCGAGGAGGAGG   536
           | |||||||||||||||| || |||| ||||||||| || ||| || |   ||||   ||||
Qy   3930  AGCCCCAACAGAGAGGGCCCTGGGCCTGGTGTGTGGCAGGCTGCCACCTCCTCCTCCCTCTC  3989

Db    537  AGACTACCTCCTCCTCTGACACGCAAGGAGGAGGAGAGGTGTCTGCTGCTGGTCATCAAGTC   596
           || ||  || |||  |    || |||  |||| |||| || | || ||||| |||||||||
Qy   3990  ---CT--CTGGTCCTGGG-CACCCTGGAGGTGCCTGCTGGGTCCACAGATC-CAACAGATC  4040

Db    597  CTCCCCAGAGTCCTCAGGGAGGCGCTTCCTCCTCCATTTCCGTCTACTACACTTTATGA   656
           ||||||||||| | | | |||||| || ||| || || |  ||  ||||| || | |
Qy   4041  CTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCACTACTACCATCAACTTCACTCGACAGA  4100

Db    657  GCCAATTCGATGAGGGCTCCAGCAGTCAAGAGAGAGAGGAGAGCCAAGCTCCTCGGTCGACC   716
           | ||   |  | || ||| || |||  ||| || || || |||| || ||||  ||| |
Qy   4101  GGCAACCCAGTGAGGGTTCCAGCACCCGTGAAGAGGAGGAGGGCCAAGCACCTCTTGTATC-  4156

Db    717  CAGCTCAGCTGGAGTTCATGTTCCAAGAAGCACTGAAAATTGAAGGTGGCTGAGTTGGTTC   776
           |||| |||| |||| |   | |||||||| || || |   ||||  | ||||| || ||
Qy   4157  -A--TC--CTGGAGTCCTTGTTCCGACAGTAATCACTAAGAGAGTGGCTGATTTGGTTG  4211

Db    777  ATTTCCTGCTCCACAAATATCGAGTCAAGGAGCCGGTCACAAAGGCAGAAATGCTGGAGA   836
           ||| |||||||| |||||||||||| || || ||| |||||||||| |||||||||| ||
Qy   4212  GTTTTCTGCTCCTCAAATATCGAGCCAGGAGCCAGGCACAAAGGCAGAAATGCTGGAGA  4271

Db    837  GCGTCATCAAAAATTACAAGCACTAGTTTCCTGTGATCTTCGGCAAAGCCCTCCGAGTTCA   896
           | ||||||||||||||||||||||||| ||||  |||||||||| || || || | || |
Qy   4272  GTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCT  4331

Db    897  TGCCAGTTGATCTTTGGCACTGATGTGAAGGAGGGTGACCCCGGCCACTCCTACATCC   956
           || ||||| |||| ||||| |||| |||||| | || |||  |  ||||| || |
Qy   4332  TGCAGTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGCCACTCCTATGTCC  4391

Db    957  TTGTCACTGCTCTGCTTGGCCTCTGTGCGATAGCATGCTCGGTGATGGTCATAGCAGTCCCA  1016
           || |||||| ||| | ||| | || |||||| || || |||| ||  | || || ||||||
Qy   4392  TTGTCACTGCTTAGGTCTCCTATGATGGGCCTGCTGGGTGATAATCAGATCTGGGTGCTGG  4451

Db   1017  AGGCCGCCCTCTGATCATTGTCCTGGGTGTGATCTAACCAAAGACAACTGCGCCCCTG  1076
           | | | |||| ||| ||  || |||| | | ||| |||||| || ||| | | |||
Qy   4452  AGAGAGGCTTCCGTCGCACGTGATCGGGTCATGATTGCAATGGAGGCGGCCAGCTCTG  4511

Db   1077  AAGAGGTTTATCTGGAAGCGGTTGAGTGTGAGAGTGTATGTTGGGAGGAGCACATGT  1136
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Qy   4512  AGGAGAAATCTGGGAGGAGCTGAGTGTGAGTGTGATGGGGAGGAGCAGAGCACAGTG  4571

Db   1137  TCTACGGGGAGCCAGGAGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAACTACCTGGAGT  1196
           |||  || ||| ||||| ||||||| || || || || |||||| |||| |||||||||
Qy   4572  CCTATGGGAGCCAGGAGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGT  4631

Db   1197  ACCGGGCAGGTGCCCGGCAGTGATCCTGCGCCACTACGAGTTCCTGTGGGGTTCCAAGGCCC  1256
           || |||| ||| || | | |||| || |||||||| |||| ||| ||  ||| |||||||
Qy   4632  AC--GGCAGGTGCCGCGACAGTGATCCTGCTATGAGTTCCTGTGGGGTTCCAAGGGGCCC  4690

Db   1257  ACGCTGAAACCAGCTATGAGAAGGGTCATAAAATTATTTGGTCATGCTCAATGCAAGAGAGC  1316
           |||||||||| |  ||||| ||||  |   | ||||| || || || ||||| | ||||
Qy   4691  TCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTCATGCTCAGTGCAAGAGTTC  4750

Db   1317  CCATCTGCTACCATCCCTTTATGAGGAGGTTTCTGGAGGAGCAAGAGGGAGTCTGAG  1376
           |||| ||| || ||||  ||  | | |||| |   || |||||||| || ||||||
Qy   4751  GCTTTTTCTTCCTCCATCCCTGCCTGAGCAGCTTGAGCAGCTTTGAGAGAGGGAGTCTGAG  4810

Db   1377  CACCAGCCGCAGCCGCGGGGCCA  1397
           || || |  ||| ||||||||| |
Qy   4811  CATGAGTTGCAGCCAAGGCCA  4831
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RESULT  .12
LOCUS           I36934          1947 bp    DNA               PAT        21-APR-1997
DEFINITION      Sequence 19 from patent US 5612201.
ACCESSION       I36934
NID             g2084894
KEYWORDS        .
SOURCE          Unknown.
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Db  838 GATGTTGGCATTGACATGAAGGAAGTGGACCCCGC-GGCCACTCCTACGTCCTTGTCAC 896
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Qy 4339 GGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCCACCCACTCCTATGTCCTTGTCAC 4398

Db  897 CTGCTTCTTCCTCCTACAATGCCTGCTGGTGATGATGCAGAGCCCCGGAGACCCGG 956
        ||||| |||| ||| |||||||||||||||||||||||||| ||||| |||| ||||
Qy 4399 CTGCCTAGGTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGG 4458

Db  957 CCTTCTGATTATGGTCTTGACCATGATCTTAATGAGGGCCACTGTGCCCCTGAGGAGGC 1016
        | |||||||| | || ||| |  |||||||| ||||||||||||| ||||||||||||
Qy 4459 CTTCCTGATAATTGTCCTGGTCATGAATGGCCGGCGGCCCATGCCTCCTGAGGAGGA 4518

Db 1017 AATCTGGGAAGCGTTGAGTGTAATGG---TGTATGATGGGATGGAGCA--GTTTCTTTGG 1071
        ||||| |||||| |||| |||| |||    |||||||||| ||||||  |||||| | ||
Qy 4519 AATCTGGGAGGAGGACTGAGTGTGTGATGGAGGTGTATGATGGGGACACAGTGCCTATGG 4578

Db 1072 GCAGCTGAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAACTACCTGCAATACCGCCA 1131
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Qy 4579 GGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAAGTACCTGGAGTACGGC-A 4637

Db 1132 GGTGCCCAGCAGTGATCCCCGTGCTACCAGTTCCTGTGGGTCAAGGGCCCCATTGA 1191
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Qy 4638 GGTGCCCGACAGTGATCCCGCCTATGAGTTCCTGTGGGTCCAAGGGCCCCTTCGCTGA 4697

Db 1192 AACCAGCTATGTGAAAGTTCCTGGAGTAGTGCAGCCAGGGTCAGTACTAAAGAGAGCATTTC 1251
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Qy 4698 AACCAGCTATGTGAAAGTTCCTTGAGTAGTTGATCAAGGTCAGTGCAAGAGTTCCTTTTTT 4757

Db 1252 CTACCCATCCCTGCATGAAGAGGAGGCTTTGGGAGAGGAGAGAGAGAGTCTGAGCGAAGT 1311
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Qy 4758 CTTCCCATCCCTGCGTGAAGCAGCTTTGCAAGCAGTTCAGTGCAGGGAGAGTCTGAGCATGAGT 4817

Db 1312 TGCAGCCAGGGCCAGTGGG 1330
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Qy 4818 TGCAGCCAAGGGCCAGTGGG 4836


RESULT 13
LOCUS       I36935       1810 bp       DNA       PAT       21-APR-1997
DEFINITION  Sequence 20 from patent US 5612201.
ACCESSION   I36935
NID         g2084895
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1810)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J., De Smet,C. and
            Chomez,P.
  TITLE     Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 20 18-MAR-1997;
FEATURES    Location/Qualifiers
  source    1. .1810
            /organism="unknown"
BASE COUNT    402 a    463 c    508 g    437 t
ORIGIN

Query Match         9.9%;  Score 562;  DB 25;  Length 1810;
Best Local Similarity  79.3%;  Pred. No. 0.00e+00;
Matches 1146;  Conservative 0;  Mismatches 242;  Indels 57;  Gaps 33;

Db  100 TGTTTCCCTGTATGTATACCAGAGCCCCCTCTGGCATCAGAACAGCAGGAACCCCACAG 159
        || ||| | |||   |  ||||||||| ||||||| | ||||| |||||||||||| ||
Qy 3518 TGTTTGCCCTGGCGATGCACACCAGGCCCCCACCTGCCCCAGGACACATAGGACTTCCACAG 3577

Db  160 TTCCTGGCCCTACCAGCCTTTGTCAGTCCTGGAGCCTTGGCCTTCAGCAGGAGGCTGC 219
        |||||| | |||| ||||||| |||| |  | | |  ||||| || | |||||||| |
Qy 3578 AGTCTGGCCCTCACCT-CCCTACTGTCAGTGCTGTAGAATCGACCTCTGCTGCGGGCCGGGGT 3636

Db  220 ACCCTGAGATGCCCCTCTCAATTTCTCCTTCAGGTTCGCAGAGAACAGGCCAGCC---AGG 276
        | ||||||| |||||  ||||||| ||||| ||||| || ||||||||||||| |   |||
Qy 4684 AGGGCCCTGCGTCTGAAACCAGCTATGTGAAAGTCCTTGAAGTCCTTGATGGTCATTCAGTCAGTGCA 4743
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Left/lower column:

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Db 3637 ACCCTGAG-TACCCTCTCACTTCCTCCTTCAGGTTTCAGGGGGACAGGCCAACCCAGAGG 3695
        || | ||   |  |  |||||| |||| |||||||| |||||||||| || | ||| | |
Qy  277 A--GG-TCA--GGAGGCCCCAGAAGAGCACTGA--AGAAGACCTGTAAGTAGACACCTTTG 328

Db 3696 ACAGGATTCCCTGGAGGCCACAGGCACCCAAGGAGAAGAATCTGTAAGTAGGCCTTTG 3755
        || |||||||| ||||||  || |||||| |||||| || ||| |||||| |||||||
Qy  329 TTAGGGCATCCAGGGTGTAGTACCCAGTGAGGCCTCTGAGCCTCCGGCCTTCCTCTCCCCAG 388

Db 3756 TTAGAGTCTCCAAGGTCAGTTCTCAGCTGAGGCCTGAGGCCTCCACACTCCCTCTCCCCAG 3815
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Qy  389 GCCTGTGGTCTCAATTGCCAGTGCCCAGGTCCGGCCCACACTC-T-CCTGCTGCCCTGACCTGAG 446

Db 3816 GCCTGTGGTCTTCATTGCCCAGGTCCTTCCCACACTCTGCCTGCCTGCCCTGACGAGGAGA 3875
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Qy  447 TCATCATGCTTCTTGGCAGAGAGTCAGGGTCCCACTGCTGCAAGCCTGAGGAGGCCTTCAGGCGCC 506

Db 3876 TCATCATGTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAGGCCCTTGAGGCCC 3935
        |||| |||||||| | |||| ||||| ||||| |||||||||||||| ||||||||||
Qy  507 AAGGAGGAGCCACCAGGGCTTATGGATGTGCAGATTCCCACAGCTGAGGAGCAGAGGCTG 566

Db 3936 AACAAGAGGC--CCTGGGCCT--GG-TGTGT-G--TGC-AG-GCTGCC----CA----C- 3975
        || |||||||  | ||| | |  || || || |  |   || | ||     | |    |
Qy  567 CATCCTCCTCTACTCTGATCATGGGAACCCTTGAGGAGGTTGACTGATTCTGGGTCAC 626

Db 3976 C-TCCTCTCCTCCTCTGGTCTCTGGGTCCTCAAGGGCCCTTCCGCTCAA 4034
        | ||||||||| || ||||| |||| || || |||||| ||||||||||
Qy  627 CAAGTCCTCCCCAGAGTCCTGAGGGTGCCTCCTCTCCCGACTGTCACCGACGCACTC 686

Db 4035 CAGATCCTCCCCAGAGTCCCCAGAGCTCCCAGGGAGCCTTTCCCACATCAACTTCACTC 4094
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Qy  687 TGTGGAGCCAATCGATGAGGGTTCCAGCAGCAATGAGAGGGGCCAAGCACCTCCC 746

Db 4095 GACAGAGGCAACCCAGTGAGGTTCCAGCAGGTTCCAGCAGCCCGTGAAGAGGGGGCAAGCACCTCTT 4154
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Qy  747 CGGACCCAGCTCACCTGGAGTCCCTGTTCCGGGAAGCACTTGATGGCTGAGAAAGTGGCTGAGT 806

Db 4155 --GT---A--TC--CTGGAGTCCTGTTGTTCCGGACAGTAATCACTGGAGGTGGCTGTGATT 4205
        |  |  |  |  ||| || || |  ||||||||| || || ||||| |||||| ||| |||
Qy  807 TAGTTCGTTCGTCCTCCCGCCCCAAATATCAAATTAAGGAGCCGGTCACAAAGGCAGAAATGC 866

Db 4206 TGGTTGGTTTCTGCTCCTCCCAAATATCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGC 4265
        |||||||||||||||||||| ||||||||||| || || ||||| |||||||||||||||||||||
Qy  867 TTGAGAGTGTCATCAAAAATTACAAGAACCACTTCCTGATATCTTCAGCGAGAGATGGTAATGG 926

Db 4266 TGGAGAGTGTCATCAAAAATTACAAGAACACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTG 4325
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Qy  927 AGTGCATGCAGGTGATCTTTGGCCATTGATGTGAAGGAAGTGGACCCTGCCCGGCCCACTCCT 986

Db 4326 AGTCCTTGCAGGTGGTCTTTGGCCATTGTTTGGCAGTGGCAGGGAGCAGACCCCCACCTGTGATGATGG 4385
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Qy  987 ACATCCTTGTCACCTGCTTCACCTGGTGGTGATGATGCAGAGTA 1046

Db 4386 ATGTCCTTGTCACCTGCTTCACCTGGTGGTGGGTGATAATCAGATCA 4445
        | ||||||||||| |||||||||| ||||| ||| |||| ||| ||
Qy 1047 CGCCCAAGACCCGCCTCTCGATAATCGTTCCTGGCAGCCGCG 1106

Db 4446 TGCCCAAGACACCGGCCTTCCTGATAATTGTCCTGGTTGCAATGGGAGGGCCGCCATG 4505
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Qy 1107 CCCCGGAGGAGGCAATCTGGGAAGCCATTGAGTGTGATGGGGTGAGGAGGAG 1166

Db 4506 CTCCTGAGGAGGAAATCTGGGAGGAGGACTGAGTGTGATGGAGG--TGTATGGGGAGGAG 4564
        || ||||||||||||||||| | | |||| |||||| |||| ||  ||| || ||||||
Qy 1167 CACAGTGCTCATTGGAAGCTCAGGAAGTCTCACCCAAGAGTGGCTCCAAGAGAACTAC 1226

Db 4565 CACAGTGCCTATGGGGAGCCCAGGAAGCCTGCTCACCCAAGATTTGGTGCAGGAAAAGTAC 4624
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Qy 1227 CTGGAGTACCGGCCAGGGCCCGCCAGTCGATCCTGGCCTTCGTGTGGGTCCGTACGGGTCCA 1286

Db 4625 CTGGAGTACGGC-AGGTCCGGACAGTGATCCCGACCGCTATGAGTTCCTGTGGGGTCCA 4683
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Qy 1287 AGGGCCCTTGCTGAAACCAGCTATGTGAAAGTTCTTGAAGTCCTTGATGGTCAATGCA 1346

Db 4684 AGGGCCCTTGCTGAAACCAGCTATGTGAAAGTCCTTGAAGTCCTTGATGGTCAGTCAGTGCA 4743
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Db   1347  AGAGTTCGCATTTCTACCATCCCTGCGATGAACGACGGCTTTGGGAGAGGAGAAAGGAGTT  1406
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Qy   4744  AGAGTTCGCTTTTTTCTTCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGGAAG-AGG-  4801

Db   1407  TGAGCAGGAGTTGCAGCTAGGCCAGTAGGTTGTGGGAGGGCCTGGGCCCAGTGCA  1466
           |||| |||  |||| |||||||| |||| |||
Qy   4802  -GAGTCTGAGCATGAGTTGCAGCAA--GGCCAG--TGGGAGGGGACTGGGCCAGTGCA  4856

Db   1467  CGTTCCAGGGCCACATCCACCA-CTTTCCCTGC-TC-TGTTACATGAGGCCATTCTTCA  1523
           | |||||||| | |||||  |||  ||| || |||||| ||||||| |||||||||
Qy   4857  CCTTCCAGGGCCGCGTTCCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCA  4916

Db   1524  CTCTG  1528
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Qy   4917  CTCTG  4921


RESULT  14
LOCUS        I36938           1107 bp    DNA             PAT       21-APR-1997
DEFINITION   Sequence 23 from patent US 5612201.
ACCESSION    I36938
NID          g2084898
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 1107)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 23 18-MAR-1997;
FEATURES              Location/Qualifiers
     source           1..1107
                      /organism="unknown"
BASE COUNT      269 a    283 c    295 g    260 t
ORIGIN

Query Match      6.9%;  Score 392;  DB 25;  Length 1107;
Best Local Similarity  75.6%;   Pred. No. 2.39e-280;
Matches  838;  Conservative   0;  Mismatches 236;  Indels 35;  Gaps  17;

Db      1  AGAGAACAGGCCAACCTGGAGGACAGGAGTCCCAGGAGGAACCCAGAGGATCACTGGAGGA   60
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Qy   3674  AGGGGACAGGCCAACCCAGGAGGACAGGATTCCCTGGAGGCCACCCA-AGGA         3732

Db     61  GAACAAGTGTAAGTAGGCCTTTGTTAGATTCCATGGTTCATATCTCATCTGAGTCTGT  120
           |||||| || ||||||||| |||| || ||||| |||| |||| ||||| |||||||||
Qy   3733  GAAGATCTGAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTCAGCTGCTGAGGCCTC  3792

Db    121  TCTCACGGTCCCCTCTCCCCAGGC-TGTGGGGCCCCATCACCCCAGATATTTCCCCACAGT  179
           || ||| || ||||||||||||||| ||| |||| | |||||||||| ||||||
Qy   3793  TCACACACTCCCTCTCTCCCCCAGGCCTGTGGGTCTTCATTGCCCAGCCTCTGCCCACACT  3852

Db    180  TCGGCCTGCTGACCTAACCAGAGTCATCATGCCTCTTGAGCAAAGAAGTCAGCACTGCAA  239
           |||||||||||||| || |||||||||| |||||||||||||||| |||||||||||||||
Qy   3853  CCTGCCTGCTGCCGCCGAGAGTCATCATGCCTCTTGAGCAGAGCAGAGAGTCTGCACTGCAA  3912

Db    240  GCCTGAGGAAGCC-TTCAGGCCAGGAAGAGACCTGGGCCTGGGGTGCACAGGCTCT  298
           |||| |||| || ||||| ||||| | || ||||||||||| ||| | ||||| ||
Qy   3913  GCCTGAGGAGTTCCTCGGGGTCTTCCCAGAGGTCTCCAGGTGTGTGCAGGCTG-  3971

Db    299  CCAAGCTGAGGAGGAGCAGGAGGCGTGCCTTCTCTCACTACTCTGAATGTGGGCACTCTAGA  358
           ||||||  || ||||||||| ||  ||| || ||| |||| || |||||
Qy   3972  -C---C------CT-CCT-C--CTCCTCTCCGTCTGTGGCTCCTGGCACCCTGGA  4011

Db    359  GGAGTTGCCTGCTGCTGAGTCACCAAGTCCTCCAGGAAGAGTCCTTCTC  418
           |||||||| |||||||| |||||||| |||||| ||||||||||| ||
Qy   4012  GGAGGTCGCACCACTGCTGGGCTCAACAGATCCTCCAGGAGCCCTCCGCCTT  4071

Db    419  TCCCACTGCCATCGGATGCCATCTTTGGGACGCCATCTGATGAGGGCTTGGCAGCCCAAGA  478
           |||||| |||| |                ||| |  ||||||||
Qy   4072  TCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGA  4131

Db    479  AAAGGAGGGCCAAGTACCTGCCTCGACCTGATAGACCCTGAGTCCTTTCCCAAGATAT    538
           | ||||||||||| |||||   | | |||||||     |||  || | |||
Qy   4132  AGAGGAGGGGCCAAGCACCTCT--TG---T-AT--CCTGGAGTCCTTGTTCCAGCAGT   4182

Db    539  ACTACATGACAAGATAATTGATTTGGTTCATTTATT-CTCCGCAAGTATCGAGTCAAGGG   597
           | | ||||||||| ||||| |||||| ||| || ||  |||||||||||| |||||||||
Qy   4183  AATCACTAAGAGAGTGGCTGATTTGGTTTGGTTTCTGCTCCTCCCAAATATCGAGCCAGGGA   4242

Db    598  GCTGATCACAAGGCAGAAATGCTGGGGAGTGTCATCAAAAATTATGAGGACTACTTTCC   657
           || ||| || |||||| ||| ||||| |||| |||||||||| | |||| ||| ||||
Qy   4243  GCCAGTCACAAAGGCACAAAATGCAGAAATGCTGGACGTGTCATCAAAAATTACAAGCACTGTTTTCC   4302

Db    658  TGAGATATTTAGGGAAGGAGGCCTCTGCATGCAACTGCCTTCTTCTTTGGCATTTGGCATTGTGAAGA  717
           ||||| |  ||| || ||||||||| || |||| ||||| |||| | |||| | |||||| ||||
Qy   4303  TGAGATCTTCGGCAAAGCCTCTGAGTCCTGAGTCATTTTGCAGTCTGGTCTTTGCATTGTGACGTGAAGGA   4362

Db    718  AGTGGACCCCACTAGCCACTCCTATGTCCTATGCACCTCCCTGCACCTCTTATGATGG  777
           ||  |||||| ||| || || || |||| |||| || || || ||  ||| |||||||
Qy   4363  AGCAGACGTGACCCCCACCCGGCCACTCCTATGTCCTATGCCTCCTAGGTCTCCTATGATGG  4422

Db    778  CATCACAGTGTAATGAGCAGAGCATGCCCAAGTCTGGCCTCCTGATAAAGTCCTGGGTGT  837
           ||| |||||| | |  |||||| |||||||| || || ||||| |||| ||||||||||||
Qy   4423  CCTGCTCGGTGGTGATAATCAGATCATGCCCCAAGACAGCCTTCCTGATAATTGTCCCTGGTCAT  4482

Db    838  AATCTTCATGAGGGAACTGCATCCCTGAGAAGGTTATGTGGGAAGTCCTGAGCATTAT  897
           |||| |||||| ||||||||||||||| |||||| |||||| ||||||  |||||||
Qy   4483  GATTGCAATGAGGAGGCGGCCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGAT  4542

Db    898  GGGGGTGTATGCTGGAGGGAGCACTTCCTTGGGAGCGCCCAAGAGGCTCCTTACCCA  957
           || ||||| ||||||||||||| || ||| ||||||||| ||||||||| |||| |
Qy   4543  GGAGGTGTATGATGGGGAGGGAGCACAGTGCCATGGGGAGGAGCAGGAAGCTGCTCACCCA  4602

Db    958  AAATTGGGTGCAGGAAAAGTACCTGGTTGTACCGGCAGTGCCCGGCACGTGATCCTGCATG  1017
           | ||| || |||| || ||||||||| ||||| |||| ||||| ||| | |||| ||||
Qy   4603  AGATTTGGTGCAGGAAAAGTACCTGGAGTTAC-GGCAGGTGCCCGGAGTCCCGAGCACG  4661

Db   1018  CTATGAGTTCCTGTGGGGTCCAAGGGCCCACGTGAGCACCGAAGATGAAAGTTCTTGA  1077
           |||||||| ||||||| ||||| |||| ||| |||||| |||| | |||||| || |||
Qy   4662  CTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGCTGAAACCAGCTATGTGAAAGTCCTTGA  4721

Db   1078  GTACATAGCCAATGCCAATGGAGGGATC  1106
           ||| || ||| ||||| || |||||||
Qy   4722  GTATGTGATCAAGGTCAGTGCAAGAGTTC  4750


RESULT  15
LOCUS        I36927           943 bp    DNA             PAT       21-APR-1997
DEFINITION   Sequence 12 from patent US 5612201.
ACCESSION    I36927
NID          g2084887
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 943)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 12 18-MAR-1997;
FEATURES              Location/Qualifiers
     source           1..943
                      /organism="unknown"
BASE COUNT      192 a    294 c    264 g    193 t
ORIGIN

Query Match      6.2%;  Score 350;  DB 25;  Length 943;
Best Local Similarity  79.7%;   Pred. No. 3.71e-246;
Matches  758;  Conservative   0;  Mismatches 150;  Indels 43;  Gaps  20;

Db      1  GGATCCTCCACCCCAGTAGAGTGGGGACCTCACAGAGTCTGGCCAACCCTCCTGACAGTT   60
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```
Qy  3307 GGGTCATCCACTGCATGAGAGTGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCA 3366
         ||||  ||||| ||  ||||||||| ||||||||| ||| |||||||||| ||
Db    61 CTGGGAATCCGTGGCTGCGTTGCTGCTGCACATTGGGGCCCGTGGATTCCTCTCCCA 120
         ||| || || |||||  ||||  |||| ||||||||  ||  |||||||||||||| ||
Qy  3367 CTGAGAAGCCAGGGCTGTGCCTTGCGGTCTGCACCCTGAGGGCCCGTTGGATTCCTCTTCC- 3425

Db   121 GGAATCAGGAGCTCCAGGACAAGGCAGTGAGGACTTGGTCTGAGGCAGTGTCCTCAGGT 180
         ||||||||||||||||  |||| ||||||||||||||||||| |||||||||||||||
Qy  3426 ----T--GGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGT 3479

Db   181 CACACAGAGTAGAGGGGGCTCAGATAGTGCCAACGGTGAAGGTTTGCCTTGGATTCAAACCA 240
         ||||||||| | |||| || || ||||||| ||| |||||| |||||||| || || ||
Qy  3480 CACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCA 3539

Db   241 AGGGCCCCACCTGCCCCAGAACACAT-GGACTCCAGAGCGCCTGGCCTCACCCTCAATAC 299
         ||||||||||||| ||| |||||||| || |||||| | |  ||||||||| || ||
Qy  3540 AGGGCCCCACCTGCCACAGGACACACATAGGACTCGGCCTCACC-TCCCTAC 3598

Db   300 TTTCAGTCCTGCAGCCTGCAGGCTCAGCATGCCGCTGGCCGGATGTACCCTGAGGTGCCCTCTCACTT 359
         | ||||||| | |  ||| | ||||||||| || ||||||||| ||||||||| | |||||||||||
Qy  3599 TGTCAGTCCTGTAGAATCGACCTCTGCTGCCGGCCTGTGGGCCGGTCGTGTACCCTGAG-TACCCTCTCACTT 3657

Db   360 CCTCCTTCAGGTTCTGAGGGACAGGGCTGACCTGGAGGACCAGAGGGCCCCCG--G--AG- 414
         ||||||||||||| || ||||| | |  |||||| ||| | |||| |  |||| |  |  |
Qy  3658 CCTCCTTCAGGTTTTCAGGGGACAGGGCCCAACCCAGGACAGGATTCCCTGGAGGCCACA 3717

Db   415 GAGCA-CTG-AAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTCCATT 472
         ||| |       |||||| |||| ||||| ||||| ||||||| |||||||||||
Qy  3718 GAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGTCTCCAAGGTTC---- 3773

Db   473 CAGTACTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCCCAGGCCAGTGGGTCTCCATT 532
         |||| ||||||||| |||||  ||  |||||||||||||||||||||||||||||| |||
Qy  3774 -AGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCCTGGGGTCTTCATT 3832

Db   533 GCCCAGCTCCTGCCCACACTCCGCGCCTTGTTGCCCTGACCAGAGTCATCATGCCTCTTGAG 592
         |||||||||| ||||||||| |  | ||| |||  ||||||||||| || |||||||||||
Qy  3833 GCCCAGCTCCTGCCCACACTCCTGCCTGCTCCTGACGAGAGTCATCATGTCTCTTGAG 3892

Db   593 CAGAGGAGTCAGCACTGCAAGCCTTCAAGCCTTGAGGAGGAAGGCCTGAGGCCCGGGGC 652
         |||||||||||||||||| |||||||||| || |||||| |  ||||||||||||||||
Qy  3893 CAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGC 3952

Db   653 CTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGGCAGGAGGCTGCCCTCCTCCTCCTCTAGT 712
         |||||||| || ||||| |||||||  |     |  |   ||| |||||||||||||| |
Qy  3953 CTGGTGTGTGTGCAGGCTGCCAC--CT----- -C-----CT-CCTCCTC-TCCTCT-G- 3994

Db   713 GTAGTTGAAGTCACCCTGGGGAGGTGCCGCTGCCGGACCAGATCCTCCCCAGAGT 772
         || |  | ||||||||||||||||||| ||| ||| ||||||| |||||||||||
Qy  3995 GTCCTGG--G-CACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGT 4051

Db   773 CCTCAGGGAGCCTCCAGCCTCCCCACTACCCTCTCTGAGCCAATCCTAT 832
         |||||||||||||||||| |  ||||||||||| ||| || || ||
Qy  4052 CCTCAGGGAGCCTCCGGGCCTTTCCCACTACCACTTCACTCGACAGAGGCAACCCAGT 4111

Db   833 GAGGACTCCAGCAACCAAGAAGAGGAGGGGGCCAAGCACCTTCCCTGACCTGAGTCTGAG 892
         |||| ||| |||||| || |||| || | ||||||| ||| || |  ||||| ||||
Qy  4112 GAGGGGTTCCAGCAGCGGCGAAGGAGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTG 4171

Db   893 TTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGTTGGTTCATTTTCTGCTC 943
         |||| ||| | |||||| ||||| || |||||| ||||| ||||||||||
Qy  4172 TTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTC 4222
```

Search completed: Tue Apr 7 20:33:44 1998
Job time : 4483 secs.

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**************************************
*                                    *
*   M P S R C H           (TM)       *
*                                    *
**************************************
```

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 20:42:40 1998;   MasPar time 486.01 Seconds
                                           1340.532 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411a-1
Description: (1-5674) from 5541104.seq
Perfect Score: 5674
N.A. Sequence: 5674 1 CCCGGGGCACCACTGGCATC..........TAATGATCTTGGGTGGATCC 5674
Comp: GGGCCCCGTGGTGACCGTAG..........ATTACTAGAACCCACCTAGG

Scoring table: TABLE default
                  Gap 6

Nmatch   STD :   Dbase 0: Query 0

Searched: 159649 seqs, 57412152 bases x 2

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Database: n-geneseq30
                  1:n-geneseq1

Statistics: Mean 10.653; Variance 6.314; scale 1.687

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                           SUMMARIES

Result   % Query
No. Score Match Length DB ID   Description   Pred. No.
---- ----- ----- ------ --- ------ ----------------------------- --------
  1 5674   100.0 5674   1 Q72477 Tumour rejection antig   0.00e+00
  2 5672   100.0 5674   1 Q32352 MAGE-1 nucleic acid.   0.00e+00
  3 5650   99.6   5724   1 Q98902 Tumour rejection antig   0.00e+00
  4 2419   42.6   2419   1 Q72476 Tumour rejection antig   0.00e+00
  5 2419   42.6   2419   1 Q32351 Antigen E gene.   0.00e+00
  6 2415   42.6   2419   1 T05086 MZ2-MEL antigen E prec   0.00e+00
  7 2413   42.5   2420   1 Q72472 Tumour rejection antig   0.00e+00
  8 2413   42.5   2420   1 Q85435 Human melanoma antigen   0.00e+00
  9 1483   26.1   4157   1 Q72478 Tumour rejection antig   0.00e+00
 10 1481   26.1   4157   1 Q32353 MAGE-2 gene.   0.00e+00
 11 1399   24.7   2531   1 Q72483 Tumour rejection antig   0.00e+00
 12 1399   24.7   2531   1 Q72482 Tumour rejection antig   0.00e+00
 13 1397   24.6   2531   1 Q32357 MAGE-4 gene.   0.00e+00
 14 1395   24.6   2531   1 Q32358 MAGE-41 gene.   0.00e+00
 15 1225   21.6   2305   1 Q72486 Tumour rejection antig   0.00e+00
 16 1225   21.6   2305   1 T01165 MAGE-51 gene.   0.00e+00
 17 1225   21.6   2305   1 Q32361 MAGE-51 genomic DNA.   0.00e+00
 18 943   16.6   2226   1 Q32360 MAGE-5 cDNA.   0.00e+00
 19 943   16.6   2226   1 Q72485 Tumour rejection antig   0.00e+00
 20 832   14.7   1084   1 Q67866 H6/MAGE-1 expression c   0.00e+00
 21 832   14.7   1094   1 Q67865 H6/MAGE-1 expression c   0.00e+00
 22 811   14.3   1640   1 Q72480 Tumour rejection antig   0.00e+00
 23 795   14.0   1640   1 Q32355 MAGE-3 cDNA.   0.00e+00
 24 683   12.0   1068   1 Q72484 Tumour rejection antig   0.00e+00
 25 681   12.0   1068   1 Q32359 MAGE-4 cDNA.   0.00e+00
 26 645   11.4   1412   1 Q72490 Tumour rejection antig   0.00e+00
 27 645   11.4   1412   1 T01169 MAGE-9 gene.   0.00e+00
 28 641   11.3   1412   1 Q32365 MAGE-9 genomic DNA.   0.00e+00
 29 611   10.8   1947   1 T01167 MAGE-7 gene.   0.00e+00
 30 611   10.8   1947   1 Q32363 MAGE-7 genomic DNA.   0.00e+00
 31 611   10.8   1947   1 Q72488 Tumour rejection antig   0.00e+00
 32 562   9.9   1810   1 T01168 MAGE-8 gene.   0.00e+00
 33 562   9.9   1810   1 Q72489 Tumour rejection antig   0.00e+00
 34 562   9.9   1810   1 Q32364 MAGE-8 genomic DNA.   4.32e-249
 35 392   6.9   1107   1 T01171 MAGE-11 gene.   4.32e-249
 36 392   6.9   1107   1 Q72492 Tumour rejection antig   4.32e-249
 37 392   6.9   1107   1 Q32367 MAGE-11 genomic DNA.   3.77e-219
 38 350   6.2   943   1 Q32481 Tumour rejection antig   3.77e-219
 39 350   6.2   943   1 Q32356 MAGE-31 gene.   3.30e-158
 40 264   4.7   379   1 T63345 Human MAGE-3 DNA.   7.21e-152
 41 255   4.5   386   1 T63349 Baboon MAGE-3 homologu   6.06e-147
 42 248   4.4   384   1 T63346 Baboon MAGE-3 homologu   3.14e-118
 43 207   3.6   1866   1 T41492 DNA encoding MAGE-Xp1   1.17e-112
 44 199   3.5   920   1 Q72491 Tumour rejection antig   1.17e-112
 45 199   3.5   920   1 Q32366 MAGE-10 genomic DNA.
```

                           ALIGNMENTS

```
RESULT   1
ID   Q72477 standard; DNA; 5674 BP.
AC   Q72477;
DT   22-JUN-1995  (first entry)
DE   Tumour rejection antigen MAGE-1 encoding DNA.
KW   Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH                    Location/Qualifiers
FT   Key
FT   CDS              3881..4711
FT   /*tag=      a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; US02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Example 26; Page 59; 105pp; English.
CC   Q72477 is the DNA sequence which encodes melanoma antigen-1
CC   (MAGE-1). Another melanoma antigen MAGE-3 is encoded by Q72470,
CC   this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence  5674 BP;    1276 A;   1644 C;    1569 G;    1185 T;

Query Match         100.0%;  Score 5674;  DB 1;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db     1 CCCGGGGCACCACTGGCATCCTCCCCTCCCCTACCACCCCCAATCCTCCCTTTACGCCACCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1 CCCGGGGCACCACTGGCATCCTCCCCTCCCCTACCACCCCCAATCCTCCCTTTACGCCACCC 60

Db    61 ATCCAAACATCTTCACGCTCACGCCCAGGCAGGCAGAATCGGTTCCACCCTG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 ATCCAAACATCTTCACGCTCACGCCCAGGCAGGCAGAATCGGTTCCACCCTG 120
```

Left column:

```
Db   121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGGCCACTGACTTGAGCATTAGTGG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGGCCACTGACTTGAGCATTAGTGG 180

Db   181 TTAGAGAGAAGCGAGGTTTTCGGTTCGGTTGAGATCGGTGAGGGGCCGGGAAGCGGGG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 TTAGAGAGAAGCGAGGTTTTCGGTTCGGTTGAGATCGGTGAGGGGCCGGGAAGCGGGG 240

Db   241 CCCAGCTCTGTAAGGACCAAGGTGACATCCTGAGGGAGGACTGAGGACCACTTACCCC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 CCCAGCTCTGTAAGGACCAAGGTGACATCCTGAGGGAGGACTGAGGACCACTTACCCC 300

Db   301 AGATAGAGACCCCAAATAATCCCTTCATGCCAGTCCTGACCATCTGGTGGTGACTTC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 AGATAGAGACCCCAAATAATCCCTTCATGCCAGTCCTGACCATCTGGTGGTGACTTC 360

Db   361 TCAGGCTGGGCCACCCCCCAGCCCCTGCTTAAAACCACTGGGACTCGAAGTCAGAG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 TCAGGCTGGGCCACCCCCCAGCCCCTGCTTAAAACCACTGGGACTCGAAGTCAGAG 420

Db   421 CTTCCGTGATCAGGGAAGGGCTGCTTAGGAGAGGCAGCGTCCAGGCTCCAGACAT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CTTCCGTGATCAGGGAAGGGCTGCTTAGGAGAGGCAGCGTCCAGGCTCCAGACAT 480

Db   481 CATGCTCAGGATTCTCAACCTGAGGGTCCCTAAGACCCGTGACCCAAC 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 CATGCTCAGGATTCTCAACCTGAGGGTCCCTAAGACCCGTGACCCAAC 540

Db   541 CCCCACTCCAATGCTCACTCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 CCCCACTCCAATGCTCACTCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Db   601 CCCCACATCCCCACCCCACCCCATCCCTGATGCCCAGCCATTCCACCCT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601 CCCCACATCCCCACCCCACCCCATCCCTGATGCCCAGCCATTCCACCCT 660

Db   661 CACCCCCACCCCACCCCACCCCACGCCCACCCCAGCCAGGATCCGGTTCCG 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 CACCCCCACCCCACCCCACCCCACGCCCACCCCAGCCAGGATCCGGTTCCG 720

Db   721 CCAGGAAACATCGGGTGCCCGGATGTGACGCCACTGACTTGCGCCATTGTGGGGCAGAGA 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721 CCAGGAAACATCGGGTGCCCGGATGTGACGCCACTGACTTGCGCCATTGTGGGGCAGAGA 780

Db   781 GAAGCGAGGTTTCCATTCTGAGGACGGCGGCTCGGCCGAAGGAACCTGACCCAGG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   781 GAAGCGAGGTTTCCATTCTGAGGACGGCGGCTCGGCCGAAGGAACCTGACCCAGG 840

Db   841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA 900

Db   901 GAGAGCCCAAATATTCCAGCCCTGCTGCCCTGCTCTTCAGAGGCTTGGCCACCCGGGAA 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 GAGAGCCCAAATATTCCAGCCCTGCTGCCCTGCTCTTCAGAGGCTTGGCCACCCGGGAA 960

Db   961 CGTCTCAGGCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAGACCAGGTTC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961 CGTCTCAGGCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAGACCAGGTTC 1020

Db  1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACTCAGAGGCTGGTTAGGAGAGG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACTCAGAGGCTGGTTAGGAGAGG 1080

Db  1081 GCAGGGCACAGGCTCTGCCCAGGCATCAAGATCAGCAGGAGGCTGTGGCCC 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1081 GCAGGGCACAGGCTCTGCCCAGGCATCAAGATCAGCAGGAGGCTGTGGCCC 1140

Db  1141 CCAAGAGCTGCCACTCCAATCCCACTCCGCATTCGCACCCCACCCCAAACC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1141 CCAAGAGCTGCCACTCCAATCCCACTCCGCATTCGCACCCCACCCCAAACC 1200
```

Right column:

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Db  1201 CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1201 CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC 1260

Db  1261 ACCCTCCAGCCCCCAGCCACCAGCCCCCAACCCTTCTGCCACCTCACCCTCACTGCCCCCAAC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261 ACCCTCCAGCCCCCAGCCACCAGCCCCCAACCCTTCTGCCACCTCACCCTCACTGCCCCCAAC 1320

Db  1321 CCCACCCTCATCTCTCTCATGTGCCCCATGCCCCATTCTGGCAGAATCC 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1321 CCCACCCTCATCTCTCTCATGTGCCCCATGCCCCATTCTGGCAGAATCC 1380

Db  1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGGCCGATGTGAAACCACTGACT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGGCCGATGTGAAACCACTGACT 1440

Db  1441 TGAACCTCACAGATCTGAGAGAGCCAGGTTCATTTAATGGTTCTGAGGGGCGGCTTGAG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441 TGAACCTCACAGATCTGAGAGAGCCAGGTTCATTTAATGGTTCTGAGGGGCGGCTTGAG 1500

Db  1501 ATCCACTGAGGGAGTGGTTTTAGGCTCTGTGTGAGGAGCAAGGTGAGATGCTGAGGAGG 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1501 ATCCACTGAGGGAGTGGTTTTAGGCTCTGTGTGAGGAGCAAGGTGAGATGCTGAGGAGG 1560

Db  1561 ACTGAGGAGGCACACACCCCAGGTAGATGCCCAAAATGATCCAGTACCACCCCTGCTG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1561 ACTGAGGAGGCACACACCCCAGGTAGATGCCCAAAATGATCCAGTACCACCCCTGCTG 1620

Db  1621 CCAGCCCTGGACCCACCCCGGCCAGGACAGATGTCTCAGCTGGACACCCCGTCCGTCC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1621 CCAGCCCTGGACCCACCCCGGCCAGGACAGATGTCTCAGCTGGACACCCCGTCCGTCC 1680

Db  1681 CACTGCCACTTAACCCACAGGGGCAATCTGTAGTGTAGTGCCCAGCATCCTATAGCTTATGGACCGG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681 CACTGCCACTTAACCCACAGGGGCAATCTGTAGTGTAGTGCCCAGCATCCTATAGCTTATGGACCGG 1740

Db  1741 GGTCAGGAGAGGCAGGGCCCAGGCCATCGGCGCCCGGCATTAGGGTCAGG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741 GGTCAGGAGAGGCAGGGCCCAGGCCATCGGCGCCCGGCATTAGGGTCAGG 1800

Db  1801 ACCCTGGGAGGGAACTGAGGGTTCCCACCACCTGTCTCCTCATCTCCACCGCCACC 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801 ACCCTGGGAGGGAACTGAGGGTTCCCACCACCTGTCTCCTCATCTCCACCGCCACC 1860

Db  1861 CCACTCACATTCCCATACCCCTACCCCCCACCCCCAACCTCATCTGTCAGAATCCCTGCTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861 CCACTCACATTCCCATACCCCTACCCCCCACCCCCAACCTCATCTGTCAGAATCCCTGCTG 1920

Db  1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCACTGACCTTGACCTCCCCATCCA 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCACTGACCTTGACCTCCCCATCCA 1980

Db  1981 GGGTCTGATGGGAGGGAAGGGCTTGAACAGGGGCCTCAGGGGAGGGGAGGGGCCTAC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 GGGTCTGATGGGAGGGAAGGGCTTGAACAGGGGCCTCAGGGGAGGGGAGGGGCCTAC 2040

Db  2041 TGGGAGATGAGGGAGGACCTCAGAGGACGCACCCCACCCCTGTCTGAG 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041 TGGGAGATGAGGGAGGACCTCAGAGGACGCACCCCACCCCTGTCTGAG 2100

Db  2101 ACTGAGGCTGCCACTTCTGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101 ACTGAGGCTGCCACTTCTGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160

Db  2161 GTGGGACCCCAGGGCCTGCAAGGCTTACGCGGAGGAAGAGAGAGGGACTTCAGGGGACCTT 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161 GTGGGACCCCAGGGCCTGCAAGGCTTACGCGGAGGAAGAGAGAGGGACTTCAGGGGACCTT 2220

Db  2221 GGAATCCAGATCAGTGTGCCAGGTCCCTGAGAGGTCCAGGGCACGTGCCACATATG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 GGAATCCAGATCAGTGTGCCAGGTCCCTGAGAGGTCCAGGGCACGTGCCACATATG 2280

Db  2281 GCCCATATTTCCTGCATCTTTGAGGTGACAGGAGCAGAGAGCTGTGTGGTGCTGAGAAGTGGGCC 2340
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Qy   2281 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     2281 GCCCATATTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGTGTCTGAGAAGTGGGGCC 2340

Db   2341 TCAGGTCAACAGAGGGAGGAGAGTTCCAGGTCCAGGGGCCCTTCCCCTTCATG 2400
     2341 TCAGGTCAACAGAGGGAGGAGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCTTCATG 2400

Qy   2401 AGGACTGGGGATATCCCCGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT 2460
     2401 AGGACTGGGGATATCCCCGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT 2460

Db   2461 TTAGTAGTCTAGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520
     2461 TTAGTAGTCTAGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520

Qy   2521 CAGGCAGGAGTTGGGGGCCCTCAGGGAGATGGGGTCTTGGGTAAAGGGGGGATGTCT 2580
     2521 CAGGCAGGAGTTGGGGGCCCTCAGGGAGATGGGGTCTTGGGTAAAGGGGGGATGTCT 2580

Db   2581 ACTCATGTCAGGGGTTGAGGAATGCACAGGGCTGGCAGGAGAATAAAGATGAGT 2640
     2581 ACTCATGTCAGGGGTTGAGGAATGCACAGGGCTGGCAGGAGAATAAAGATGAGT 2640

Qy   2641 GAGACAGACAAGGCTATTGGAATCCACACCCAGAACAACCCAGACACC 2700
     2641 GAGACAGACAAGGCTATTGGAATCCACACCCAGAACAACCCAGACACC 2700

Db   2701 TCACCCAGGATGTGGCTTCTTTTCACTCCGTTTCCAGATCTGGGCAGGTGAGGACCT 2760
     2701 TCACCCAGGATGTGGCTTCTTTTCACTCCGTTTCCAGATCTGGGCAGGTGAGGACCT 2760

Qy   2761 CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCTGTCTAAAGACAGAGCG 2820
     2761 CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCCATCTGTCTAAAGACAGAGCG 2820

Db   2821 GTCCCAGGATCTGCCATGCTGCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG 2880
     2821 GTCCCAGGATCTGCCATGCTGCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG 2880

Qy   2881 GACCAGAACACTGAGGGAGACTGCACAGCAGAAATCAGCCCCTGCCCCTGTCACCCCAGAG 2940
     2881 GACCAGAACACTGAGGGAGACTGCACAGCAGAAATCAGCCCCTGCCCCTGTCACCCCAGAG 2940

Db   2941 AGCATGGGGCTGGGCCGTCTGCCCAGGTCCTTCCGTATCCTGGGATCATTGATGTCAGGG 3000
     2941 AGCATGGGGCTGGGCCGTCTGCCCAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000

Qy   3001 ACGGGAGGAGGCCTTGGTCTGAGAAGGCTGCGCTGCCGCTCAGTCAGTCAGTCTCCAGGCC 3060
     3001 ACGGGAGGAGGCCTTGGTCTGAGAAGGCTGCGCTGCCGCTCAGTCAGTCAGTCTCCAGGCC 3060

Db   3061 CTGCCAGGAGTCAAGGTGAGGACCAGGAGGCGGCACCCACCTCACCTCCACCAGGACA 3120
     3061 CTGCCAGGAGTCAAGGTGAGGACCAGGAGGCGGCACCCACCTCACCTCCACCAGGACA 3120

Qy   3121 GAATTTGATATCTCTTGCTCCCCTTAGGCACGTGTGGCCAGATGTTT 3180
     3121 GAATTTGATATCTCTTGCTCCCCTTAGGCACGTGTGGCCAGATGTTT 3180

Db   3181 GTCCCCTCCTGTCCTTATCATGGATGGGTGAACTCTTGATTTGGATTTCTCAG 3240
     3181 GTCCCCTCCTGTCCTTATCATGGATGGGTGAACTCTTGATTTGGATTTCTCAG 3240

Qy   3241 ACCAGCAAAAGGGCAGGATCGGGGATGTCGCCTGCCAGGAAAAATATAGGCCCTGCCTGAGAA 3300
     3241 ACCAGCAAAAGGGCAGGATCGGGGATGTCGCCTGCCAGGAAAAATATAGGCCCTGCCTGAGAA 3300

Db   3301 CAGAGGGGGTCATCCACTGCATGAGTCGGGATGTGGGGATGTCCAGGCCTCCAGCCCTCCTG 3360
     3301 CAGAGGGGGTCATCCACTGCATGAGTCGGGATGTGGGGATGTCCAGGCCTCCAGCCCTCCTG 3360
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Qy   3361 GTAGCACTGAGAAGCCAGGGCTGTGCCTTGCGGTCGCTGCACCCTGAGGGCCCGTGGATTCCT 3420
     3361 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   3421 CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGGCCTGGTCTGAGACAGTATCCTCAGGTC 3480
     3421 CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGGCCTGGTCTGAGACAGTATCCTCAGGTC 3480

Qy   3481 ACAGAGCAGAGGATGACACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGACACCACAA 3540
     3481 ACAGAGCAGAGGATGACACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGACACCACAA 3540

Db   3541 GGGCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG 3600
     3541 GGGCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG 3600

Qy   3601 TCAGTCCTGTAGAATCGACCCTGCTGCCGGCTGCCCGGTGACCCTGAGTACCCTCACTTCCT 3660
     3601 TCAGTCCTGTAGAATCGACCCTGCTGCCGGCTGCCCGGTGACCCTGAGTACCCTCACTTCCT 3660

Db   3661 CCTTCAGGTTTCAGGGGGACAGCCACAGAGGACAGGATTCCCTGAGGGCCACAGAG 3720
     3661 CCTTCAGGTTTCAGGGGGACAGCCACAGAGGACAGGATTCCCTGAGGGCCACAGAG 3720

Qy   3721 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTTCAGTTCAGTTCTTC 3780
     3721 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTTCAGTTCAGTTCTTC 3780

Db   3781 AGCTGAGGCCTCCACACTCCCTCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCT 3840
     3781 AGCTGAGGCCTCCACACTCCCTCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCT 3840

Qy   3841 CCTGCCCCACACTCCTGCTCCCCGACGAGTCATCATGTCTCTTGAGCAGAGGAG 3900
     3841 CCTGCCCCACACTCCTGCTCCCCGACGAGTCATCATGTCTCTTGAGCAGAGGAG 3900

Db   3901 TCTGCACTGCAAGCCTGAGGAGGCCCACAAGAGGCCCTGGGCCTGGTGTG 3960
     3901 TCTGCACTGCAAGCCTGAGGAGGCCCACAAGAGGCCCTGGGCCTGGTGTG 3960

Qy   3961 TGTGCAGGCTGCCACCTCCTCTCCTCCTCTGGCCTGGGCACCCTGCTGGAGAGGTGCC 4020
     3961 TGTGCAGGCTGCCACCTCCTCTCCTCCTCTGGCCTGGGCACCCTGCTGGAGAGGTGCC 4020

Db   4021 CACTGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGAGTCCTCGGCCTTTCCCACTAC 4080
     4021 CACTGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGAGTCCTCGGCCTTTCCCACTAC 4080

Qy   4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140
     4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140

Db   4141 GCCAAGCACCTCTTGTATCCTGAGTCCTTGTTCCTGTTCCGACGAGTAATCACTAAGGAGGTGGC 4200
     4141 GCCAAGCACCTCTTGTATCCTGAGTCCTTGTTCCTGTTCCGACGAGTAATCACTAAGGAGGTGGC 4200

Qy   4201 TGATTTGGTTGGTTTTCTGCCTCCTCAAATATCAGCACTGTTTCCTGAGATCTTCGGCAGA 4260
     4201 TGATTTGGTTGGTTTTCTGCCTCCTCAAATATCAGCACTGTTTCCTGAGATCTTCGGCAGA 4260

Db   4261 AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTCGGCAAAGC 4320
     4261 AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTCGGCAAAGC 4320

Qy   4321 CTCTGAGTCCTTGCACCTGGTCTTTGGCATTGGCATTGGGTGAAGGAAGCAGACCCCACCGGCCA 4380
     4321 CTCTGAGTCCTTGCACCTGGTCTTTGGCATTGGCATTGGGTGAAGGAAGCAGACCCCACCGGCCA 4380

Db   4381 CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGCCTGGGTGATAATCA 4440
     4381 CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGCCTGGGTGATAATCA 4440

Qy   4441 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGGTCATGATTGGTCAATGCAATGGAGGGGCCG 4500
     4441 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGGTCAATGCAATGGAGGGGCCG 4500
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Db   4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGAGGTGTATGATGGGAG 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGAGGTGTATGATGGGAG 4560

Db   4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGAGATTTGGTGCAGGAAAA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGAGATTTGGTGCAGGAAAA 4620

Db   4621 GTACCTGGAGTACGGCAGTGCCCGACAGTGATCCGCACGCTATGAGTTCCTGTGGGGT 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4621 GTACCTGGAGTACGGCAGTGCCCGACAGTGATCCGCACGCTATGAGTTCCTGTGGGGT 4680

Db   4681 CCAAGGGCCCTGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4681 CCAAGGGCCCTGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740

Db   4741 GCAAGAGTTCGCTTTTTCTTCCCATCCTGCGTGAAGCAGCAGTTTGAGAGAGGAGGAAGAG 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4741 GCAAGAGTTCGCTTTTTCTTCCCATCCTGCGTGAAGCAGCAGTTTGAGAGAGGAGGAAGAG 4800

Db   4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT 4860

Db   4861 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4861 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT 4920

Db   4921 GAAGAGCAGTGCTCAGTGTTCTCAGTAGTAGTTCTGTTCTATTGGTGACTTGGAGATT 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4921 GAAGAGCAGCGTCAGTGTTCTCAGTAGTAGTTCTGTTCTATTGGTGACTTGGAGATT 4980

Db   4981 TATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTTTTTTAAGGGGATGTTGAATGAAC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4981 TATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTTTTTTAAGGGGATGTTGAATGAAC 5040

Db   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100

Db   5101 TAAGAGTTCTGTGTTTATTCAGATTGGGAAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5101 TAAGAGTTCTGTGTTTATTCAGATTGGGAAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Db   5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGAGATAA 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGAGATAA 5220

Db   5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280

Db   5281 ATTTTTAAAGATATATGCATAAGAATTCATACCTGGATTTCCTTGGCTTCTTGGCTTGGC 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5281 ATTTTTAAAGATATATGCATAAGAATTCATACCTGGATTTCCTTGGCTTCTTGGCTTGGC 5340

Db   5341 TAAATCTGAATAAAAGAATTCTTCCTGTTCTTCCCATGCCACTGAGCA 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5341 TAAATCTGAATAAAAGAATTCTTCCTGTTCTTCCCATGCCACTGAGCA 5400

Db   5401 TCTGCTTTTTGGAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGCTAAGCCAGACTCATAC 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5401 TCTGCTTTTTGGAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGCTAAGCCAGACTCATAC 5460

Db   5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAGTGAATCGAGGTGGCAAGATGTC 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAGTGAATCGAGGTGGCAAGATGTC 5520

Db   5521 CTCTAAAGATGTAGGGAAAAGTGAGGGTGAGAGGGTGAGGGCTTCCCGGTGAGAGTG 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5521 CTCTAAAGATGTAGGGAAAAGTGAGGGTGAGAGGGTGAGGGCTTCCCGGTGAGAGTG 5580
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Db   5581 GTGGAGTGCAATGCCCTGAGCTGGGCGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5581 GTGGAGTGCAATGCCCTGAGCTGGGCGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Db   5641 GGGGGAGCTGATTGTAATGAATCTTGGTGGATCC 5674
          |||||||||||||||||||||||||||||||||
Qy   5641 GGGGGAGCTGATTGTAATGAATCTTGGTGGATCC 5674
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RESULT  2
ID    Q32352  standard; DNA; 5674 BP.
AC    Q32352;
DT    22-APR-1993  (first entry)
DE    MAGE-1 nucleic acid.
KW    melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW    tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS    Homo sapiens.
FH                       Location/Qualifiers
FT    Key
FT    CDS                3881..4711
FT    /*tag=   a
PN    WO9220356-A.
PD    26-NOV-1992.
PF    22-MAY-1992; U04354.
PR    23-MAY-1992; US-705702.
PR    09-JUL-1991; US-728838.
PR    23-SEP-1991; US-764364.
PR    12-DEC-1991; US-807043.
PA    (LUDW-) LUDWIG INST CANCER RES.
PI    Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI    Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR    WPI; 92-415460/50.
PT    Nucleic acid mol. encoding a human tumour rejection antigen
PT    precursor - useful as an immunostimulant in a vaccine for
PT    treating and preventing cancers, also useful in diagnosis
PS    Disclosure: Page 71-73; 142pp; English.
CC    The sequences given in Q32352-69 represent a new family of genes
CC    referred to as melanoma antigens (MAGE).  The cDNAs of this gene
CC    family were identified during the isolation of the antigen E gene.
CC    The MAGE cDNAs, when tested, did not transfer expression of antigen
CC    E, but they did show substantial homology to the antigen E cDNA
CC    sequence.  The MAGE DNAs share a certain degree of homology with each
CC    other and are expressed in tumour cells including several types of
CC    human tumor cells as well as in human tumors.  MAGE expression is not
CC    restricted to melanomas.  MAGE refers to a family of tumor rejection
CC    antigen precursors.  The antigens resulting from these genes are
CC    referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC    See also Q32351.
SQ    Sequence 5674 BP;     1277 A;     1644 C;     1568 G;     1185 T;

Query Match             100.0%;  Score 5672;  DB 1;  Length 5674;
Best Local Similarity   100.0%;  Pred. No. 0.00e+00;
Matches 5673;    Conservative    0;  Mismatches    0;  Indels    1;  Gaps    0;
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Db      1 CCCGGGGCACCACTGGCATCCTCCCCTACCACCCCCCAATCCTCCCCTTACGGCCACCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 CCCGGGGCACCACTGGCATCCTCCCCTACCACCCCCCAATCCTCCCCTTACGGCCACCC 60

Db     61 ATCCAAACATCTTCACGCTCACGCCCAAGCCAGGCCAGGAATCGGTTCCACCCTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ATCCAAACATCTTCACGCTCACGCCCAAGCCAGGCCAGGAATCGGTTCCACCCTG 120

Db    121 CTCTCACCCAGGGAAGCCCCAGTGCCCAGATGTGACGGCCGCCACTGACTGAGCATTAGTGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 CTCTCACCCAGGGAAGCCCCAGTGCCCAGATGTGACGGCCGCCACTGACTGAGCATTAGTGG 180

Db    181 TTAGAGAGAAGCGAGGTTTTCGGTTCGGTTCCACCCTG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTTCGGTTCCACCCTG 240

Db    241 CCCAGCTCTGTGTAAGGAGCCAAGGTGACATGCCAAGGTGACTGAGGGACCCACTTACCCC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 CCCAGCTCTGTGTAAGGAGCCAAGGTGACATGCCAAGGTGACTGAGGGACCCACTTACCCC 300
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Db  301  AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCTGGACCATCTGGTGGTTGGACTTC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301  AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCTGGACCATCTGGTGGTTGGACTTC  360

Db  361  TCAGGCTGGGCCACCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  361  TCAGGCTGGGCCACCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG   420

Db  421  CTCCGTGTGATCAGGGAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  421  CTCCGTGTGATCAGGGAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT   480

Db  481  CATGCTCAGGATTCTCAAGGAGGCTGAGGGTCCCAAGACCCTCCGTGACCCAAC        540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  481  CATGCTCAGGATTCTCAAGGAGGCTGAGGGTCCCAAGACCCTCCGTGACCCCAAC       540

Db  541  CCCACTCCAATGCTCACTCCCGTGACCCAACCCTCTTCATTGTCATTCCAACCCCA      600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  541  CCCACTCCAATGCTCACTCCCGTGACCCAACCCTCTCATTGTCATTCCAACCCCCA      600

Db  601  CCCCACAATCCCCACCCCACCCCACCCTCAACCCTGATGCCCATCCCCAGCCATTCCACCCT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  601  CCCCACAATCCCCACCCCACCCCACCCTCAACCCTGATGCCCATCCCCAGCCATTCCACCCT  660

Db  661  CACCCCCACCCCACCCCACCCCAGCGCCACTCCAGCGGATCGGTTCCG            720
         |||||||||||||||||||||||||||||||||||||||||||||
Qy  661  CACCCCCACCCCACCCCACCCCAGCGCCACTCCAGCGGATCCGTTCCG           720

Db  721  CCAGGAAACATCCGGGTGCCCGATGTGACGCCACTGACTGTGGGGCAGAGA         780
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  721  CCAGGAAACATCCGGGTGCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA   780

Db  781  GAAGCCGGAGGTTTCCATTCTGAGGGACGGCGTGAGTTCGGCGAAGGAACCTGACCCAGG  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  781  GAAGCGGAGGTTTCCATTCTGAGGGACGGCGTGAGTTCGGCGAAGGAACCTGACCCAGG   840

Db  841  CTCTGTGAGGAGCAAGGTCTGGAATCAGAGGTTGCTGTGAGGGACTGAGAGCTGAGGAGG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  841  CTCTGTGAGGAGCAAGGTCTGGAATCAGAGGTTGCTGTGAGGGACTGAGAGCTGAGGAGG  900

Db  901  GAGAGCCCCAAATATTCCAGCCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGGAGA      960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  901  GAGAGCCCCAAATATTCCAGCCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGGAAGA     960

Db  961  CGTCTCAGCCTGGGCTGCCCCCAGACCCCGCTCCTGCTCTCCAAAAGCCTTGAGAGAGTTC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  961  CGTCTCAGCCTGGGCTGCCCCCAGACCCCGCTCCTGCTCTCCAAAAGCCTTGAGAGTCTCTGAG 1020

Db 1021  TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGAGGTCAGGAGGCAGGAGGACTGGTTAGGAGAGG 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1021  TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGAGGTCAGGAGGCAGGAGGACTGGTTAGGAGAGG 1080

Db 1081  GCAGGGCACAGGCTCTGCCAGCTCAAGATCAGCACCCCAAGAGAGGGGCTGTGGGCCC   1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1081  GCAGGGCACAGGCTCTGCCAGCTCAAGATCAGCACCCCAAGAGAGGGGCTGTGGGCCC   1140

Db 1141  CAAGAGACTGCACTCCAATCCCCACTCCCACTCCCATTCGGCATTCCCACCCACC      1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1141  CCAAGAGACTGCACTCCAATCCCCACTCCCACTCCCATTCGGCATTCCCACCCACC     1200

Db 1201  CCATCTCCTCCAGCTCAGCTGCCCAGCACCAGCTCCTGCCACCTCCGTCACCCTGACCACC  1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1201  CCCATCTCCTCCAGCTCAGCTGCCCAGCACCAGCTCCTGCCACCTCCGTCACCCTGACCACC 1260

Db 1261  ACCCTCCAGCCCCAGCCCAACCCTTCTCCCCACCTCACTGTGCCACCTCTCATGTTGCCCCACTTCGGCAGAATCC 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1261  ACCCTCCAGCCCCAGCCCAACCCTTCTCCCCACCTCACTGTGCCACCTCTCATGTTGCCCCACTTCGGCAGAATCC 1380

Db 1381  GGTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 1381  GGTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAG 1440

Db 1441  TGAACCTCACAGATCTGAGAGAAGCCAGTTCATTTAATGGTTCTGAGGGGCGGCTTGAG  1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1441  TGAACCTCACAGATCTGAGAGAAGCCAGTTCATTTAATGGTTCTGAGGGGCGGCTTGAG  1500

Db 1501  ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGAGTGCTGAGGGAGG  1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1501  ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG   1560

Db 1561  ACTGAGGAGGCACACACCACCACCAGGACCCCAAAATGATCCAGTACTACCACCCCTGCTG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1561  ACTGAGGAGGCACACACCACCACCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620

Db 1621  CCAGCCCTGGACCCGCCCAGGCCAGGCCCCAGGACAGTGTCAGCTGACCACCCCCGTCCGTCC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1621  CCAGCCCTGGACCCGCCCAGGCCAGGCCCCAGGACAGTGTCAGCTGACCACCCCCGTCCGTCC 1680

Db 1681  CACTGCCACTTAACCCACCACAGGGCAATCTGTAGTCATATGTGACCCGGCCAGGGGCAGGGTT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1681  CACTGCCACTTAACCCACCACAGGGCAATCTGTAGTCATATGTGACCCGGCCAGGGGCAGGGTT 1740

Db 1741  GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCACCACCTTATGTGACCTTATGTGACTTAGGGTCAGG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1741  GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCACCACCTTATGTGACCTTATGTGACTTAGGGTCAGG 1800

Db 1801  ACCCTGGAGGGAACTGAGGGTTCCCACCCCTACCCCAACCTGTCTCCATCTCACCGCCACC  1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1801  ACCCTGGAGGGAACTGAGGGTTCCCACCCCTACCCCAACCTGTCTCCATCTCACCGCCACC  1860

Db 1861  CCACTCACATTCCCATACTACCCCAACCTACTACTCCTGCTCCGATCTCGACTTGACGTGACTCCGCTG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1861  CCACTCACATTCCCATACTACCCCAACCTACTACTCCTGCTCCGATCTCGACTTGACGTGACTCCGCTG 1920

Db 1921  TCAACCCACGGAAGCCACGGACCACGGATCCCGCCCACTCAAATA               1980
         |||||||||||||||||||||||||||||||||||||||||||||
Qy 1921  TCAACCCACGGAAGCCACGGACCACGGATCCCGCCCACTCAAATA              1980

Db 1981  GGGTCTGATGGAGGGGAGGGGCTTGAACAGGGCCTCAGGGGAGGGGGCCCTAC        2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1981  GGGTCTGATGGAGGGGAGGGGCTTGAACAGGGCCTCAGGGGAGGGGGCCCTAC       2040

Db 2041  TGCGAGATGAGGGAGGGGCCTCAGAGGGCACCCGCACCACCCGTCTCTGAG         2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2041  TGCGAGATGAGGGAGGGGCCTCAGAGGGCACCCGCACCACCCGTCTCTGAG        2100

Db 2101  ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGACTCAGATTGCATGGGGG     2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2101  GCCCATATTTCCTGCATCTTTGCTGCATCTTTGCCTCAAGATGTGCCCCCTTCATG    2160

Db 2161  GTGGGGACCAGGCCTCGCAAGGCTTACGCGGAGGAAGAGAGGAGGGGACCTT       2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2161  GTGGGGACCAGGCCTCGCAAGGCTTACGCGGAGGAAGAGAGGAGGGGACCTT      2220

Db 2221  GGAATCCAGATCAGTGTGCCAATCCCAGGGGGCACGGTGGCCACACATATG        2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2221  GGAATCCAGATCAGTGTGCCAATCCCAGGGGGCACGGTGGCCACACATATG       2280

Db 2281  GCCCATATTTCCTGCATCTTTGCTGCATCTTTGCCCCAAGATGTGCCCCTTCATGGGGGCC 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2281  GCCCATATTTCCTGCATCTTTGCTGCATCTTTGCCCCAAGATGTGCCCCTTCATGGGGGCC 2340

Db 2341  TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCCATATGGCCCAAGATGTGCCCCCTTCATG 2400
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Qy 2341  TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCCATATGGCCCAAGATGTGCCCCCTTCATG 2400

Db 2401· AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGACTCCACACAGTCCGGCTGTCCCCTT   2460
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Qy 2401  AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGACTCCACACAGTCCGGCTGTCCCCTT   2460

Db 2461  TTAGTAGCTCTAGGGGGACCAGATCAGGGATGCGGTATGTTCCATTCTCACTTGTACCA   2520
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Qy  2461 TTAGTAGCTCTAGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520
Db  2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGGATGGGGTCTTGGGGTAAAGGGGGATGTCT 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGGATGGGGTCTTGGGGTAAAGGGGGATGTCT 2580
Db  2581 ACTCATGTCAGGGGAATTGGGGGTTGAGGAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581 ACTCATGTCAGGGGAATTGGGGGTTGAGGAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640
Db  2641 GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGGTCAGCCCTGGACACC 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641 GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGGTCAGCCCTGGACACC 2700
Db  2701 TCACCCAGGATGTGGCTTCTTTTCACTTCCTGTTTCCAGATCTGGGGCAGGTGAGGAGGACCT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701 TCACCCAGGATGTGGCTTCTTTTCACTTCCTGTTTCCAGATCTGGGGCAGGTGAGGAGGACCT 2760
Db  2761 CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGTCTAAAGACAGAGCG 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2761 CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGTCTAAAGACAGAGCG 2820
Db  2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGTGAGGAACATGAGGGAGACTGAGGGTACCCCAG 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGTGAGGAACATGAGGGAGACTGAGGGTACCCCAG 2880
Db  2881 GACCAGAACAACTGAGGGAGACTGCACAGAGAAATCAGCCCTGCCCCTGCTCACCCCAGAG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881 GACCAGAACAACTGAGGGAGACTGCACAGAGAAATCAGCCCTGCCCCTGCTCACCCCAGAG 2940
Db  2941 AGCATGGGCTGGGCGCTCTGCCGAGTCCTTCCGTTATCCTGGATCATTGATGTCAGGG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941 AGCATGGGCTGGGCGCTCTGCCGAGTCCTTCCGTTATCCTGGATCATTGATGTCAGGG 3000
Db  3001 ACGGGGAGGCCTTGGTCTGGTCTCAGGTGAGGAGCGTCCCAGGCC 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001 ACGGGGAGGCCTTGGTCTGGTCTCAGGTGAGGAGCGTCCCAGGCC 3060
Db  3061 CTGCCAGGAGTCAAGGTGAGGAGGTCACCAAGCGGGGACCAAGCGGGCAGCACATTAATTCCAAT 3120
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Qy  3061 CTGCCAGGAGTCAAGGTGAGGAGGTCACCAAGCGGGGACCAAGCGGGCAGCACATTAATTCCAAT 3120
Db  3121 GAATTTGATATCTCTTGCTGCCCTTCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT 3180
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Qy  3121 GAATTTGATATCTCTTGCTGCCCTTCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT 3180
Db  3181 GTCCCCTCCTGTCCTCCATTCCTTATCATGGATGTGAACTCTTGATTTGGATTTCTCAG 3240
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Qy  3181 GTCCCCTCCTGTCCTCCATTCCTTATCATGGATGTGAACTCTTGATTTGGATTTCTCAG 3240
Db  3241 ACCAGCAAAAGGCAGGATCCAGGGCCCTGCCAGGAGAAAAATATAAGGGCCCTGCGTGAGAA 3300
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Qy  3241 ACCAGCAAAAGGCAGGATCCAGGGCCCTGCCAGGAGAAAAATATAAGGGCCCTGCGTGAGAA 3300
Db  3301 CAGAGGGGGTCATCCACTGCAGTGGGATGGGGATGGGGATGGGGATCCAGCGTCCAGCCCACCCTCCTG 3360
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Qy  3301 CAGAGGGGGTCATCCACTGCAGTGGGATGGGGATGGGGATGGGGATCCAGCGTCCAGCCCACCCTCCTG 3360
Db  3361 GTAGCACTGAGAAGCCAGGCTGTGCTTGCGGTCTGAGCGGTGCCAGCAGTGCACCACCAA 3420
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Qy  3361 GTAGCACTGAGAAGCCAGGCTGTGCTTGCGGTCTGAGCGGTGCCAGCAGTGCACCACCAA 3420
Db  3421 CTTCCTGGAGCTCCAGGAACCAGGCCTTGGTCTGACAGCAGTATCCTTCAGGTC 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421 CTTCCTGGAGCTCCAGGAACCAGGCCTTGGTCTGACAGCAGTATCCTTCAGGTC 3480
Db  3481 ACAGCAGAGGATGCACAGGGTGCCAGCAGTGTTGCCCTGAATGTGCACCACCAA 3540
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Qy  3481 ACAGCAGAGGATGCACAGGGTGCCAGCAGTGTTGCCCTGAATGCACCACCAA 3540
Db  3541 GGGCCCCACCTGCCACCAGGACACATAGGACTCCCAGAGTCTGGCCCTCACCTCCCTACTG 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541 GGGCCCCACCTGCCACCAGGACACATAGGACTCCCAGAGTCTGGCCCTCACCTCCCTACTG 3600
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Db  3601 TCAGTCCTGTAGAATCGACCCTGCTGGCCGCGGCTGTGCCCGCTGAGTACCCTCCACTTCCT 3660
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Qy  3601 TCAGTCCTGTAGAATCGACCCTGCTGGCCGCGGCTGTGCCCGCTGAGTACCCTCCACTTCCT 3660
Db  3661 CCTTCAGGTTTTCAGGGGACAGGCCAACCAGGCCAACCCAGAGGACGATCCCCTGGAGGCCCACAGAG 3720
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Qy  3661 CCTTCAGGTTTTCAGGGGACAGGCCAACCAGGCCAACCCAGAGGACGATCCCCTGGAGGCCCACAGAG 3720
Db  3721 GAGCACCAAGGAGAAGATCTGTAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTC 3780
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Qy  3721 GAGCACCAAGGAGAAGATCTGTAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTC 3780
Db  3781 AGCTGAGGGCCTCACACACTCCCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCT 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781 AGCTGAGGGCCTCACACACTCCCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCT 3840
Db  3841 CCTGCCCACACTCCTGCCTGCCTGCCCTGCCCTGACGAGAGTCATCATGGTCTTGAGCAGAGGAG 3900
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Qy  3841 CCTGCCCACACTCCTGCCTGCCTGCCCTGCCCTGACGAGAGTCATCATGGTCTTGAGCAGAGGAG 3900
Db  3901 TCTGCACTGCAAGCCTGAGGAAGCCCTGAGGCCCAACAAGAGAGCCCTGGCCCTGGTGTG 3960
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Qy  3901 TCTGCACTGCAAGCCTGAGGAAGCCCTGAGGCCCAACAAGAGAGCCCTGGCCCTGGTGTG 3960
Db  3961 TGTGCAGGCTGCCACCTCCTGGTCCTCGGCACCCTGGAGGAGGTGCC 4020
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Qy  3961 TGTGCAGGCTGCCACCTCCTGGTCCTCGGCACCCTGGAGGAGGTGCC 4020
Db  4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTCAGGGAGCCTTCCGCCTTCCCACTAC 4080
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Qy  4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTCAGGGAGCCTTCCGCCTTCCCACTAC 4080
Db  4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGTTCCAGCAGCCGTGAAGAGGAGGG 4140
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Qy  4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGTTCCAGCAGCCGTGAAGAGGAGGG 4140
Db  4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTCACAAGAAGGTGGC 4200
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Qy  4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTCACAAGAAGGTGGC 4200
Db  4201 TGATTTGGTTGGTTTTCTGCTCCTCCAAATATCAGCCAGTCAGGGAGCCAGGGAGCCCAAAGGCAGA 4260
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Qy  4201 TGATTTGGTTGGTTTTCTGCTCCTCCAAATATCAGCCAGTCAGGGAGCCAGGGAGCCCAAAGGCAGA 4260
Db  4261 AATGCTGGAGAGTGTCATCAAAAATTACAAGACACTGTTTTCCTGAGATCTTCGGCAAAGC 4320
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Qy  4261 AATGCTGGAGAGTGTCATCAAAAATTACAAGACACTGTTTTCCTGAGATCTTCGGCAAAGC 4320
Db  4321 CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGAAGGAGGAGCAGACCCCACCGGCCA 4380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4321 CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGAAGGAGGAGCAGACCCCACCGGCCA 4380
Db  4381 CTCCTATGTCTGTCACCTGCCTAGGTCTCTCCTATGATGGGCTGCTGGGTGATAATCA 4440
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Qy  4381 CTCCTATGTCTGTCACCTGCCTAGGTCTCTCCTATGATGGGCTGCTGGGTGATAATCA 4440
Db  4441 GATCATGCCCAAGACAGCTTCCTGAGTAATTGTCCTGGTCATGATTGTCCTGGTGCAGGGGCGG 4500
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Qy  4441 CCATGCTCCTGAGGGGGAAATCTGGGAGGAAATCTGGGAGGGGTATGATGGGGAG 4500
Db  4501 CCATGCTCCTGAGGGGGAAATCTGGGAGGGGTATGATGGGGAG 4560
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Qy  4501 CCATGCTCCTGAGGGGGAAATCTGGGAGGGGTATGATGGGGAG 4560
Db  4561 GGAGCACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA 4620
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Qy  4561 GGAGCACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA 4620
Db  4621 GTACCTGAGTACGGCCAGGTACCGGGACAGTGCCGGACAGTCCCGGACGATCCCGGACGACTG 4680
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Qy  4621 GTACCTGAGTACGGCCAGGTACCGGGACAGTGCCGGACAGTCCCGGACGATCCCGGACGACTG 4680
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DE   Tumour rejection antigen (MAGE-1) gene.
KW   Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb;
KW   diagnosis; immunoassay; cancer; ss.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   CDS            3881..4711
FT   /tag=    a
FT   /product= Tumour rejection antigen MAGE-1.
FT   /note= "the CDS is not indicated in the text of the
FT   specification but is suggested in the layout
FT   of the sequence."
PN   WO9520974-A1.
PD   10-AUG-1995.
PF   05-JAN-1995; U00095.
PR   01-FEB-1994; US-190411.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (SLOK ) MEMORIAL SLOAN-KETTERING CANCER CENT.
PI   Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
PI   Stockert E, Van der bruggen P;
PN   WO9520974-A1.
DR   WPI; 95-283606/37.
PT   New monoclonal antibody binding specifically to MAGE-1 - useful for
PT   diagnosis and monitoring of cancer, also new hybridomas, recombinant
PT   MAGE-1 and immunogenic peptide(s)
PS   Disclosure; Page 16-19; 33pp; English.
CC   A monoclonal antibody directed against the tumour rejection antigen
CC   (MAGE-1) can be used to detect MAGE-1 in samples by standard
CC   immunoassay methods for diagnosis and monitoring of cancer etc. The
CC   monoclonal antibody is designated MA454 and is produced by the
CC   hybridoma deposited as ATCC HBB11540. The monoclonal antibody is
CC   specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
CC   Peptide fragments of MAGE-1 (See R80618-20) may be useful as
CC   immunogens for production of the monoclonal antibody and antisera.
SQ   Sequence 5724 BP;    1282 A;    1589 G;    1200 T;

Query Match             99.68%;    Score 5650;   DB 1;   Length 5724;
Best Local Similarity 100.0%;    Pred. No. 0.00e+00;
Matches 5650;    Conservative   0;    Mismatches   0;    Indels   0;    Gaps   0;

Db     1 CCCGGGCACCACTGCATCCTCCCCCAATCCTCCTTACGCCACCG   60
         ||||||||||||||||||||||||||||||||||||||||||||
Qy     1 CCCGGGCACCACTGCATCCTCCCCCAATCCTCCTTACGCCACCG   60

Db    61 ATCCAAACATCTTCACGCTCACCCGGTCCACCCCTG  120
         ||||||||||||||||||||||||||||||||||||
Qy    61 ATCCAAACATCTTCACGCTCACCCGGTCCACCCCTG  120

Db   121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGGTGACGTGACTTGAGCATTAGTGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGGTGACGTGACTTGAGCATTAGTGG  180

Db   181 TTAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGTGAGGGAGGAAGCGGG  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 TTAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGTGAGGGAGGAAGCGGG  240

Db   241 CCCAGCTCGTGTAAGGAGGCAAGTGACATGCTGAGGGAGGACTGGGGGACCCACTTACCCCC  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 CCCAGCTCGTGTAAGGAGGCAAGTGACATGCTGAGGGAGGACTGGGGGACCCACTTACCCCC  300

Db   301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTTCCTGGACCATCTGGTGTGGACTTC  360
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Qy   301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTTCCTGGACCATCTGGTGTGGACTTC  360

Db   361 TCAGGCTGGGCCACCCAGCCCCTGCTTAAACCACTGGGAGGGGTCCAGGGCTCGAAGTCAGAG  420
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Qy   361 TCAGGCTGGGCCACCCAGCCCCTGCTTAAACCACTGGGAGGGGTCCAGGGCTCGAAGTCAGAG  420

Db   421 CTCCGTGTGATCAGGAGGCTGCTTAGGAGAGGGCAGCGTCCAGGGCTCTCGCCAGACAT  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 CTCCGTGTGATCAGGAGGCTGCTTAGGAGAGGGCAGCGTCCAGGGCTCTCGCCAGACAT  480

Db   481 CATGCTGTGATCCAGGATTCTCAAGGAGGCTGCCTAAGACCCCACTCCCGTGACCCAAC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT  4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT  4740

Db  4741 GCAAGAGTTGCCTTTTCTTCCCATCCCGCGTGAAGCAGCTTTGAGAGAGGAAGAG  4800
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Qy  4741 GCAAGAGTTGCCTTTTCTTCCCATCCCGCGTGAAGCAGCTTTGAGAGAGGAAGAG  4800

Db  4801 GGAGTCTGAGCATGAGTTGCAGCCAGGGGGACTGGGCCAGTGCACCTT  4860
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4801 GGAGTCTGAGCATGAGTTGCAGCCAGGGGGACTGGGCCAGTGCACCTT  4860

Db  4861 CCAGGGCGGCGTCCAGCAGCTTCCCCGCCCTCGTGTGACATGAGGCCCATTCTTCACTCT  4920
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4861 CCAGGGCGGCGTCCAGCAGCTTCCCCGCCCTCGTGTGACATGAGGCCCATTCTTCACTCT  4920

Db  4921 GAAGAGAGCCGTCAGTGTTCTCAGTAGTTTCTGTTCTATTGGGTGACTTGGAGATT  4980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4921 GAAGAGAGCCGTCAGTGTTCTCAGTAGTTTCTGTTCTATTGGGTGACTTGGAGATT  4980

Db  4981 TATCTTTGTCTCTTTTGGAATTGTTCAAATGTTTTTTTTAAGGGATGGTGAATGAAC  5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4981 TATCTTTGTCTCTTTTGGAATTGTTCAAATGTTTTTTTTAAGGGATGGTGAATGAAC  5040

Db  5041 TTCAGCATCCAAGTTATGAATGACACAGCAGTCTGTGTATATAGTTTAAGGG  5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5041 TTCAGCATCCAAGTTATGAATGACACAGCAGTCTGTGTATATAGTTTAAGGG  5100

Db  5101 TAAGAGTCTGTGTTTATTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT  5160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5101 TAAGAGTCTGTGTTTATTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT  5160

Db  5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGAGATAA  5220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGAGATAA  5220

Db  5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAA  5280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280

Db  5281 ATTTTTAAAGATAATGCATACCTGGATTTCCTTGGCTTCTTTGAGAAGTGAAGAGAAAT  5340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5281 ATTTTTAAAGATAATGCATACCTGGATTTCCTTGGCTTCTTTGAGAAGTGAAGAGAAAT  5340

Db  5341 TAAATCTGAATAAAGAATTCTTCGTGTTCACTGCGTCTTTTCTTCCATGCCACTGAGCA  5400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5341 TAAATCTGAATAAAGAATTCTTCGTGTTCACTGCGTCTTTTCTTCCATGCCACTGAGCA  5400

Db  5401 TCTGCTTTTGGAAGGCCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC  5460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5401 TCTGCTTTTGGAAGGCCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC  5460

Db  5461 CCACCCATAGGGTGTGTAGAGGTCGTAGGAGTGGAGTCGCAGTCACGTAATCGAGGTGGCAAGATGTC  5520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5461 CCACCCATAGGGTGTGTAGAGGTCGTAGGAGTGGAGTCGCAGTCACGTAATCGAGGTGGCAAGATGTC  5520

Db  5521 CTCTAAAGATGTAGGGAAAGTGAGAGGGTGTGAGGGGTCCGGGTGAGAGTG  5580
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5521 CTCTAAAGATGTAGGGAAAGTGAGAGGGTGTGAGGGGTCCGGGTGAGAGTG  5580

Db  5581 GTGGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCATTTTGGGAAACTGCAGTTCCTTCT  5640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5581 GTGGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCATTTTGGGAAACTGCAGTTCCTTCT  5640

Db  5641 GGGGGAGGCTGATTGTAATGATCTTGGGTGGATCC  5674
         |||||||||||||||||||||||||||||||||||
Qy  5641 GGGGGAGGCTGATTGTAATGATCTTGGGTGGATCC  5674
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RESULT   3
ID   Q98902 standard; DNA; 5724 BP.
AC   Q98902;
DT   28-FEB-1996 (first entry)

Left column:

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Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCCCACTCCAATGCTCACTCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541 CCCCACTCCAATGCTCACTCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Db    601 CCCCACATCCCCACACCCCATCCTGATGCCATCCGCCCAGCCATTCCACCCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601 CCCCACATCCCCACACCCCATCCTGATGCCATCCGCCCAGCCATTCCACCCT 660

Db    661 CACCCCACCCCACCCAGCCCAGGCAGGATCCGGTTCCG 720
              |||||||||||||||||||||||||||||||||||||
Qy    661 CACCCCACCCCACCCAGCCCAGGCAGGATCCGGTTCCG 720

Db    721 CCAGGAAACATCCGGTGCCGGATGTGACCGCCACTGACTTGCGCATTGTGGGCAGAGA 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 CCAGGAAACATCCGGTGCCGGATGTGACCGCCACTGACTTGCGCATTGTGGGCAGAGA 780

Db    781 GAAGCCAGGTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 GAAGCCAGGTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Db    841 CTCTGTGAGGAGGCAAGGTGAGAGGTGAGGGAGGACTGAGGACCCCGCCACTCCCAAATA 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGTGAGGGAGGACTGAGGACCCCGCCACTCCCAAATA 900

Db    901 GAGAGCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCCGCCGGGAAGA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 GAGAGCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCCGCCGGGAAGA 960

Db    961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTTCCAAAAGCCTTCGAGACACCAGGTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTTCCAAAAGCCTTCGAGACACCAGGTTC 1020

Db   1021 TTTCTCCCAAGCTCTGAATCAGAGGTTGCTTGTGACCAGGGCAGGACTGGTTAGGGACAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021 TTTCTCCCAAGCTCTGAATCAGAGGTTGCTTGTGACCAGGGCAGGACTGGTTAGGGACAGG 1080

Db   1081 GCAGGGCCACAGGGCTCTGCCAGGCAGATCAGCAAGATCAGCACCCAGAGGAGAGGGCTGTGGGCCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081 GCAGGGCCACAGGGCTCTGCCAGGCAGATCAGCAAGATCAGCACCCAGAGGAGAGGGCTGTGGGCCC 1140

Db   1141 CCAAGACTGCACTCCAATCCCCACTTCGCATTCCCCATTCGCATTCCACCCCAACC 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 CCAAGACTGCACTCCAATCCCCACTTCGCATTCCCCATTCGCATTCCACCCCAACC 1200

Db   1201 CCCATCTCCTCAGCTACACCTCCACCTCCGTCACCTGACCACC 1260
              ||||||||||||||||||||||||||||||||||||||||||
Qy   1201 CCCATCTCCTCAGCTACACCTCCACCTCCGTCACCTGACCACC 1260

Db   1261 ACCCTTGCCCTGCTCTTCAACCCAGCCCAGCCCGGTAGGGCCCGGTGAAACCACTGACT 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261 ACCCTTGCCCTGCTCTTCAACCCAGCCCAGCCCGGTAGGGCCCGGTGAAACCACTGACT 1320

Db   1321 CCCACCCTCATCTCTCCATCGTGCCCCCTCCCCACTCGCTCCCCATTCTGGCAGAATCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 CCCACCCTCATCTCTCCATCGTGCCCCCTCCCCACTCGCTCCCCATTCTGGCAGAATCC 1380

Db   1381 GGTTTGCCCCTGTCCTCAACCCAGGAAGCCCTGGTAGGCCCGGATGTGAAACCACTGACT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381 GGTTTGCCCCTGTCCTCAACCCAGGAAGCCCTGGTAGGCCCGGATGTGAAACCACTGACT 1440

Db   1441 TGAACCTCACAGATCTGAGAGGAGAGCCAGGTTCATTTAATGGTTCATTTAATGGTTCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441 TGAACCTCACAGATCTGAGAGGAGAGCCAGGTTCATTTAATGGTTCATTTAATGGTTCT 1500

Db   1501 ATCCACTGAGGGAGGTTGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501 ATCCACTGAGGGAGGTTGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560

Db   1561 ACTGAGGAGGCACACCCCAGGTAGATGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1561 ACTGAGGAGGCACACCCCAGGTAGATGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620
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Right column:

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Db   1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCTGCTGACCTGACTGGACCACCCCGTCCGTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCTGCTGACCTGACTGGACCACCCCGTCCCGTCC 1680

Db   1681 CACTGCCACTTAACCACCAGGGCAATCTGTAGTCATAGCTTTATGTGACCCGGGCAGGGTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1681 CACTGCCACTTAACCACCAGGGCAATCTGTAGTCATAGCTTTATGTGACCCGGGCAGGGTT 1740

Db   1741 GGTCAGGAGGAGGCAGGGCCCAGGCATCAAGGTCAGCATCCGCCCGCCCGCCATTAGGGTCAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1741 GGTCAGGAGGAGGCAGGGCCCAGGCATCAAGGTCAGCATCCGCCCGCCCGCCATTAGGGTCAGG 1800

Db   1801 ACCCTGGGAGGGACTGAGGTTCCCACCCACCACCTGTCTCCATCTCCACCGCCACC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1801 ACCCTGGGAGGGACTGAGGTTCCCACCCACCACCTGTCTCCATCTCCACCGCCACC 1860

Db   1861 CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTACTCTGTCAGAATCCCTGCTG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1861 CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTACTCTGTCAGAATCCCTGCTG 1920

Db   1921 TCAACCCACCGGAAGCCACGGGAATGGCGGCCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1921 TCAACCCACCGGAAGCCACGGGAATGGCGGCCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980

Db   1981 GGGTCTGATGGAGGGAAGGGCTTGAACAGGGCCTTCAGGGGAGCAGAGGAGCAGGGCCCTAC 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1981 GGGTCTGATGGAGGGAAGGGCTTGAACAGGGCCTTCAGGGGAGCAGAGGAGCAGGGCCCTAC 2040

Db   2041 TGGCGAGATGAGGGAGGCCCTCAGAGGACCCTAGGACACCGCACCCGCACCCGTCTGAG 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2041 TGGCGAGATGAGGGAGGCCCTCAGAGGACCCTAGGACACCGCACCCGCACCCGTCTGAG 2100

Db   2101 ACTGAGGCTGCCACTTCTGGCCTCCAAGAATCAGAACGATGGGACTCGATTGCATGGGG 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2101 ACTGAGGCTGCCACTTCTGGCCTCCAAGAATCAGAACGATGGGACTCGATTGCATGGGG 2160

Db   2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGAGGAGGAAGAGGGACTCAGGGGACCTT 2220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGAGGAGGAAGAGGGACTCAGGGGACCTT 2220

Db   2221 GGAATCCAGATCAGTGTGGACCTCGGCCTCCGGCCGTGCCACGGTGCCACATATG 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2221 GGAATCCAGATCAGTGTGGACCTGTGACCTCCGGCCGTGCCACGGTGCCACATATG 2280

Db   2281 GCCCATATTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2281 GCCCATATTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340

Db   2341 TCAGGTCAACAGAGGGAGAGTTCAGGACTCCATATGGCCCAAGATGTGCCCCCTTCATG 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2341 TCAGGTCAACAGAGGGAGAGTTCAGGACTCCATATGGCCCAAGATGTGCCCCCTTCATG 2400

Db   2401 AGGACTGGGGATATCCCGGCTCAGAAAGAAGGACTCCACACAGTCAGTCTGCTCCCCTT 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2401 AGGACTGGGGATATCCCGGCTCAGAAAGAAGGACTCCACACAGTCAGTCTGCTCCCCTT 2460

Db   2461 TTAGTAGCTCTAGGGGACCAGGCGGTATGTTCCATTCTCACTTGTACCA 2520
              |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2461 TTAGTAGCTCTAGGGGACCAGGCGGTATGTTCCATTCTCACTTGTACCA 2520

Db   2521 CAGGCAGGAAGTTGGGGGCCCTCAGGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2521 CAGGCAGGAAGTTGGGGGCCCTCAGGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT 2580

Db   2581 ACTCATGTGAGGGGAGTTGGGGGTTGAGGAAGCACAGGGCTGGAAGAATAAAGATGAGT 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2581 ACTCATGTGAGGGGAGTTGGGGGTTGAGGAAGCACAGGGCTGGAAGAATAAAGATGAGT 2640

Db   2641 GAGACAGACAAGGCTATTGGAATCCCAGAACCCAAAGGGGTCAGCCCTGGACACC 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2641 GAGACAGACAAGGCTATTGGAATCCCAGAACCCAAAGGGGTCAGCCCTGGACACC 2700
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Thu Apr 9 08:15:25 1998

(DNA sequence alignment — "Db" query and "Qy" database rows, paired with identity bars, numbered in increments of 60 from 2701 to 4920)

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CC   Q72476 encodes tumour rejection antigen E, another sequence
CC   Q72470 encodes melanoma antigen-3 (MAGE-3) a tumour rejection
CC   antigen precursor. Melanomas characterised by the expression of
CC   MAGE-3 can be detected, or monitored, by contacting a test sample
CC   with an agent that can recognise MAGE-3. The melanoma can be treated
CC   by the administration of cytolytic T cells specific for the complex of
CC   antigen D (the mature rejection antigen derived from MAGE-3) and a human
CC   leucocyte antigen (esp. HLA-A1).
SQ   Sequence 2419 BP;      562 A;     581 C;     677 G;     599 T;

Query Match            42.6%;  Score 2419;  DB 1;  Length 2419;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 2419;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db      1 GGATCCAGGCCCGCCAGGAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3256 GGATCCAGGCCCGCCAGGAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC 3315

Db     61 ACTGCATGAGAGTGGGGATGTCACAGCCAGCCCTCGGTAGCACTGAGAAGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3316 ACTGCATGAGAGTGGGGATGTCACAGCCAGCCCTCGGTAGCACTGAGAAGC 3375

Db    121 CAGGGCGTGTCGTCTGCGGTCTGCACCCTGGATTCCTCCTTCCTTCCTGGAGCTCCA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3376 CAGGGCGTGTCGTCTGCGGTCTGCACCCTGGATTCCTCCTTCCTTCCTGGAGCTCCA 3435

Db    181 GGAACCAGCAGTGAGGCCTTGTGTCAGTATCTCAGGTCACAGAGCAGAGGATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3436 GGAACCAGCAGTGAGGCCTTGTGTCAGTATCTCAGGTCACAGAGCAGAGGATG 3495

Db    241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGGCTCCACCTGCCA 300
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGGCTCCACCTGCCA 3555

Db    301 CAGGACACATAGGACTCGGGCTGGAGATGCTAAGGTAAGCCAGACTCATAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3556 CAGGACACATAGGACTCGGGCTGGAGATGCTAAGGTAAGCCAGACTCATAC 3615

Db    361 CGACCTCGCTGCTCGCCGCGTGTACCCTGAGTACCCTCCACTTCCTTCCTTCCTCAGGTTTTCAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3616 CGACCTCGCTGCTCGCCGCGTGTACCCTGAGTACCCTCCACTTCCTTCCTTCCTCAGGTTTTCAG 3675

Db    421 GGACAGGCCAACCCAGAGGACGAATTCCCTGGAGGCCACCAAGGAGGAA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3676 GGACAGGCCAACCCAGAGGACGAATTCCCTGGAGGCCACCAAGGAGGAA 3735

Db    481 GATCTGTAAGTAGGCCTTTGTTAGAGCTGTTCAGTGTTCATTGCCCAGGTCTTCATTGCCCAGGTCTTCA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3736 GATCTGTAAGTAGGCCTTTGTTAGAGCTGTTCAGTGTTCATTGCCCAGGTCTTCATTGCCCAGGTCTTCA 3795

Db    541 CACACTCCTCTCTCCCCAGGCTGTGGGTCTTCATTGCCCAGGTCTTCATTGCCCAGGTCTTGCCACACTCCT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3796 CACACTCCTCTCTCCCCAGGCTGTGGGTCTTCATTGCCCAGGTCTTCATTGCCCAGGTCTTGCCACACTCCT 3855

Db    601 GCCTGCTGCCCTGCCCCTGACGAGAGCTCATCATGTCTCTTGAGCAGGAGTCTGCACTGCAAGCC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3856 GCCTGCTGCCCTGCCCCTGACGAGAGCTCATCATGTCTCTTGAGCAGGAGTCTGCACTGCAAGCC 3915

Db    661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCGTCGTGTGTGCAGGCTGCCAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCGTCGTGTGTGCAGGCTGCCAC 3975

Db    721 CTCCTCCTCCTCTGGTCCTCGTGGGCACCCTGGAGGAGGTGCCCACTGTCGGTCAAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3976 CTCCTCCTCCTCTGGTCCTCGTGGGCACCCTGGAGGAGGTGCCCACTGTCGGTCAAC 4035

Db    781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTTCCAGGCCGTGAAGAGGAGGGGCCAAGCC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTTCCAGGCCGTGAAGAGGAGGGGCCAAGCC 4095

Db    841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCCAAGCACCTCTTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCCAAGCACCTCTTG 4155
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Qy   4861 CCAGGGCCGCGGTCCAGCAGCTTCCCGCTGCGTGACATGAGCCCATTCTTCACTCT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GAAGAGAGCGGGTCAGTGTTCTCAGTAGTAGGTTCTTCGTTCTTATTGGTGACTTGGAGATT 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4921 GAAGAGAGCGGGTCAGTGTTCTCAGTAGTAGGTTCTTCGTTCTTATTGGTGACTTGGAGATT 4980

Db   4981 TATCTTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGGTTGAATGAAC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4981 TATCTTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGGTTGAATGAAC 5040

Db   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG 5100

Db   5101 TAAGAGTCTGTGTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5101 TAAGAGTCTGTGTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Db   5161 AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5161 AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220

Db   5221 AGAACTAAAGAAATTAAGACATGACAGAGTCAATTCTTGCCTTATACCTCAGTTCTATTCTGTAAA 5280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5221 AGAACTAAAGAAATTAAGACATGACAGAGTCAATTCTTGCCTTATACCTCAGTTCTATTCTGTAAA 5280

Db   5281 ATTTTAAAGATATATGCATACCTGGATTCCTTCTTGGCTTCTTGGCTCTTTCTCATGCACTGAGCA 5340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5281 ATTTTAAAGATATATGCATACCTGGATTCCTTCTTGGCTTCTTGGCTCTTTCTCATGCACTGAGCA 5340

Db   5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTCTCCATGCACTGAGCA 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTCTCCATGCACTGAGCA 5400

Db   5401 TCTGCCTTTTGGAAGGCCCTGGGTTAGTAGTGGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5401 TCTGCCTTTTGGAAGGCCCTGGGTTAGTAGTGGGAGATGCTAAGGTAAGCCAGACTCATAC 5460

Db   5461 CCACCCATAGGGTCGTAGAGTCTAGGAGTCGCAGTCGCAGTGCAAGATGTC 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5461 CCACCCATAGGGTCGTAGAGTCTAGGAGTCGCAGTCGCAGTGCAAGATGTC 5520

Db   5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAAGTGAGAGGGTGAGGGTCCGGGTGAGAGTG 5580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAAGTGAGAGGGTGAGGGTCCGGGTGAGAGTG 5580

Db   5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Db   5641 GGGGGAGCTG 5650
          ||||||||||
Qy   5641 GGGGGAGCTG 5650
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RESULT  4
ID   Q72476 standard; DNA; 2419 BP.
AC   Q72476;
DT   21-JUN-1995 (first entry)
DE   Tumour rejection antigen E encoding DNA.
KW   Tumour rejection antigen E; melanoma antigen-3; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
OS   Homo sapiens.
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Disclosure; Page 58; 105pp; English.
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Db   901  TATCCTGGAGTCCTTGTTCCGACAGTAATCACTAAGGAGGTGCTGATTTGGTTGGTTT  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4156  TATCCTGGAGTCCTTGTTCCGACAGTAATCACTAAGGAGGTGCTGATTTGGTTGGTTT  4215

Db   961  TCTGCTCCTCAAATATCAGCCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4216  TCTGCTCCTCAAATATCAGCCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT  4275

Db  1021  CATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4276  CATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA  4335

Db  1081  GCTGTGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4336  GCTGTGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGT  4395

Db  1141  CACCTGCCTAGGTCTCTCCTATGATGCGCTGGGTGATAATCATGCCCAAGAC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4396  CACCTGCCTAGGTCTCTCCTATGATGCGCTGGGTGATAATCATGCCCAAGAC  4455

Db  1201  AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGCGGCCATGCTCCTGAGGA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4456  AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGCGGCCATGCTCCTGAGGA  4515

Db  1261  GGAAATCTGGGAGGAGCTGAGTGTGATGGAGTGTATGATGGGAGGCACAGTGCCTA  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4516  GGAAATCTGGGAGGAGCTGAGTGTGATGGAGTGTATGATGGGAGGCACAGTGCCTA  4575

Db  1321  TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTCGAGGAAAAGTACCTGGAGTACGG  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4576  TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTCGAGGAAAAGTACCTGGAGTACGG  4635

Db  1381  CAGTGCCGGACAGTGATCCCGGCGACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4636  CAGTGCCGGACAGTGATCCCGGCGACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT  4695

Db  1441  GAAACCAGCTATGTGAAAGTCCTTGAGTGTGATCAAGGTCAGTGCAAGAGTTCGCTTT  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4696  GAAACCAGCTATGTGAAAGTCCTTGAGTGTGATCAAGGTCAGTGCAAGAGTTCGCTTT  4755

Db  1501  TTCTTCCCATCCCGCTGCGTGAAGCAGCTTTGAGAGAGGAAGGAGTCTGAGCATGA  1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4756  TTCTTCCCATCCCGCTGCGTGAAGCAGCTTTGAGAGAGGAAGGAGTCTGAGCATGA  4815

Db  1561  GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTCCCGTCCA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||
Qy  4816  GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTCCCGTCCA  4875

Db  1621  GCAGCTTCCCCGTGCCTGCCTCCGTGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGGCGGTCAG  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4876  GCAGCTTCCCCGTGCCTGCCTCCGTGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGGCGGTCAG  4935

Db  1681  TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT  1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4936  TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT  4995

Db  1741  TTGGAATTGTTCAAATGTTTTTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4996  TTGGAATTGTTCAAATGTTTTTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT  5055

Db  1801  TATGAATGACAGCAGCAGTCACACAGTTCTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5056  TATGAATGACAGCAGCAGTCACACAGTTCTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT  5115

Db  1861  TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5116  TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA  5175

Db  1921  AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGAGATGAGAAAGAAATT  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5176  AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGAGATGAGAAAGAAATT  5235

Db  1981  AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5236  AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA  5295

Db  2041  TGCATACCTGGATTTCCTTGGCTTCTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5296  TGCATACCTGGATTTCCTTGGCTTCTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG  5355

Db  2101  AATTCTTCCTGTTCACTGGCTCTTTCTTCCTCCATGCACTGAGCATCTGCTTTTTGGAAG  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5356  AATTCTTCCTGTTCACTGGCTCTTTCTTCCTCCATGCACTGAGCATCTGCTTTTTGGAAG  5415

Db  2161  GCCCTGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGAACTCATACCCACCCATAGGGTCG  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5416  GCCCTGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGAACTCATACCCACCCATAGGGTCG  5475

Db  2221  TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5476  TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG  5535

Db  2281  GAAAAGTGAGAGAGGGGTGAGGGTGTGGGCTCCGGTGGAGTGGTGGTGAGTGTCAATGC  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5536  GAAAAGTGAGAGAGGGGTGAGGGTGTGGGCTCCGGTGGAGTGGTGGTGAGTGTCAATGC  5595

Db  2341  CCTGAGCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCTCGGGGGAGCTGATTGT  2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5596  CCTGAGCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCTCGGGGGAGCTGATTGT  5655

Db  2401  AATGATCTTGGGTGGATCC  2419
          |||||||||||||||||||
Qy  5656  AATGATCTTGGGTGGATCC  5674
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RESULT  5
ID   Q32351 standard; DNA; 2419 BP.
AC   Q32351;
DT   22-APR-1993  (first entry)
DE   Antigen E gene.
KW   Stable; antigen; E; D; F; A; human; melanoma; cell line; MZ2-MEL;
KW   cytolytic T cell; MEL3.1; open reading frame; homology; MAGE;
KW   melanoma antigen; ss.
OS   Homo sapiens.
PN   WO922056-A.
PD   26-NOV-1992.
PF   22-MAY-1992; U04354.
PR   23-MAY-1991; US-705702.
PR   09-JUL-1991; US-728838.
PR   23-SEP-1991; US-764364.
PR   12-DEC-1991; US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure; Page 69-70; 142pp; English.
CC   This sequence encodes the stable antigen E.  This antigen is expressed
CC   along with antigens "D, F and A" by the human melanoma cell line MZ2-
CC   MEL.  These antigens are all recognised by cytolytic T cells.  A
CC   subline of MZ2-MEL is MEL3.1 which only expresses antigen E.  This
CC   cell line was chosen as a source for the isolation of this sequence.
CC   This sequence was found to contain three exons. The open reading frame
CC   for antigen E was contained within the first two exons.  An ATG is
CC   located at position 66 of exon 3 and is followed by an 828 base pair
CC   reading frame.  The three exons contain 65, 73 and 1551 base pairs.
CC   During the isolation of this sequence two different but closely reated
CC   cDNAs were also identified.  These cDNAs, when tested, did not
CC   transfer expression of antigen E, but they did show substantial
CC   homology to the antigen E cDNA sequence.  These new cDNAs represent a
CC   new family of genes refered to as melanoma antigens (MAGE) (see also
CC   Q32352-69).
SQ   Sequence   2419 BP;   562 A;   581 C;   677 G;   599 T;
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Query Match          42.6%;    Score 2419;    DB 1;    Length 2419;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  2419;  Mismatches    0;  Conservative    0;  Indels    0;  Gaps    0;

Db       1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC 3315

Db      61 ACTCGATGAGAGTGGGATGTCACAGAGTCAGCCACCCTTCTGTAGCACTGAGAAGC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3316 ACTCGATGAGAGTGGGATGTCACAGAGTCAGCCACCCTTCTGTAGCACTGAGAAGC 3375

Db     121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCCTCTTCCTGGAGCTCCA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCCTCTTCCTGGAGCTCCA 3435

Db     181 GGAACCAGCAGTGAGGGCCTTGGTCTGAGACAGTATCCTCAGTCACGAGAGCAGGAGGATG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3436 GGAACCAGCAGTGAGGGCCTTGGTCTGAGACAGTATCCTCAGTCACGAGAGCAGGAGGATG 3495

Db     241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555

Db     301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCCACCTCCTACTGTCAGTCCTGTAGAAT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCCACCTCCTACTGTCAGTCCTGTAGAAT 3615

Db     361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCCTCCTTCCTCACTTCCTCAGGTTTTCAG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCCTCCTTCCTCACTTCCTCAGGTTTTCAG 3675

Db     421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735

Db     481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTCAGCTGAGGCCTCTCA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTCAGCTGAGGCCTCTCA 3795

Db     541 CACACTCCCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCAGCTCCACACTCCT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3796 CACACTCCCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCAGCTCCACACTCCT 3855

Db     601 GCCTGCTGCCCGACGAGTCATCATGTCTCTTGAGCAGGAGGAGTCTGCACTGCAAGCC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3856 GCCTGCTGCCCGACGAGTCATCATGTCTCTTGAGCAGGAGGAGTCTGCACTGCAAGCC 3915

Db     661 TGGAGGAAGCCCTGAGGCCTCAGGGAGTTCCAGCAGCCCTGAAGCAGAGGGCCCGTGTGTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3916 TGGAGGAAGCCCTGAGGCCTCAGGGAGTTCCAGCAGCCCTGAAGCAGAGGGCCCGTGTGTG 3975

Db     721 CTCCTCCTCTCCTCCGTCTCGGCACCCTGGAGGAGGTGCCCCACTACCACCATCAACTTCACTCG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    3976 CTCCTCCTCTCCTCCGTCTCGGCACCCTGGAGGAGGTGCCCCACTACCACCATCAACTTCACTCG 4035

Db     781 AGATCCTCCCAGAGTCTCAGGGAGTCCTCAGGGAGCCTCCCCAGAGGAGGAGCCCAGCCTCTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4036 AGATCCTCCCAGAGTCTCAGGGAGTCCTCAGGGAGCCTCCCCAGAGGAGGAGCCCAGCCTCTG 4095

Db     841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCCAGCAGAGGGGCCCAAGCCACCACCTCTTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCCAGCAGAGGGGCCCAAGCCACCACCTCTTG 4155

Db     901 TATCCTGGAGTCCTGTTCCCAGCAGTAATCACTACTAAGAAGAGGTGGCTGATTTGGTTGGTTT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4156 TATCCTGGAGTCCTGTTCCCAGCAGTAATCACTACTAAGAAGAGGTGGCTGATTTGGTTGGTTT 4215

Db     961 TCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGGAGAGTGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4216 TCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGGAGAGTGT 4275
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Db    1021 CATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4276 CATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335

Db    1081 GCTGGTCTTGGCATTGACGTGAAGGAAGGAGCAGAGCCCACCGGCCACTCCTATGTCCTTGT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4336 GCTGGTCTTGGCATTGACGTGAAGGAAGGAGCAGAGCCCACCGGCCACTCCTATGTCCTTGT 4395

Db    1141 CACCTGCCTAGGTCTCTCCTATGATGGGCCTGGGTGATAATCAGATCATGCCCAAGAC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4396 CACCTGCCTAGGTCTCTCCTATGATGGGCCTGGGTGATAATCAGATCATGCCCAAGAC 4455

Db    1201 AGGCTTCCTGATAATTGTCTCGGTCATGATTGCAATGCAGCCGGCCATCCTCCTGAGGA 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4456 AGGCTTCCTGATAATTGTCTCGGTCATGATTGCAATGCAGCCGGCCATCCTCCTGAGGA 4515

Db    1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 4575

Db    1321 TGGGGAGCCCAGGAGCCCTGCTCACCCCAAGATTTGGTGCAGGAAAAGTAGCTGGAGTACGG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4576 TGGGGAGCCCAGGAGCCCTGCTCACCCCAAGATTTGGTGCAGGAAAAGTAGCTGGAGTACGG 4635

Db    1381 CAGTGCCGGACAGTGATCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCCTGCT 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4636 CAGTGCCGGACAGTGATCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCCTGCT 4695

Db    1441 GAAACCAGCTATGTGAAAGTCCTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4696 GAAACCAGCTATGTGAAAGTCCTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 4755

Db    1501 TTCTTCCCATCCCGCGTCAAGCAGTTTGAGCAGCAGGAGGAGTCTGAGCATGA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4756 TTCTTCCCATCCCGCGTCAAGCAGTTTGAGCAGCAGGAGGAGTCTGAGCATGA 4815

Db    1561 GTTGCAGGCCAAGGCAGTGGGGACTGGGGCCAGTGCACCTTCCAGGGCCGCGCTCCA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4816 GTTGCAGGCCAAGGCAGTGGGGACTGGGGCCAGTGCACCTTCCAGGGCCGCGCTCCA 4875

Db    1621 GCAGCTTCCCCTGCCCTGTGTGACATGAGGCCCATTCTCACTCTGAAGAGAGCGGGTCAG 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4876 GCAGCTTCCCCTGCCCTGTGTGACATGAGGCCCATTCTCACTCTGAAGAGAGCGGGTCAG 4935

Db    1681 TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTCACTTGGGACTTGGAGATTTATCTTGTCTCTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4936 TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTCACTTGGGACTTGGAGATTTATCTTGTCTCTT 4995

Db    1741 TTGGAATTGTTCAAATGTTTTTTTTAAGGGATAATAACAGCAGTGGGATCCAAGTT 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    4996 TTGGAATTGTTCAAATGTTTTTTTTAAGGGATAATAACAGCAGTGGGATCCAAGTT 5055

Db    1801 TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAATAACAGTCTGTGTT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5056 TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAATAACAGTCTGTGTT 5115

Db    1861 TTATTCAGATTGGAAATCCATTCTATTTTGTGAATTGGGATAATAGATGAGATAAAGAAATT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5116 TTATTCAGATTGGAAATCCATTCTATTTTGTGAATTGGGATAATAGATGAGATAAAGAAATT 5175

Db    1921 AGTACTTAGAAATGAAAAATGAGCAGTAAAATAGATGAGTAAAAGAACTAAAGAAATT 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5176 AGTACTTAGAAATGAAAAATGAGCAGTAAAATAGATGAGTAAAAGAACTAAAGAAATT 5235

Db    1981 AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5236 AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA 5295

Db    2041 TGCATAACCTGGATTTCCTTGGCTTCTTGAGAATGTAAATGAAATTAAAATCTGAATAAAG 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    5296 TGCATAACCTGGATTTCCTTGGCTTCTTGAGAATGTAAATGAAATTAAAATCTGAATAAAG 5355

Db    2101 AATTCTTCCTGTTCACTGCTGCTCTTTTCTTCCCATGCACTGCAGCACTGCTCTCTGCTGTTTTGGAAG 2160
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Qy   5356 AATTCTTCCGTTCACTGGCTCTTTCTTCTCCATGCACTGAGCACTGCTTTTTGGAAG 5415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5416 GCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 5475
Db   2221 TAGAGTCTAGGAGCTGCAGTCAGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5476 TAGAGTCTAGGAGCTGCAGTCAGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 5535
Db   2281 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGTGAGAGTGGTGGTGAGTGTCAATGC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5536 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGTGAGAGTGGTGGTGAGTGTCAATGC 5595
Db   2341 CCTGAGCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5596 CCTGAGCTGGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 5655
Db   2401 AATGATCTTGGGTGGATCC 2419
          |||||||||||||||||||
Qy   5656 AATGATCTTGGGTGGATCC 5674
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RESULT   6

ID   T05086 standard; DNA; 2419 BP.
AC   T05086;
DT   26-FEB-1996 (first entry)
DE   MZ2-MEL antigen E precursor gene.
KW   Melanoma; MZ2-MEL; tumour rejection antigen; cancer; diagnosis; ss.
OS   Homo sapiens.
PN   WO9523874-A1.
PD   08-SEP-1995.
PF   23-FEB-1995; U02203.
PR   01-MAR-1994; US-204727.
PR   10-MAR-1994; US-209172.
PR   01-SEP-1994; US-299849.
PR   30-NOV-1994; US-346774.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI   De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI   Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
DR   WPI; 95-320586/41.
PT   Determn. of cancerous condition(s) - using a nucleic acid as a
PT   primer to determine expression of a MAGE tumour rejection antigen
PT   precursor
PS   Example 20; Page 69-70; 121pp; English.
CC   A gene sequence (T05086) hybridizes with a 2.4 kb fragment from
CC   human melanoma cell line MZ2-MEL but not with E- antigen loss
CC   variants of MZ2-MEL. This E precursor antigen gene sequence was
CC   obtd. from a cosmid derived from DNA of the E+ subclone MZ2-MEL 43.
SQ   Sequence 2419 BP; 560 A; 581 C; 601 G; 677 T;

Query Match   42.6%; Score 2415; DB 1; Length 2419;
Best Local Similarity   99.9%;
Matches 2417; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Db      1 GGATCCAGGCCCTGCCAGGAAAAATAATAAGGGCCCTGCCTGAGAACAGAGAGGGTCATCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3256 GGATCCAGGCCCTGCCAGGAAAAATAATAAGGGCCCTGCCTGAGAACAGAGAGGGTCATCC 3315
Db     61 ACTGACATGAGAGTGGGGATGTCACAGAGTCCAGCCCCCACCCCTCCTGGTAGCACTGAAGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3316 ACTGACATGAGAGTGGGGATGTCACAGAGTCCAGCCCCCACCCCTCCTGGTAGCACTGAAGC 3375
Db    121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCTCTTCCTGGATTCCTCCA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCTCTTCCTGGATTCCTCCA 3435
Db    181 GGAACCAGGCAGTGAGGCCCTTGGTTGGTCAGATCCTGAGACAGTATCCTCAGGTCACAGAGGATG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3436 GGAACCAGGCAGTGAGGCCCTTGGTTGGTCAGATCCTGAGACAGTATCCTCAGGTCACAGAGGATG 3495
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Db    241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCACCTGCCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCACCTGCCA 3555
Db    301 CAGGACACATAGGACTCCACAGAGTCTGGCCTGCCTAGACTCATACCCACCCATAGGAAT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTGCCTAGACTCATACCCACCCATAGGAAT 3615
Db    361 CGACCTTCGTCGTCCGGCCGGCTGTACCCTGAGTACCCTCACTTCCTCCTCCTCAGGTTTCAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3616 CGACCTTCGTCGTCCGGCCGGCTGTACCCTGAGTACCCTCACTTCCTCCTCCTCAGGTTTCAG 3675
Db    421 GGACAGGCCAACCAGAGACAGGATTCCCTGAGGCCACAGAGGAGCCACCAAGGAGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3676 GGACAGGCCAACCAGAGACAGGATTCCCTGAGGCCACAGAGGAGCCACCAAGGAGCA 3735
Db    481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGCTGAGTCTCAGCTCCGCCCACACTCCT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGCTGAGTCTCAGCTCCGCCCACACTCCT 3795
Db    541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCAATTGCCCAGCTCCTGCCCCACACTCCT 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCAATTGCCCAGCTCCTGCCCCACACTCCT 3855
Db    601 GCCTGCTGCCCTGAGCGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3856 GCCTGCTGCCCTGAGCGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
Db    661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTCGGTGTGTGTGCAGGCTGCCAC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTCGGTGTGTGTGCAGGCTGCCAC 3975
Db    721 CTCCTCCTCCTCCTCTGTCCTGGTCCTCTGTGCTCCTGGGCCACCCTGCTCGGTCAAC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3976 CTCCTCCTCCTCCTCTGTCCTGGTCCTCTGTGCTCCTGGGCCACCCTGCTCGGTCAAC 4035
Db    781 AGATCCTCCCAGAGTCCTCAGGGAGCCTCCGGCCTTTCCCACTACCATCAACTTCACTCG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4036 AGATCCTCCCAGAGTCCTCAGGGAGCCTCCGGCCTTTCCCACTACCATCAACTTCACTCG 4095
Db    841 ACAGAGGCCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGCAGCAGCAGGGGCCAAGCACCTCTTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4096 ACAGAGGCCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGCAGCAGCAGGGGCCAAGCACCTCTTG 4155
Db    901 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTACGAAGGTGGCTGATTTGGTTGGTTT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4156 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTACGAAGGTGGCTGATTTGGTTGGTTT 4215
Db    961 TCTGCCTCCTCAAATATCAGCCGCCAGGGAGCCAGTGCACAAAGGCCACAAAGCTGGAGAGTGT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4216 TCTGCCTCCTCAAATATCAGCCGCCAGGGAGCCAGTGCACAAAGGCCACAAAGCTGGAGAGTGT 4275
Db   1021 CATCATTAATTACAAGCACTGTTTTCCTGGAAGATCCTCGGCCAAAGCCTCTGAGTCCTTGCA 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4276 CATCAAAAATTACAAGCACTGTTTTCCTGGAGATCCTCGGCCAAAGCCTCTGAGTCCTTGCA 4335
Db   1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCACTCCTATGTCCTTGT 4395
Db   1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455
Db   1201 AGGCTTCCTGATAATTGTCCTGTCGATTGCAATGGAGGGCGGCCATGCCCTGAGGA 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4456 AGGCTTCCTGATAATTGTCCTGTCGATTGCAATGGAGGGCGGCCATGCCCTGAGGA 4515
Db   1261 GGAAATCTGGGAGGACTGAGTGTATGAGGTGTGATGGAGGACAGTGTTA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4516 GGAAATCTGGGAGGACTGAGTGTATGAGGTGTGATGGAGGACAGTGTCCTA 4575
Db   1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGTCGAGGAAAAGTACCTGGAGTACGG 1380
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Qy   5656 AATGATCTTGGGTGGATCC 5674

RESULT 7
ID    Q72472 standard; DNA; 2420 BP.
AC    Q72472;
DT    21-JUN-1995   (first entry)
DE    Tumour rejection antigen E precursor gene DNA.
KW    Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3;
KW    cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
OS    Homo sapiens.
PN    WO9423031-A.
PD    13-OCT-1994.
PF    17-MAR-1994; U02877.
PR    26-MAR-1993; US-037230.
PA    (LUDW-) LUDWIG INST CANCER RES.
PI    Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR    WPI; 94-333192/41.
PT    New tumour rejection antigen precursor MAGE3 - useful in
PT    treatment and diagnosis of cancer
PS    Example 20; Page 28; 105pp; English.
CC    Q72472 is the tumour rejection antigen E precursor gene, another
CC    gene Q72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection
CC    antigen precursor. Melanomas characterised by the expression of MAGE-3
CC    can be detected, or monitored, by contacting a test sample with an
CC    agent that can recognise MAGE-3. The melanoma can be treated by the
CC    administration of cytolytic T cells specific for the complex of antigen
CC    D (the mature rejection antigen derived from MAGE-3) and a human
CC    leucocyte antigen (esp. HLA-Al).
SQ    Sequence 2420 BP;   562 A;   582 C;   677 G;   599 T;

Query Match               42.5%;   Score 2413;   DB 1;   Length 2420;
Best Local Similarity   100.0%;    Pred. No. 0.00e+00;
Matches 2419;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

Db      1 GGATCCAGGCCCTGCCAGGAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3256 GGATCCAGGCCCTGCCAGGAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC 3315

Db     61 ACTGCATGAGAGTGGGATGTCACAGAGTCCAGCACCCTCGTGTAGCACTGAGAAGC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3316 ACTGCATGAGAGTGGGATGTCACAGAGTCCAGCACCCTCGTGTAGCACTGAGAAGC 3375

Db    121 CAGGGCGTGTCGTTGCCGTCGCACCCTGAGGGCCGTGGATTCCTTCCTGGAGCTCCA  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3376 CAGGGCGTGTCGTTGCCGTCGCACCCTGAGGGCCGTGGATTCCTTCCTGGAGCTCCA 3435

Db    181 GGAACCAGCAGTGAGGCCTTGGTCAGACAGTATCCTCAGGTCACAGAGTCAGAGGATG  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3436 GGAACCAGCAGTGAGGCCTTGGTCAGACAGTATCCTCAGGTCACAGAGTCAGAGGATG 3495

Db    241 CACAGGGTGCCAGCAGTGAATGTTGCCCTGAATGCACAGCAAGGGCCCACCTGCCA  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3496 CACAGGGTGCCAGCAGTGAATGTTGCCCTGAATGCACAGCAAGGGCCCACCTGCCA 3555

Db    301 CAGGACACATAGGACTCCAGAGTCTGGCCTCACCTCCTCCACTCTCAGTCCTGTAGAAT  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3556 CAGGACACATAGGACTCCAGAGTCTGGCCTCACCTCCTCCACTCTCAGTCCTGTAGAAT 3615

Db    361 CGACCTCTGCTGCCGGCGTGTACCCTGATTCCTCCACTTCCTCCACTCCTCCAGGTTTCAG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3616 CGACCTCTGCTGCCGGCGTGTACCCTGATTCCTCCACTTCCTCCACTCCTCCAGGTTTCAG 3675

Db    421 GGGACAGGCCAACCAGGACAGGATTCCTGGAGGGCCCACCAGGAGGCCACCAAGGAGAA  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3676 GGGACAGGCCAACCAGGACAGGATTCCTGGAGGGCCCACCAGGAGGCCACCAAGGAGAA 3735

Db    481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGTTCAGTTCAGCTGAGGCCTCTCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGTTCAGTTCAGCTGAGGCCTCTCA 3795

Db    541 CACACTCCCTCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT  600
          |||||||||||||||||||||||||||||||||||||||||
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Qy   4576 TGGGGAGCCCAGGAAGCTGCTCACCCAGAGTTGGTGCAGGAAAGTACCTGGAGTACGG 4635
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1381 CAGGTGCCGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4636 CAGGTGCCGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT 4695

Db   1441 GAACCAGCTATGTGAGTAGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4696 GAACCAGCAGCTATGTGAGTAGTGATCAAGG'CAGTGCAAGAGTTCGCTTT 4755

Db   1501 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGGAGGAGAGGGAGTCTGAGCATGA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4756 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGGAGGAGAGGGAGTCTGAGCATGA 4815

Db   1561 GTTGCAGCCAAGGCCAGTGGAGGGGGACTGGGCCAGTGCACCTTCCAGGCCGCGTCCA 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4816 GTTGCAGCCAAGGCCAGTGGAGGGGGACTGGGCCAGTGCACCTTCCAGGCCGCGTCCA 4875

Db   1621 GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCAATTCTTCACTCTGAAGAGAGCGGTCAG 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4876 GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCAATTCTTCACTCTGAAGAGAGCGGTCAG 4935

Db   1681 TGTTCTCAGTAGTAGGTTTCGTGTCTATTGGGTGACTTGGAGATTTATCTTGTCTCTT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4936 TGTTCTCAGTAGTAGGTTTCGTGTCTATTGGGTGACTTGGAGATTTATCTTGTCTCTT 4995

Db   1741 TTGGAATTGTTCAAATGTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4996 TTGGAATTGTTCAAATGTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT 5055

Db   1801 TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTAAGGGTAAGAGTCTTGTGTT 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5056 TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTAAGGGTAAGAGTCTTGTGTT 5115

Db   1861 TTATTCAGATTGGGAAAATCCATTCTATTTGTGAATTGGGATAATAACAGCAGTGGAATA 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5116 TTATTCAGATTGGGAAAATCCATTCTATTTGTGAATTGGGATAATAACAGCAGTGGAATA 5175

Db   1921 AGTACTTAGAAATGTGAAAAATGAGACAGTAAAATAGATGAGATAAAGAACTAAAGAAATT 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5176 AGTACTTAGAAATGTGAAAAATGAGACAGTAAAATAGATGAGATAAAGAACTAAAGAAATT 5235

Db   1981 AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5236 AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA 5295

Db   2041 TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5296 TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG 5355

Db   2101 AATTCTTCCTGTTCACTGGCTCTCTTTCTTCCCCATGCACTGCATCTGCAGCATCTGCTTTTGGAAG 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5356 AATTCTTCCTGTTCACTGGCTCTCTTTCTTCCCCATGCACTGCATCTGCAGCATCTGCTTTTGGAAG 5415

Db   2161 GCCCTGGGTTAGTAGTGGAGATGCTAAGTAAGCCAGAGCTCATACCCCATACCCATAGGGTCG 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5416 GCCCTGGGTTAGTAGTGGAGATGCTAAGTAAGCCAGAGCTCATACCCCATACCCATAGGGTCG 5475

Db   2221 TAGAGTCTAGGAGCTGCAAGTCACGTAATCGAGGTGCAAGATGTCCTCTAAAGATGTAGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5476 TAGAGTCTAGGAGCTGCAAGTCACGTAATCGAGGTGCAAGATGTCCTCTAAAGATGTAGG 5535

Db   2281 GAAAAGTGAGAGAGGGTGAGGGTGGGGGCTCCGGTGGGCTGTGAGCAGTGGTGTCAATGC 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5536 GAAAAGTGAGAGAGGGTGAGGGTGGGGGCTCCGGTGGGCTGTGAGCAGTGGTGTCAATGC 5595

Db   2341 CCTGAGCTGGGGCATTTGGGGCTGCAGTTCCTTGTTAGAGTCTCCAAGTTCAGTTCAGCTGATTGT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5596 CCTGAGCTGGGGCATTTGGGGCTGCAGTTCCTTGTTAGAGTCTCCAAGTTCAGTTCAGCTGATTGT 5655

Db   2401 AATGATCTTGGGTGGATCC 2419
          |||||||||||||||||||
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Qy 3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCACACTCCT 3855
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GCCTGCTCGCCCTGACGAGAGTCATCATGTCTTGAGCAGGAGTCTGCACTGCAAGCC 660
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3856 GCCTGCTCGCCCTGACGAGAGTCATCATGTCTTGAGCAGGAGTCTGCACTGCAAGCC 3915

Db   661 TGAGGAAGCCCTTGAGGCCCAACAGAGAGGCCCTGGCCTGGTGTGCAGGCTGCCAC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3916 TGAGGAAGCCCTTGAGGCCCAACAGAGAGGCCCTGGCCTGGTGTGCAGGCATGCCAC 3975

Db   721 CTCCTCCTCCTCCTCTGTCTCTGGGCACCCTGGAGAGGTGCCCACTGCTGGGTCAAC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3976 CTCCTCCTCCTCCTCTGTCTCTGGGCACCCTGGAGAGGTGCCCACTGCTGGGTCAAC 4035

Db   781 AGATCCTCCCAGAGTCCTCAGGGAGTCCTCCGCCTTCCCACCACCATCAACTTCACTCG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4036 AGATCCTCCCAGAGTCCTCAGGGAGTCCTCCGCCTTCCCACCACCATCAACTTCACTCG 4095

Db   841 ACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGGCCAAGCACCTCTTG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGCCAAGCACCTCTTG 4155

Db   901 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAGAGGTGGCTGATTTGGTTGGTTT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4156 TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAGAGGTGGCTGATTTGGTTGGTTT 4215

Db   961 TCTGCTTCCTCAAATATCGAGCCAGGAGGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4216 TCTGCTTCCTCAAATATCGAGCCAGGAGGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275

Db 1021 CATCAAAAATTACAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4276 CATCAAAAATTACAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335

Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCACCGGCCACTCCTATGTCCTTGT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCACCGGCCACTCCTATGTCCTTGT 4395

Db 1141 CACCTGCTAGGTCTCTCCTATGATGGCTCGGCTGGTGATAATCAGATCATGCCCAAGAC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4396 CACCTGCTAGGTCTCTCCTATGATGGCTCGGCTGGTGATAATCAGATCATGCCCAAGAC 4455

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGCGGCCATGTCTCCTGAGGA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGCGGCCATGTCTCCTGAGGA 4515

Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGAGTGTATGATGGGAGGGAGCACAGTGCCTA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4516 GGAAATCTGGGAGGAGCTGAGTGTGAGTGTATGATGGGAGGGAGCACAGTGCCTA 4575

Db 1321 TGGGGAGCCAGGAGAGTGCTCACCAGGAGAGTTGGTGCAGGAAAAAGTACCTGGAGTACCG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4576 TGGGGAGCCAGGAGAGTGCTCACCAGGAGAGTTGGTGCAGGAAAAAGTACCTGGAGTACG 4634

Db 1381 GCAGGTGCCGGACAGTGATCCCGGACAGCTGTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4635 GCAGGTGCCGGACAGTGATCCCGGACAGCTGTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG 4694

Db 1441 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTCAATCAAGGTCAGTGCAAGAGTTCGCTT 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4695 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTCAATCAAGGTCAGTGCAAGAGTTCGCTT 4754

Db 1501 TTTCTTCCATCCCTGCCTGAACCAGCTTGAAGCAGAGGAGTCTTGAGCATG 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4755 TTTCTTCCATCCCTGCCTGAACCAGCTTGAAGCAGAGGAGTCTTGAGCATG 4814

Db 1561 AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCCAGTTCCAGGGCCGCGTCC 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4815 AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCCAGTTCCAGGGCCGCGTCC 4874

Db 1621 AGCAGCTTCCCCGCTGCCCTGGTGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGCGGTCA 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4875 AGCAGCTTCCCCGCTGCCCTGGTGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGCGGTCA 4934

Db 1681 GTGTTCTTCAGTAGTAGTAGGTTTCTGTTCTCATTGGGTGACTTGGAGATTTATCTTGTTCCT 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4935 GTGTTCTTCAGTAGTAGTAGGTTTCTGTTCTCGTTCTCATTGGGTGACTTGGAGATTTATCTTTGTGTCTCT 4994

Db 1741 TTTGGAATTGTTCAAATGTTTTTTTTTTTTAAGGATGGTGAATGAACTTCAGCATCCAAGT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4995 TTTGGAATTGTTCAAATGTTTTTTTTTTTTAAGGATGGTGAATGAACTTCAGCATCCAAGT 5054

Db 1801 TTATGAATGACAGCAGTCACACAGTTCTGTGTATAGTTAAGGGTAAGAGTCTTGTGT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5055 TTATGAATGACAGCAGTCACACAGTTCTGTGTATAGTTAAGGGTAAGAGTCTTGTGT 5114

Db 1861 TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5115 TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT 5174

Db 1921 AAGTACTTAGAAGTGAAAAATGACCAGTAAAATAGATGAGTAAAGAACTAAAGAAAT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5175 AAGTACTTAGAAATGTGAAAAATGACCAGTAAAATAGATGAGTAAAGAACTAAAGAAAT 5234

Db 1981 TAAGAGATAGTCAATTCTGCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5235 TAAGAGATAGTCAATTCTGCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 5294

Db 2041 ATGCATACCTGATTTCCTTGGCTTCTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5295 ATGCATACCTGGATTTCCTTGGCTTCTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 5354

Db 2101 GAATTCTTCCTGTCACTGGCTCTCTTTCTTCTTCTCCATGCACTGCGAGCACTGCTTTTTGGAA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5355 GAATTCTTCCTGTCACTGGCTCTCTTTCTTCTTCTCCATGCACTGCGAGCACTGCTTTTTGGAA 5414

Db 2161 GGCCCTGGTTAGTAGTGGAGATGCTAAGGTAAGGTAAGCTGTAAGACTCATACCCCATAGGGTC 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5415 GGCCCTGGTTAGTAGTGGAGATGCTAAGGTAAGGTAAGCTGTAAGACTCATACCCCATAGGGTC 5474

Db 2221 GTAGAGTCTAGGAGCTGCAGTAATCGAGGTGCACGTAATCGAGGTGCCAAGATGTCCTCTAAAGATGTAG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5475 GTAGAGTCTAGGAGCTGCAGTCGAGTAATCGAGGTGCACGTAATCGAGGTGCCAAGATGTCCTCTAAAGATGTAG 5534

Db 2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGGAGTGTGGTGTCAATG 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGGAGTGTGGTGTCAATG 5594

Db 2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTCGCAGTCGCAGTCGAGTCGATTG 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy 5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTCGCAGTTCCTTCTGGGGGAGCTGAGTG 5654

Db 2401 TAATGATCTTGGGTGGATCC 2420
         ||||||||||||||||||||
Qy 5655 TAATGATCTTGGGTGGATCC 5674

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PT   Human melanoma antigen, MAGE-1, peptide(s) - useful for
PT   stimulating immune response against melanoma
PS   Example 1; Fig 1; 59pp; English.
CC   Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
CC   to produce the C-terminal MAGE-1 peptides described in R70915 to
CC   R70969. These peptides are useful for defining epitopes that
CC   engender a HLA-restricted cytotoxic lymphocyte activity against
CC   MAGE-1 antigens. Compsns. containing these peptides can be
CC   administered, as a vaccine to patients susceptable to MAGE
CC   associated tumours, e.g. melanomas.
SQ   Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T;

Query Match      42.5%;  Score 2413;  DB 1;  Length 2420;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 2419;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  1;


Db      1 GGATCCAGGCCCTGCCAGGAAAAAATATAAGGGCCCTGCGTGAGAACAGAGAGGGGTCATCC    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3256 GGATCCAGGCCCTGCCAGGAAAAAATATAAGGGCCCTGCGTGAGAACAGAGAGGGGTCATCC  3315

Db     61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCTTCCTGTAGCACTGAGGAAGC   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCTTCCTGTAGCACTGAGGAAGC  3375

Db    121 CAGGGCTGTGTCGTGCTTGCCACCCTGAGGGCCCTGGATTCCTTCTTCCTGGAGCTCCA   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3376 CAGGGCTGTGTCGTGCTTGCCACCCTGAGGGCCCTGGATTCCTTCTTCCTGGAGCTCCA  3435

Db    181 GGAACCAGGCAGTGAGGCCTTGGCTGAGACAGTATCCTCAGGTCACAGAGCCAGAGGATG   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3436 GGAACCAGGCAGTGAGGCCTTGGCTGAGACAGTATCCTCAGGTCACAGAGCCAGAGGATG  3495

Db    241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCGAGTCGGCTGGGCCCCCACCTGCCA   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCGAGTCGGCTGGGCCCCCACCTGCCA  3555

Db    301 CAGGACACATAGGACTCCACAGAGTCTGGCCTGGCCTCCCTACTGTCAGTCCTGTAGAAT   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTGGCCTCCCTACTGTCAGTCCTGTAGAAT  3615

Db    361 CGACCTCTGCTGCCGGCTGTACCCTGAGTACCCTGAGTTGCCAGGTTTTCAG   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3616 CGACCTCTGCTGCCGGCTGTACCCTGAGTACCCTGAGTTGCCAGGTTTTCAG  3675

Db    421 GGGAACAGGCCAACCCAGAGGACAGGATTCCCTGGAGCAGGCACCAAGGAGAA   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3676 GGGAACAGGCCAACCCAGAGGACAGGATTCCCTGGAGCAGGCACCAAGGAGAA  3735

Db    481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTTGTAGAGTTCAGTTCTTCAGCGTGAGGCCTCA   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTTGTAGAGTTCAGTTCTTCAGCGTGAGGCCTCA  3795

Db    541 CACACTCCCTCTCTCCCAGCCTGTGGGTTCATTGCCCAGCTCCTGCCCACACTCCT   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3796 CACACTCCCTCTCTCCCAGCCTGTGGGTTCATTGCCCAGCTCCTGCCCACACTCCT  3855

Db    601 GCCTGCTGCCCTCTCCTGGCACCTGAGCAGGAGTCTGCACTGCAAGCC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3856 GCCTGCTGCCCTCTCCTGGCACCTGAGCAGGAGTCTGCACTGCAAGCC  3915

Db    661 TGAGGAGCCCTTGAGGCTCCTCAGGGACGTCCTGGGCTGTGTGTGTCGAGGCTGCCAC   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3916 TGAGGAGCCCTTGAGGCTCCTCAGGGACGTCCTGGGCTGTGTGTGTCGAGGCTGCCAC  3975

Db    721 CTCCTCCTCCTCCTGGTCCTGGGCACCCTGAGGGAGTTGCACTGCTGGGTCAAC   780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3976 CTCCTCCTCCTCCTGGTCCTGGGCACCCTGAGGGAGTTGCACTGCTGGGTCAAC  4035

Db    781 AGATCCTCCCAGAGTCCTCAGGGAGCCTCAGGGACCTCCCCTTCCCACTACCATCAACTTCACTCG   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4036 AGATCCTCCCAGAGTCCTCAGGGAGCCTCAGGGACCTCCCCTTCCCACTACCATCAACTTCACTCG  4095

Db    841 ACAGAGGCAACCCAGTGAGGGTCCAGCAGCGTGAAGAGGAGGGGCCAAGCACCTCTTG   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4096 ACAGAGGCAACCCAGTGAGGGTCCAGCAGCGTGAAGAGGAGGGGCCAAGCACCTCTTG  4155

Db    901 TATCCTGGAGTCCTGTTCCTGAGCAGTAATCACTAAGAAGAAGGTGGCTGATTGGTTGGTTT   960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4156 TATCCTGGAGTCCTGTTCCTGAGCAGTAATCACTAAGAAGAAGGTGGCTGATTGGTTGGTTT  4215

Db    961 TCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4216 TCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT  4275

Db   1021 CATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4276 CATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA  4335

Db   1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGAGACCCCACGGCCACTCCTATGTCCTTGT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGAGACCCCACGGCCACTCCTATGTCCTTGT  4395

Db   1141 CACCTGCCTAGGTCTCTCCTGGTGAATGGGCCTGCTGGTGATAATCAGATCATGCCCAAGAC  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4396 CACCTGCCTAGGTCTCTCCTGGTGAATGGGCCTGCTGGTGATAATCAGATCATGCCCAAGAC  4455

Db   1201 AGGCTTCCTGATAATTGTCCTGGTCATGATGGGGCCGGCCATGCTCCTGAGGA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4456 AGGCTTCCTGATAATTGTCCTGGTCATGATGGGGCCGGCCATGCTCCTGAGGA  4515

Db   1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGGAGTGTGATGAGTGGGGAGCCACAGTGCCTA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGGAGTGTGATGAGTGGGGAGCCACAGTGCCTA  4575

Db   1321 TGGGGAGCCCAGGAAGCTGCTCACCCAGATTGGTGCAGGAAAAGTACCTGGAGTACCG  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Qy   4576 TGGGGAGCCCAGGAAGCTGCTCACCCAGATTGGTGCAGGAAAAGTACCTGGAGTAC-G  4634

Db   1381 GCAGGTGCCGGACAGTGATCCCGACGCGTATGAGTTCCTGTGGGTCCAAGGGCCCTCGC  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4635 GCAGGTGCCGGACAGTGATCCCGACGCGTATGAGTTCCTGTGGGTCCAAGGGCCCTCGC  4694

Db   1441 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAGAGTTCGCTT  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4695 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAGAGTTCGCTT  4754

Db   1501 TTTCTTCCCATCCTGCGTGAAGCAGCTTTGAGAGAGGGAAGGAGGAGTCTGAGCATG  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4755 TTTCTTCCCATCCTGCGTGAAGCAGCTTTGAGAGAGGGAAGGAGGAGTCTGAGCATG  4814

Db   1561 AGTTGCAGCCAAGGCCAGTGGAGGGGACTGGGCCCAGTGCACCTTCCAGGGCCCGCGTCC  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4815 AGTTGCAGCCAAGGCCAGTGGAGGGGACTGGGCCCAGTGCACCTTCCAGGGCCCGCGTCC  4874

Db   1621 AGCAGCTTCCCCTGCCTCGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGGGGTCA  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4875 AGCAGCTTCCCCTGCCTCGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGGGGTCA  4934

Db   1681 GTGTTCTCAGTAGTAGGTTTCGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT  1740
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Qy   4935 GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT  4994

Db   1741 TTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGTTGAATGAACTTCAGCATCCAAGT  1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4995 TTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGTTGAATGAACTTCAGCATCCAAGT  5054

Db   1801 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTAAGGGTAAGAGTCTTGTGT  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5055 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTAAGGGTAAGAGTCTTGTGT  5114

Db   1861 TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATATAATAACAGCAGTGGAAT  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5115 TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATATAATAACAGCAGTGGAAT  5174

Db   1921 AAGTACTTAGAAATGTGAAAAATGAAAATAGATAGCAGTAAAATAGATAGAGAATAGAACTAAAGAAAT  1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5175 AGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAAT 5234
          ||||| ||||  |||||| |||||
Db   2154 CATGGGGGTGGGACCCAGCCTGCAAGGGGAGGAAGAGGAGGGAGGACTCAGG 2213

Db   1981 TAAGAGATAGTCAATTCTTGCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040
          ||||||||||||||||||||||||||||||||||||
Qy    918 GGACCTTGGAGTCCAGATCAGTGCAACCTTGGC-TGGGGGATCCTGGCACAGTGGCC 976

Qy   5235 TAAGAGATAGTCAATTCTTGCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 5294
          ||||||||||||||||||||||||||||| ||  |||
Qy   2214 GGACCTTGGAAATCCAGATCAGTGTGGACCTGGGGGATCCTGGCACGGTGGCC 2273

Db   2041 ATGCATACCTGGATTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAA 2100
          ||||||||||||||||||||||||||||||
Qy    977 GAATGTGCCCCGTGCTCATTGCACCTCAGGGTGACAGAGATTGAGGGCTGTGGTCTGA 1036

Qy   5295 ATGCATACCTGGATTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAA 5354
          |||||||  | ||||| | |||
Qy   2274 ACATATGGCCCCATATTTCCTGCATCTTTGAGGTGACAG-GACA-GAG--CTGTGTCTGA 2329

Db   2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTTTCTCCATGCACTGAGCATCTGCTTTTTGGAA 2160
          |||||||||||||||||||||| |
Qy   1037 GGGCTGGGGACTTCAGGTGCCAGAGGGAGGAAAATCCCAGGATCTGCCGGACCCAGGGTGTG 1096

Qy   5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTTTCTCCATGCACTGAGCATCTGCTTTTTGGAA 5414
          | |||| ||| || ||| || |
Qy   2330 GAAGTGGGGCCCTCAGGTCAACAGAGGAGGAGAGTTCCAGGATCCATATGCCCAAGATGTG 2389

Db   2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCATAGGGTC 2220
          |||||||||||||||||||||||||||||||||
Qy   1097 CCCCCTCATGAGGACTCCCATACCCCGGGAACCTGATCTCAGGATGCCACAGAGTCTG 1156

Qy   5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCATAGGGTC 5474
          || |||| || || ||| || ||
Qy   2390 CCCCCTCATGAGGACTGGGGATATCCCCGGGCTCAGAAAGAAGAGGGACTCCACACAGTCTG 2449

Db   2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280
          |||||||||||||||||||||||||||||||
Qy   1157 GAAGTAAATTGTTCTTAGCTCTCTGGGGAACCTGATCTCAGGGATGCCCTAAGTGACAATCT 1216

Qy   5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
          | ||||||||| |||| ||| ||  ||| |||
Qy   2450 GCTGTCCCCTTTTAGTACTCTAGGGGGACCAGATCAGGGATGCCGGTATGTTCCATTCT 2509

Db   2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGAGTGTCAATG 2340
          |||||||||||||||||||||||||||
Qy   1217 CATTTGTACCACAGGAGGAGGTGGGGAACCCTCAGGGAGATAAGGTGTTGGTGTAAAG 1276

Qy   5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGGTGAGTGTCAATG 5594
          | |||||||||| |||||||||| |
Qy   2510 CACTTGTACCACAGGAGGAGTTGGGGGCCCTCAGGGAGATGGGGTCTTGGGTAAAG 2569

Db   2341 CCCTGAGCGTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400
          |||||||||||||||||||||||||||||||
Qy   1277 AGGAGCTGTCTGCTCATTTCAGGGGGTTCCCCTTGAGAAAGGGCAGTCCTGGCAGGAGAG 1336

Qy   5595 CCCTGAGCGTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          ||| ||| |  ||||| || ||| |
Qy   2570 GGGGGATTGCTACTCATGTCAGGGAATTGGGGTTGGAGCACACAGGCGCTGGCAGGAA 2629

Db   2401 TAATGATCTTGGGTGGATCC 2420
          |||||||||||||||
Db   1337 TAAAGATGAGTAACCCACAGGAGGCCATCATAACGTTCACCCTAGAACCAAAGGGTCAG 1396

Qy   5655 TAATGATCTTGGGTGGATCC 5674
          |||||||||||||||
Qy   2630 TAAAGATGAGTGAGACAGACAAGCTATTGGAATCACACCCCAGAACCAAAGGGTCAG 2689

Db   1397 CCCTGGACAACCGACGTGGGGTAACAGGATGTGGCCCCTCCTCACTTGTCTTTCCCAGATC 1456
          |||||||||| ||||| ||| ||
Qy   2690 CCCTGGACACCTCACCCCAGGATGT--GGCT-T----CTTTTCACTCCTGTTTCCCAGATC 2742

Db   1457 TCAGGGAGTTGATGACCTTGTTTCAGAAGGTGACTCAG--TCAACACAGGGCCCC--TC 1513
          | ||| ||||||||||| ||||||||| ||| |||| ||
Qy   2743 TGGGCAGGTGAGGACCTCATCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATC 2802

Db   1514 TGGTCGACAGATGCAGTGGTTCTAGGATTCTGCCAAGCATCCAGGTGGAGAGCTGAGGTA 1573
          ||||| ||| ||| |||||||| |  |||||||||
Qy   2803 TGGTCTAAAGACAGCGGGTCCCAGGATCTGCCCATGCCTTCGGGTGAGGAACATGAGGGA 2862

Db   1574 GGATTGAGGGTACCCCTGGGCCAGAATGCAGCAAGGGGCCCCATAGAAAATCTGCCCTGC 1633
          ||||||||||||||||| |||||||||  ||
Qy   2863 GGACTGAGGGGTACCCCAGGACCAGAACACTG-AGGGGGACTGCACAGAAAATCAGCCCTGC 2921

Db   1634 CCCTGCGGTTACTTCAGAGACCCTGGGCAGGGGCTGTCAGCTGAAGTCCCTCCATTATC-T 1692
          |||||||||||| ||||| ||||| || |
Qy   2922 CCCTGCGTCGTCACCCAGAGAGCATGGGCGTCTGGGCGTCGTTCCGTTATCCT 2981

Db   1693 GGGATCCTTTGATGTCAGGGAAGGGGAGGGCCTTGGTCTGGAAGGGGCTGAGGTCAGT 1752
          ||||||| |||||||||||||| | |||||
Qy   2982 GGGATCATTGATGTCAGGGACGGGGACGCCCTTGGTCTGAGAAGGCTGCGTCAGGTCAGT 3041

Db   1753 AGAGGGAGGGGTTCAGGGCCCTGCCAGGAGTGGGACCGGACTCGTCACCC 1812
          |||||||| || ||||| || |||||||
Qy   3042 AGAGGGGAGGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGCCACCTCACCC 3101

Db   1813 AGGACACCTGGACTCCAATGAATTT-GACATCTCCTGTTCCTGTGGGACCTGGT 1871
          ||||||||||||| |
Qy   3102 AGGACACACATTAATTCCAATGAATTTTGATATCTCTTCTGCGCCCTTCCCCAAGGACCTAGG 3161

Db   1872 CACGTATGGCCAGATGTGGGTCCCCTATCTCCTTCGTACCATATCAGGGATGTGAGT 1931
          |||| |||||| |||||||||||
Qy   3162 CACGTGTGGCCCAGATGTTTGTCCCCTCC-TGTCCTTCCATTCCTTATCATGGATGTGAAC 3220

Db   1932 TCTTGACATGAGAGATTCTCAAGCCAGCAGCAAAAGGGTGGGATT-AGGCCCTACAAGGAGAA 1990
          ||||||| || || ||||| ||||||||
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RESULT   9
ID   Q72478 standard; DNA; 4157 BP.
AC   Q72478;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-2 gene.
KW   Tumour rejection antigen; melanoma antigen-2; MAGE-2; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   CDS            2598..3542
FT   /tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; US-037230.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Example 32; Page 61; 105pp; English.
CC   Q72478 is the gene which contains the coding sequence for melanoma
CC   antigen-2 (MAGE-2). Another melanoma antigen precursor MAGE-3 is encoded by
CC   Q72470, this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence 4157 BP;   953 A;   1134 C;   1185 G;   885 T;

Query Match    26.1%;  Score 1483;  DB 1;  Length 4157;
Best Local Similarity 78.8%;  Pred No. 0.00e+00;
Matches 2615;  Conservative 0;  Mismatches 622;  Indels 85;  Gaps 51;

Db    858 CAGGGGGTGGGCCCAGCCTGCGAGGAGTCAAGGGAGTGAAGAGGGAGGACTGAGG 917
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Qy  3221  TCTTGATTTG-GAT-TTCTCAGACCAGCAAGAGGGCAGGATCCAGGCCCTGCCAGGAAAA  3278
Db  1991  AGGTGAGGGCCCTGAGTGAGCACAGAGCAGGGGACCCTCCACCCAAGTAGAGTGGGACCTCA  2050

Qy  3279  ATATAAGGCCCTGCGTGAGAACAGAGAGGGGGTCATCCACTGCAGTGGGGATGTCA  3338
Db  2051  CGGAGTCTGCCAACCCTGCTGAGATCCGTGGCTGCTGGGAATCCGTGGCTGCTGCAGTCTGCA  2110

Qy  3339  CAGAGTCCAGCCACCCCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCA  3398
Db

Qy  3399  CACTGAAGGCCCGTGCATTCCTCTCCAGGAATCAGGAGCTCCAGGAACCAGCAGGTGAG  3451
Db  2111  ACTGAAGGTTGCCTGGAATGACACACAAGGCCCCACCGCC-CAGAACAAATGGGACT  2170

Qy  3452  GCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGGGGACGAGCAGCAGTGCCAGC  3511
Db  2171  GCCTTGGTCTGAGTGAGTCAGTG-CCTCAGGTCACAGAGAGGGGGACGCAGCAGGCTGAC  2229

Qy
Db  2230  ACTGAAGGTTGCCTGGAATGACACACAAGGCCCCACCGCC-CAGAACAAATGGGACT  2288

Qy  3512  AGTGAATGTTTGCCCTGAATGCACACACCAGGCACCATAGGGACT  3571
Db  2289  CCAGAGGGCCTGGCCTCACCCTCCTATTCTCAGTCCTCAGCCTGAGCATGTGCTGGCC  2348

Qy
Db  2349  GGCTGTACCCGTGAGGTGCCCTCCCCACTTCCTCTCAGTTCTCGGGGGACCAGGCTGAC  2408

Qy  3572  CCACAGAGTCTGGCCTCACC-TCCCTACTGTCAGTCCTGTAGAATCGACCCTCGCTGGCC  3630
Db  2409  AGTTAGGACCCGAGCCAGCACTGGAGAG-CATTGAAGAGAGAATCTGTAAGAGGTTAAGA  2467

Qy
Db  2468  TCAGAGGCCTCCAAGGTTCA--GTTCAGTTCTCACCTAAGGCCTCACACACGGCTCCTTCTC  2525

Qy  3631  GGCTGTACCCGTGAG-TACCCCTCAGTTCTCACTTCCTCTCAGGTTTCAGGGG-ACAGGCCAAC  3688
Db  2526  TCCCCAGGCCGTCGTGTTCCTTCATTGGCGGGCTTGGGGGAGGTACCCTGGGGAGGTTGCC  2585

Qy
Db  2586  ACCAGAGTCATCATGCCTTCCTGAGCAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTT  2645

Qy  3689  AAGTAGGACCCGAGCCACTGGAGAG-CATTGAAGAGAGAATCTGTAAGTAAGTAAGTAG  3748
Db  2646  GAGGCCCGAGGAGGAGGGGCCCTGGGCGTCGGGGTCGGGGTGTGTGGCGAGGAGCAG  2705

Qy
Db  2706  CAGACCGCTTGTCCTCTCTACTCAGTGGAAGTTACCCTGGGAGGTCGTGCTGCCC  2765

Qy  3749  GCCTTGTTGAGTCCCAAGGTTCCCAAGGTTCAGTTCTCAGCTGAGGTGTGTCCACACTCCCTCTC  3808
Db  2766  GACTTCACCGAGTCCTGCCCCAGTCTTCGCACTACCATCAAC  2825

Qy  3809  TCCCCAGGCCGTGGTCTTCAGTTGCATTGCCCGAGTCTCAGGTCACCTGCGCCCAGC  3868
Db  2826  TACACTCTTTGGAGACAATCCGATGAGGGCTCCAGCAACCAAGAGAGAGGGGCCCAAGA  2885

Qy
Db  2886  ATGTTTCCCGACCCGAGTCCGAGTTCCAGCAGCAATCAGTAGGAAGATGGTTGAGTTG  2945

Qy  3869  ACGAGAGTCATCATGCTCTCTGAGCAGGAGTCGCACTGCAAGCCTGAGGAAGCCCTT  3928
Db  2946  GTTCATTTTCTGGTCTCCAAGTATCGAGCAGGGTCACAAAGGCCAGAAATGCTG  3005

Qy
Db  3006  GAGAGTGTCATCATGCCTCAGAAATTGCCCTGGTCTTCCCTGATCTTCAGCAGAGTCCGAG  3065

Qy  3929  GAGGCCCGAGGAGGAGGGGCCCTGGGCTGGTGTGTGTGTGGCGAGGAGCAG---C-----C--  3978
Db  4027  GGGTCAACAGATTCATCTCTTGAGCAGTCCTCAGGGAGCTCCACTACCATCAAC  4087

Qy  3979  CT--CCTCCTCT-CCTCTGGT-C-CT---GG--GC-ACCCTGGAGGAGGTGCCCACTGCT  4027

Qy  4028  GGGTCAACAGATTCATCTCTTGAGCAGTCCTCAGGGAGCTCCACTACCATCAAC  4087
Db  4088  TTCACTCGACAGAGGCAACCAGTGGGTTCCAGCAGGGTCCAGGAGGGGGCCAAGC  4147
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Db  3066  TACTTGAGCTGCTGGTCTTTGGCATCGAGGTGGTGTGGAAGTGGTCCCATCAGCCACTTGTAC  3125
Qy  4328  TCCTTGCAGCTGCTGTCTTTGGCATTGACGTGAAGGAAGCAGAGCCCACCGCCCACTCCTAT  4387

Db  3126  ATCCTTGTCACCTGCCTGGGCCTTCTGCTGCTGGGCCATAATCGCTTACGATGGCCTGGGGGCCGACAATCAGTCATG  3185
Qy  4388  GTCCTTGTCACCTGCCTGGGCCTAGGTCTCTATGATGGCCTGCTGGTGATAATCAGATCATG  4447

Db  3186  CCCAAGACAGGCCTCCTGATAATCGTCTGGCCCATAATCGCAATCGAATAGAGGGCGACTGTGCC  3245
Qy  4448  CCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGCCGGCCGGCCATGCT  4507

Db  3246  CCTGGAGAGAAAATCTGGGAGAGCTGAGTATGTTGAGGTGTGTTTGAGGGGAGGGAGGAC  3305
Qy  4508  CCTGAGGAGGAAATCTGGGAGGGCTGAGTGTGTGATGGGAGTGTATGGGGAGGGAGGCAC  4567

Db  3306  AGTGTCTTCGCACATCCCAGGAGAGTCGCTCATCGCATGCAAGAATCGTGCAGGAAAACTACCTG  3365
Qy  4568  AGTGCCTATGGGAGCCCAGGAGCTGCTCACCCAAGATTGGTGCAGGAAAGTACCTG  4627

Db  3366  GAGTACCGGCAGTGCCGGCCAGTGATCCTGACGTACGAGTGCTACGAGGTCCTGTGGGGTCCAAGG  3425
Qy  4628  GAGTAC--GGCAGTGCCGGCCAGTGATCCCGACGCTATGAGTGCTCCTGTGGGGTCCAAGG  4686

Db  3426  GCCCTCATTGAAACCAGCTATGTGAAAGTCCTGCCACCATACACTAAGATCGGTGGAGAA  3485
Qy  4687  GCCCTCGCTGAAACCAGCTATGTGAAAGTCCTGAGTATGTGATCAAGGTCAGTGCAAGA  4746

Db  3486  CCTCACATTCCTACCACCCCTGCATGAACGGGCTTTGAGAGAGGAGGAAGAGTGAGTC  3545
Qy  4747  GTTCGCTTTTTCTTTCCTCCATCCCTGCGTGAACCCTGCTTTGAGAGAGGAGGAGGAGTC  4806

Db  3546  TCAGCACATGTTGCAGCCAGGGCTCGGGGCCAGTGCACCTTCCAGGG  3605
Qy  4807  TGAGCAATGAGTTGCAGCCAGGGCTCGGGGACTGGGCCAGTGCACCTTCCAGGG  4866

Db  3606  CCCCATCCATTAGCTTCCACTGCCTCGTGTGATATGAGGGCCATTCCTGCCTCTTTGAAG  3665
Qy  4867  CCGCGTCCAGCACGCTTCCCCTGCGTGTGACATGAGGCCCATTCTTCACTCT--GAAG  4924

Db  3666  AGAGCAGTCAGCATTCATGCAGTCTTAGCACAGTTCTTCGTCTCGTTGGATGACTTTGAGATTTATC  3725
Qy  4925  AGAGCAGTCTCAGTGTTCTCCAGTAGTAGGTTTCTGTTGTTCATTGGGTGACTTTGGAGATTTATC  4984

Db  3726  TTTCTTTCTGTGGAATTGTTCAAATGTTCCTTTT-AACAAATGGTTGGATGGAACTTCA  3784
Qy  4985  TTTGTTCTTTTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCA  5044

Db  3785  GCATCCAAGTTATGAATGACACTAGTCACACATAGTGCTGTTTATATAGTTAGGGGTA  3844
Qy  5045  GCATCCAAGTTTATGAATGACAGCAGTCACACA--GTTCTGTGTATATAGTTTAAGGGGTA  5102

Db  3845  AGAGTCCTGTTTTTATTCAGATTGGAAATCCATTCCATTTTGTGAGTGTCACATAAT  3904
Qy  5103  AGAGTCTGTGTTTTATTCAGATTGGAAATCCATTCCATTTCTATTTGTGAATTTGGGA--TAAT  5160

Db  3905  AACAGCAGGTGGAATATGTATTTGCCTATATTGTGAACGAATTAGCACAGTAAAAT-ACATGA  3963
Qy  5161  AACAGCAGTGGAATAAGTAACTTAGAAAATGTGAAAAATGAGCAGTAAAAATGATGAGATAA  5220

Db  3964  T--AC-AAGGAACTCAAAAGATAGTTAATTCTTGCCTTATACCTCAGTCTATTATGTAAA  4020
Qy  5221  AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTTGTAAA  5280

Db  4021  ATTA--AAA-ATATGTG--TA--TT---TTT--TTG--CTTCTTTGAGAATGCAAAAGAAAT  4068
Qy  5281  ATTTTTAAGATATATGCATAACTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT  5340

Db  4069  TAAAATCTGAATAAA---TTCTTCCTGTTCACTGCGTCCATTCTTTACCATTACTCACTCAGCA  4125
Qy  5341  TAAAATCTGAATAAGAAATTCTTCCTGTTCACTGCGTCTCTTTTCTTTCCCATGCACTGACTCAGCA  5400
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Db   4126 TCTGCTCTGTGGAAGGCCCTGG 4147
          ||||| | |||||||||||||
Qy   5401 TCTGCTTTTGGAAGGCCCTGG 5422

RESULT 10
ID   Q32353 standard; DNA; 4157 BP.
AC   Q32353;
DT   22-APR-1993 (first entry)
DE   MAGE-2 gene.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT
FT   /*tag=   a
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992;
PR   23-MAY-1991; U04354.
PR   09-JUL-1991; US-705702.
PR   23-SEP-1991; US-728838.
PR   12-DEC-1991; US-764364.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure; Page 74-75; 142pp; English.
CC   The sequences given in Q32352-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence. The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors. MAGE expression is not
CC   restricted to melanomas. MAGE refers to a family of tumor rejection
CC   antigen precursors. The antigens resulting from these genes are
CC   referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence 4157 BP;   953 A;   1135 C;   1184 G;   885 T;

Query Match   26.1%; Score 1481; DB 1; Length 4157;
Best Local Similarity   78.7%;
Matches 2614; Conservative   0; Mismatches 623; Indels 85; Gaps 51;

Qy   858 CAGGGGGTTGGGGCCCAGCCTGCGAGGAGTCAAGGGAGGGAGGAAGAGGGAGGAGGACTGAGG 917
          || ||||| ||| ||||| |||| | |-| ||||||| ||||||| |||||||| |||
Db   2154 CANGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGGAGGAGGAGGACTCAGG 2213

Db   918 GGACCTTGGAGTCCAGATCAGTGCCAACCTTGGC-TGGGGGATCCTGGCCACAGTGCC 976
          ||||||||||||||||| ||| |||| |||||-||| || |||| |||
Qy   2214 GGACCTTGGAATCAGTGTGACCTGCCGCCCTCCCGAGAGGTCCAGGGCACGGTGGCC 2273

Db   977 GAATGTGCCCCGTGCTCATTGCACCTTCAGGGTGACACAGAGAGTTGAGGGCTGGTGGTCTGA 1036
          || ||| ||| || |||| ||| ||||||||||||||||| || |||||||||
Qy   2274 ACATATGCCCCATATTTCCTGCACCATCTTTGAGGTGACAG-GACA-GAG--CTGTGGTCTGA 2329

Db   1037 GGGCTGGGACTTCAGGTCAGGTGACTTACGCGGAGGAATCCCAGGATCTGCCCGGACCCAAGGTGTG 1096
          | |||||||||||||| |||| |||||||||||||||| | ||||||||||||| |||||||
Qy   2330 GAAGTGGGGCCTGCAGGTCAACAGAGGAGGAGGATCCCAGGAGATCCCCAAGATGTG 2389

Db   1097 CCCCCTTCATGAGACTCCCCATACCCCCGGCCAGGCCCAGAAAGAAGGGGATGCCACAGAGTCTG 1156
          ||||||||||||||||| ||||| |||||||||||||||||| |||||||| |||
Qy   2390 CCCCCTTCATGAGGACTGGGGATATCCCCGGGCTCAGAAGAAGAAGAAGGGACTCCACACAGTCTG 2449

Db   1157 GAAGTAAATTGTGTTCTTTAGTCTGGGGAACCTGATCACAGGAGTGGGCCCTAAGTGACAATCT 1216
          | ||| ||| ||| ||| |||||||||||| |||||||||||| |||| ||
Qy   2450 GCTGTCCCCTTTTTAGTAGCTCAGGGGGACGATCAGGGATGGCCGGTATGTTTCCATTCT 2509

Db   2289 CCAGAGGGGCCTGGCCTCACCCTCCCTATTCTCAGTCCTGCTGCAGCCTGGCATGTGCTGCC 2348

Db   1217 CATTTGTACCACAGGCAGGAGGTTGGGGAACCCTCAGGGAGGAGATAAGGTGTTGGTGTAAAG 1276
          || ||||| ||| || |||||||||||||| |||||| ||| |||| ||| |||||
Qy   2510 CACTTGTACCACAGGCAGGAGGAGTGGGGGCCTCAGGGAGAGTGGGGGTCTTGGGGTAAAG 2569

Db   1277 AGGAGCTGTGTCTGCTCATTTCAGGGGGTTCCCCTTGAGAAAGGGCAGTCCCTGGCAGGAG 1336
          |||||| ||||||||| ||||||||||| |||| |||||| |||||||| ||||||| ||
Qy   2570 GGGGGATGTCTACTCATGTCAGGGAATTGGGGTTGAGGAAGCACAGGCGCTGGCACGGGAA 2629

Db   1337 TAAAGATGAGTAACCCACAGGAGGCCATCATAACGTTCACCCTAGAACCAAAGGGGTCAG 1396
          |||||||||| |||||||| ||||||||||| | |||||||||||||||||||||||
Qy   2630 TAAAGATGAGTGAGACGACAAGGCTATTGGAATCACACCCCAGAACCAAAGGGGTCAG 2689

Db   1397 CCCTGGCAAACCCACGTGGGGTAACAGGATGTGGCCCCTCCTCACTTGTCTTTCCAGATC 1456
          |||||||| ||| |||| | | |||||| ||| | |||| | ||||||||||
Qy   2690 CCCTGGCACACCTCACCCCAGGATGT--GGCT-T----CTTTTTCACTCCTGTTTCCAGATC 2742

Db   1457 TCAGGGAGTTGATGACCTTGTTTCAGAAGGTGACTCAG-TCAACACAGGGGCCCC--TC 1513
          ||| |||||| | ||| ||| ||||||| ||| ||||-||||||| ||| | -||
Qy   2743 TGGGGCAGGTGAGGACCTCATTCTCCAGGGTGACTCAGGTCAACGTTAGGGACCCCCATC 2802

Db   1514 TGGTCACAGATGCAGTGGTTCTAGGATCTGCCAAGCATCCAGGTGAGAGCTGAGGTA 1573
          ||||||| ||| |||||||| ||||||||||| ||| | |||||| | || ||||
Qy   2803 TGGTCTAAAGACAGAGGCGGTCCCAGGATCTGCCATGCGTTCGGTGAGGAACATGAGGGA 2862

Db   1574 GGATTGAGGGTACCCCTGGGCCAGAATGCAGCAGGGGCCCCATAGAAATCTGCCCTGC 1633
          ||| |||||||||| || | |||| ||||| ||||| | | |||| | ||| |||
Qy   2863 GGACTGAGGGTACCCCAGGACCAGAACACTG-AGGGAGACTGCACAGAAATCAGCCCTGC 2921

Db   1634 CCCTGCGGTTACTTCAGAGACTCAGAGGTCTGCAGGGGCTGTCAGCTGAAGTCCTCCATTATC-T 1692
          |||||| ||| || |||||||| |||||||||||||| |||||| |||| |||| | |||| |-|
Qy   2922 CCCTGCTGTCACCCGAGGATGTGGTCCGTCCGTCCGAGGTCCTTCCGTTATCCT 2981

Db   1693 GGGATCTTGATGTGTCAGGGAAGGGAGCCTTGGTCTGAAGGGGCTGAGTCAGGTCAGT 1752
          |||||||||| |||||||||||||||||||||||||| | | || ||||||||||||
Qy   2982 GGGATCATTGATGTGTCAGGGGGCGGAGGCCTGGTGCGCTCGAGGCTCAGGTCAGT 3041

Db   1753 AGAGGGAGGGTCTCAGCCCTGCCAGAGTGACGTGAGGACCAAGCGGACTCGTCACCC 1812
          |||||||||||| ||||||| | ||||||| ||||| ||||||||| ||||| ||||
Qy   3042 AGAGGGAGGGCGTCCCAGCCCTGCCAGGAGTCAAGGTGAGGACCAAGGCGGCCACCTCACCC 3101

Db   1813 AGGACACCTGGACTCCAATGAATTT-GACATCTCGTTGTCCTTCGCGGAGGACTCGGT 1871
          ||| | | | ||| ||| ||||||-|||| | |||| ||||| |||||||||||-
Qy   3102 AGGACACATTAATTCCAATGAATTTTGATATCTCTTGTCGTCCCCTTCCCCAAGGACCTAGG 3161

Db   1872 CACGTATGGCCAGATGTGGGTCCCCTCTATCCTCTCGTACCATATCAGGGATGTGAGT 1931
          |||||||| |||||||||||||| ||| |-||| | -|||| |||| ||||||| |
Qy   3162 CACGTGTGGCCAGATGTTGTCCCCTCC-TGTCCTTCCATTCCTTATCATGGATGTGAAC 3220

Db   1932 TCTTGACATGAGAGATTCTCAGCCAGCCAGAAAAGGTGGGATT-AGGCCTACAAGGAGAA 1990
          ||||| | |-||| ||||| ||||| |||||||| |||||| | |-| |||| |||||
Qy   3221 TCTTGATTTG-GAT-TTCTCAGACCACCAGCAGAAAAGGGCCTGGCCCTGCCAGGAAAA 3278

Db   1991 AGGTGAGGGCCCTGAGTGAGCACAGAGGAGAGAGGGGGACCCTCCACCCAAGTAGAGTGGGGACCTCA 2050
          | ||||||||||| || ||||| ||||||| |||| ||||| | | |||||||||||
Qy   3279 ATATAGGGCCCTGCGTGAGCACAGAGGGGGTCATCGATGCATGCGGGATGTCA 3338

Db   2051 CGGAGTCTGGCCAACCCTGCTGAGACTTCTGGGAATCAGCTGCTGCAGTCTGCA 2110
          |||||||||||||| ||||| ||| ||||||||||||| |||||||| |||||||
Qy   3339 CAGAGTCCAGCCACCCTCCTGGTAGCACTGAGAAGCCAGGGTGTGTCTTGCCGTCTTCA 3398

Db   2111 CACTGAAGGCCCGTGCATTCCTCCCAGAAGAATCAGGAGCTCAGCAGGCAGTGAG 2170
          |||||||||||||| ||||||||||| | -| -|| -|| | || || |||
Qy   3399 CCCTGAGGGGCCCGTGATTCCTCTCC----T--GGAGCTCAGGAACCAGGCAGTGAG 3451

Db   2171 GCCTTGGTCTGATGAGGACTG-CCTCAGGTCACAGTG--CCTCAGGTCACCAGAGTCTG 2229
          |||||||||| | | |||| | | ||| |||||||||||| |||| | |||||||
Qy   3452 GCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGGATGGATGTCAGC 3511

Db   2230 ACTGAAGGTTTGCCTGGAATGCACACCAAGGGCCCCCC-CAGAACAAATGGGACT 2288
          | ||| ||||| |||||| | ||||||||| ||||| | |||||||||||||||||
Qy   3512 AGTGAATGTTTGCCCTGAATGCACACCAAGGCCCCACCTGCCCACAGGACACATAGGACT 3571

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Qy   3572 CCACAGAGTCTGGCCTCACC-TCCCTACTGTCAGTCCTGTAGAATCGACCTCTGCTGGCC 3630
          |||  || |||||||||||  |||||||||| |||||||||||  |  ||||||||||||
Db   2349 GGCTGTACCCGAGGTGCCCTCCCCACTTCCTCTCCTTCAGGTTCTGAGGGGACAGGCTGAC 2408

Qy   3631 GGCTGTACCCTGAG-TACCCTCACTTCCTCACTTCCTCCTTCAGGTTTCAGGGG-ACAGGCCAAC 3688
          ||||||||||||||  || ||||||||||||||||||||||||||| ||||||  |||||||||
Db   2409 AAGTAGGACCCGAGGCACTCGAGAG-CATTGAAGGAGAAGATCTGTAAGTAAGCCTTTG 2467

Qy   3689 CCAGAGACAGGATTCCCTGGAGGCCACCAAGGAGCACCAAGGAGAAGATCTGTAAGTAG 3748
          | |||||||| |||| ||| ||||||| | || ||| |||| ||| ||||||||||||
Db   2468 TCAGAGCCCTCCAAGGTTCA--GTTCAGTCTCACCTAAGGCCTCACACGCTCCTTCTC 2525

Qy   3749 GCCTTTGTTGAGAGTCTCCAAGGTTCAGTTCTCAGCTGAGGCCTCTCACACTCCCTCTC 3808
          |||||||||||||| |||||||||||||||||||||||||||||| ||| ||||
Db   2526 TCCCCAGGCCTGTGGGCTCTTCATTGCCCAGCTCCTGCCCCGCACTCCTGCCTGCCCTG 2585

Qy   3809 TCCCCAGGCCTGTGGGCTCTTCATTGCCCAGCTCCTCCCACACTCCTGCCTGCGCCCTG 3868
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   2586 ACCAGAGTCATCATGCCTGCTCTTGACAGAGAGTCAGCACTGCAAGCCTGAAGAAGGCCTT 2645

Qy   3869 ACGAGAGTCATCATCTCTCTGAGCAGAGAGTCGCACTGCAAGCCTGAGGAAGCCCTT 3928
          | |||||||||||||| |||||||||||||||| |||||| |||||| ||||||||
Db   2646 GAGGCCCGAGGAGAGCCCTGGGCCTGGTGCGGCAGCCTCCTGCTACTGAGGAGCAG 2705

Qy   3929 GAGGCCCCAACAAGAGGCCCTGGGCTGGTGTGTGCAGGCTGCCAC--CT----- C-- 3978
          |||||||  || ||||||||||||| ||||||| ||||||||||| ||
Db   2706 CAGACCGCTTCTTCCCTCTACTCTAGTGGAAGTTACCCGTCGGGGAGGTGCCTGCTGCC 2765

Qy   3979 CT--CCTCCTCT-CCTCTGGT-C-CT---GG--GC-ACCCTGGAGGAGGTGCCCACTGCT 4027
          ||  |||||||| || ||| | |  |   ||  || ||||||||||||  |||||||||
Db   2766 GACTCACCCAGTCCTCCCCACAGTCCTCGACTTCTCGACTACCATCAAC 2825

Qy   4028 GGGTCAACAGATCATCTCTCTGAGCAGAGTCCTCCGAGGAGGCCTCCCACTACCATCAAC 4087
          |||| |||||| ||||||||||||||||  |||  |||||| |||||||||||||||||
Db   2826 TACACTCTTGGAGACAATCCGATGAGGCTCCAGCAACCAAGAGAGGAGGGCCCAAGA 2885

Qy   4088 TTCACTCGACAGAGGCCAACCCAGGTGAGGGTTCCAGCAGCCAGGAGGAGGGGCCCAAGC 4147
          |||||||||||  | ||| || || ||||||||||||||||||||||||||||||||||
Db   2886 ATGTTCCCGACCTGGAGTCCGAGTTCCAAGCAGCAATCAGTAGGAGAAGATGGTTGAGTTG 2945

Qy   4148 ACCTGTGTATCCTGTGGAGTCTGTTCCTGCAGCAGTAATCACTAAGAAGAGGTGGCTGATTTG 4207
          ||||||||  | |||| | |||||||||||||||||||||||||||||||||||||||||
Db   2946 GTTCATTTTCTGCTCCTCAGATCGAGCCTCCAGCTTCTCGACTAATCAAC 3005

Qy   4208 GTTGTTTTTGTCTCCTCAAATATGAGCCCAGAGTCCAACAAAAGGCAGAAATGCTG 4267
          ||| ||| |||| |||||| ||||||||||||||||| ||||||||||||||||||
Db   3006 GAGAGTGTCCTCAGAAAATTGCCAGGATCTTCAGCAGACTTCTTCCCTGATCTTCAGCAAAAGGCCTCCGAG 3065

Qy   4268 GAGAGTGTCATCAAAAAATTACAAGCACTGTTTTCCTGAGATCTTGCGGCAAAGCCTCTGAG 4327
          ||||||||| ||||| |||| | ||| |||| |||||| | |||||| ||||||| |||||
Db   3066 TACTTGCAGCTGGTCTTTGGCATCGAGGTGGTGGAAGTGGTCCCCATCAGCCACTGTAC 3125

Qy   4328 TCCTTGCAGCTGGTCTTTGGCATTGACGTGGAAGTGAAGAAGCAGACCCCCACTCCTAT 4387
          | |||||||||||||||||||| || |||||| ||| ||||| |||||  | ||| |
Db   3126 ATCCTTGTCACCTGGCCTCTCGGGCCTCCTACGATGCCATCAGTGTAC 3185

Qy   4388 GTCCTTGTCACCTGGCTCTCCCTATGATGGCCGGGTGTATAATCAGATCATG 4447
          ||||||||||||||||||||| |||||| |||||| |||||||||||||||
Db   3186 CCCAAGACAGGCAGGCCTCCTCTCGGCGCCGCCCATAATCCACGCCAATAGCTGGAGTCTGCGGTCTGCC 3245

Qy   4448 CCCAAGACAGGCAGGCGTCCCTGGCCTCGGCGCCCATAATCCACGCCAATAGTGATGAGTGCAAATGGTGCGGCCGCCATGCT 4507
          |||||||||||||||| ||||| || ||||||||||||||||||||| | ||||| ||||| ||||||||||| ||||||||
Db   3246 CCTGAGGAGAAAATCTGGGAGGAGCTGGAGTATGTTGGAGGGTGTTTGAGGGAGGGAGGAC 3305

Qy   4508 CCTGAGGAGGAGAAATCTGGGAGGAGCTGGAGTGTATGGAGGGTGTATGGAGGGAAAAGTACCTG 4567
          ||||||||| ||||| ||||||||||||||||| | || |||||| ||||||||||| |||||
Db   3306 AGTGTCTTCGCACAATCCCAGGGAGCTGCTCATCGAAGATCGTCAGAAATCCAGGGAAAAACTACCTG 3365

Qy   4568 AGTGCCTATGGGGAGCCCAGGAAGCGTCTCACCCCAGATTTGGTGCGAGAAAAGTACCTG 4627
          |||||||| | |||||||||||||| | ||||||||||| ||||| |||||| |||||
Db   3366 GAGTACCGGCAGGTGCCCGGCAGTGATCCTGCACGTTATGAGTTCCTGTGGGGTCCAAGG 3425
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Qy   4628 GAGTAC-GGCAGGTGCCGACAGCAGTCCGGACACGTCATGAGTTCCTGTGGGGTCCAAGG 4686
          ||||||  ||||||||| |||||| |||| |||| ||||| |||||||||||||||||||
Db   3426 GCCCTCATTGAAACCAGCAGTGATGAAAGTCCTGCACCACTACACTACTAAAGATCGGGAGAA 3485

Qy   4687 GCCCTCGCTGAAACCAGCAGTGATGAAAGTCCTGAGAGTCATCAAGTCAGTGCAAGA 4746
          |||||||| ||||||||||||||| ||||||||||| |||||| ||||||||||||
Db   3486 CCTCACATTCCTACCCACCCCTGCTGACGCGGCTTTGAGAGAGGGAGGAGAGTGAGTC 3545

Qy   4747 GTTCGCTTTTCTTCCTGCCATCCCTGCGTGAAGGCTTTGAGAGAGGAGGAGAGGAGGGAGTC 4806
          || ||| |||| | ||||||||||||||||  ||||| ||||||||||||||||||||||
Db   3546 TCAGCACATGTTGCAGCCAAGGGGCCAGTGGGAGGGGTCTGGGCCGTCGGGCCACCTTCCAGGG 3605

Qy   4807 TGAGCAGTAGTTGCAGCCAAGTAGCCAGTGGGAGGGGGACTGGGCCCAGTGCCACCTTCCAGGG 4866
          |||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||||
Db   3606 CCCCATCCATTAGCTTCCACTGCTCCTGCCGTGATATGAGCCCATTCCTGCCTCCTTGAAG 3665

Qy   4867 CGCCGTCCAGCCAGCTTCCCCTGCCTCCGTGTGACATGAGCCCATTCTTCACTCT--GAAG 4924
          || |||||| ||| ||| || |||||| |||||| |||||||||||| ||||| | ||||
Db   3666 AGAGCAGTCAGCATTCTTAGCAGTGAGTTTCTGTCGTGATGACTTTGAGATTTATC 3725

Qy   4925 AGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATC 4984
          ||||| |||||| ||||||||||| ||||||||| || |||||| ||||||||||||||
Db   3726 TTTCTTCCTGTGAATTGTTCAAATGTTCCTTTT-AACAAATGGTTGGATGAACTTCA 3784

Qy   4985 TTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGATGGTTGAATGAACTTCA 5044
          ||| |||| |||||||||| ||| ||||||| ||||||||||||||| |||||||||||
Db   3785 GCATCCAAGTTATGAATGACAGTAGCACACAGTAGTGCTGTTATATAGTTTTAGGGGTA 3844

Qy   5045 GCATCCAAGTTATGAATGACAGCAGTCACACA--GTTCTGTGTATATAGTTTTAAGGGTA 5102
          |||||||||||||||||||||||||||||||  ||||| ||||||||||||| |||||||
Db   3845 AGAGTCCTGTTTTATTCAGATTGGGAAATCCATTCCATTTGTGAGTGTCACATAAT 3904

Qy   5103 AGAGTCTGTGTTTTATTCAGATTGGGAAATCCATTCCATTCATTTGTGAATTGGGA--TAAT 5160
          ||||| | |||||||||||||||||||||||  ||||| |||||||||||||| || |||
Db   3905 AACAGCAGTGGAATATGTATTTGCCTATATTGTGAACGAATTAGCAGTAAAAT-ACATGA 3963

Qy   5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220
          |||||||||||||| | ||||||||||||| |||||||||||||||||| |||| ||||
Db   3964 T--AC-AAGGAACTCAAAAGATAGTTAATTCTTCGCCTATATGACTCTATTATGTAAA 4020

Qy   5221 AGAACTAAAGAAATTAAGAGATAGTAGTCAATTCTTGCCTATATCCTATATTCTGTAAA 5280
          ||||||||||||||  || ||||||| |||||||||||||||| |||||||||||||||
Db   4021 ATTA--AAA-ATATGTG--TA--TG--TTT--TTG-CTTCTTTGAGAATGCAAAAGAAAT 4068

Qy   5281 ATTTTTAAGATATATGCATAACCTGGATTTCCTTGGCTTCTTTGGAGAATGTAAGAGAAAT 5340
          ||||  ||| ||| | || |||| |||| |||| |||| ||||||||||||| |||||||
Db   4069 TAAAATCTGAATAAA---TTCTTCCTGTTCACTGGCTCATTTCTTTACCATTCACTCAGCA 4125

Qy   5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTCTTTCTTCCTCCATGCCACTGAGCA 5400
          |||||||||||||| ||||||||||||||||||||| |||||| |||||||||||||||||
Db   4126 TCTGCTCTGTGGAAGGCCCTGG 4147

Qy   5401 TCTGCTTTTGGAAGGCCCTGG 5422
          ||||||||||||||||||||
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RESULT  11
ID   Q72483 standard; DNA; 2531 BP.
AC   Q72483;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-41 gene.
KW   Tumour rejection antigen; melanoma antigen-41; MAGE-41; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             625..1578
FT   /*tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
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DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Disclosure; Page 68; 105pp; English.
CC   Q72483 is the gene which contains the coding sequence for melanoma
CC   antigen-41 (MAGE-41). Another melanoma antigen precursor. Melanomas
CC   Q72470, this is a tumour rejection antigen precursor MAGE-3 is encoded by
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence 2531 BP; 607 A; 593 C; 701 G; 630 T;

Query Match   24.7%; Score 1399; DB 1; Length 2531;
Best Local Similarity 84.3%; Pred. No. 0.00e+00;
Matches 2068; Conservative 0; Mismatches 327; Indels 57; Gaps 27;

Db   1 GGATCCAGGCCCTGCCTGAGAAATGTGAGGGCCTGAGTGAACACAGTGGGATCATCC   60
           ||||||||||||||||||||||||| |||||||||||| || || |||||||||||
Qy   3256 GGATCCAGGCCCTGCCAGGAGAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315

Db   61 ACTCCATGAGAGATGGGGACCTCACAGAGTCCAGCTGGCCCTCTTGATGGCACTGAGGGAC   120
           ||| ||||||||||||||||| ||||| |||||||| || | | |||||| |
Qy   3316 ACTGCATGAGAGATGGGGATGTCACAGAGTCCAGCGCCACCCTCCTGGTAGCACTGAGAAGC 3375

Db   121 CGGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGAGATTCCTCTCCTAGGAGCTCCA   180
           | ||||||||||||| ||||||||||| |||||||| | |||||||| | ||||||||||
Qy   3376 CAGGGCTGTGCTTGCGGGTCTGCACCCTGAGGGCCCGGATTCCTCTTCCTGGAGCTCCA 3435

Db   181 GGAACAAGGCAGTGAGGCCTTGGCTGCGCCAGCAGTGTCCTCGAGGTTACAGAGCAGGATG   240
           |||| |||||||||||||||||||||| |||||||||||||| |||||||||||||||||
Qy   3436 GGAACAGGGCAGTGAGGCCTGGCCGCAGCAGTGTATCCTCAGGTCACAGAGCAGGAGGATG 3495

Db   241 CACAGGCCGTGCCAGCAGTGAATGTTGCCCTGAATGCACACACCAAGGGCCCCACCTGCCA   300
           ||||| ||||||||||||||| |||||||||| |||||| | ||| |||||||||||||||
Qy   3496 CACAGGGCGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555

Db   301 CAAGACACATAGGACTCCAAAGAGTCTGGGCTCACCTCCTACCATCAATCCTGCAGAAT   360
           ||| |||||||||||||| |||||||||||| ||||||||| |||| | ||||||||||
Qy   3556 CAGGACACACTAGGACTCCCAGAGTCTGGGCTCGGGCTCACCTACTGTCCAGTCCTGTAGAAT 3615

Db   361 CGACCCTGCTGGCCGGCTATACCCTGAGGTGCTCTCCAGGTTCTGA   420
           | ||||||||||||||| ||| |||||| | || |||||||||||| |
Qy   3616 CGACCCTGCTGGCCGGCTGAG-TACCCTCACTTCCTCAGGTTTTTCA 3674

Db   421 GCGAGACAGGCCAACCG-GAG-ACAGGATTCCCTGGAGGCCACAGGAGCACCAAGGAGGA   478
           | |||||||||||||| | |||||||||||||| |||||||||||||||||||||||||
Qy   3675 GGGGACAGGCCAACCCAACAGAGGACGAGGACGATTCCCTGGAGGAGCAGGAGCACCAAGGAGGA 3734

Db   479 AGATCTGTAAGTAAGCCTTTGTTGTAGCCCTGAAGATTTGGTTCTCAGCTGAGGTCTCTC   538
           ||||||||||||||||||||||||| ||||||||||||||| || |||||||||||||||
Qy   3735 AGATCTGTAAGTAAGCCTTTGTTAGCCCTGAAGATTTCAGTTCTCAGCTGAGGCCTCTC 3794

Db   539 ACATGCTCCCTCTCCGTAGGCCTGTGGGTCCCTGTCTTTGCCTGCACTCT   598
           ||| ||||||||||||||||||||||||||||||| ||| |||||||||||
Qy   3795 ACACTCCCTCTCCCTCCCAGGCCTGTGGGTCTTTCATTGCCCAGTTCCCTGCCCACACTCC 3854

Db   599 TGCCTGCTGCCTGAGCAGGTCATCATGTCTCTTGAGCAGAGGAGCACCAAGGGAGA   658
           ||| |||||||||||||||||||||||||||||| |||||| |||||||||||||||
Qy   3855 TGCCTGCTGCCTGAGCAGGTCATCATGTCTCTTGAGCAGAGGAGCTCGCAAGC 3914

Db   659 CTGAGGAAGGCGTTGAGGCCCAAGAAGAGAGGCCCTGGTGGGTGCGGAGGCCTCCTA   718
           |||||||||||| | |||||||||||||||||||||| |||||||||||||||||| |
Qy   3915 CTGAGGAAGGCCCTTGAGGCCCAACAAGAGAGGCCCTGGGTGCGGAGGCTGCAGGCTGC-- 3972

Db   719 CTACTGAGGAGCAGGAGGCGTCGTCCTCCTCCTCCTCCTCGTGTGTGTCCCTGGCACCCTGG   778
           || ||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Qy   3973 ------------CA------C---CTCCTCCTCCTCCTCCTCGTGTGTGTCCCTGGCACCCTGG 4010

Db   779 AGGAAGTGCCGCTGCTGACAGTCCTCCCAGAGTCCTCAGGAGGAGGCCTTGCCT   838
           ||||| |||| ||||||| ||| ||||||||||||||| |||| ||||||||||||
Qy   5084 TGTATATAGTTTAAGGTAAGAGTCTTGTTTTATTCAGATTGGGAAATCCATTCTATT 5143

Db   4011 AGGAGGTGCCCACTGCTGGTCAACAGATCCTCCCAGAGTCCTCAGGAGGACCTCCGCCT   4070
           | |||||||| || || |||||||| || |||||||||||| ||||||||||| ||||||
Qy   839 TACCCACTACCATCAGCTTCACTTGCTCTGAGGCACCCAATGAGGGTTCAGCAGCCAAG   898

Db   4071 TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTG   4130
           ||||||||||||||||||||||| | |||||| || ||| |||||||||||||| |
Qy   899 AAGAGGAGGGGCCAAGCACCTGTTCCGAGAGCACTCAGTA   958

Db   4131 AAGAGGAGGGGCCAAGCACCTGTTATCCTGAGTCCTTGTTCCGAGCAGTAATCACTA   4190
           |||||||||||||||||||||||| | |||| | |||||||||||||||||||
Qy   959 ACAAGGTGGATGAGTTGGCTCATTTCTGCTCCGCCAAGTATCGCAGGTATCGGCAGGAGTGGTCA 1018

Db   4191 AGAAGGTGCCTGATTTGGTTGGTTTCTGCTCCTCAAATATCGACCAGGGAGGCCAGTCA   4250
           ||||| |||| | | |||| || |||||| | | ||||||||| || ||| ||| ||||
Qy   1019 CAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAGACGCGTGCTTCCTGTGATCT 1078

Db   4251 CAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAACACGTGTTTCCTGAGATCT   4310
           |||||||||||||||||||||| |||||||||||||||||| | |||||| ||| ||||
Qy   1079 TCGGCAAAGCCTCCGAGTCCTGAAGATGATCTTTGGCATTGACGTGAGGAAGTGACC 1138

Db   4311 TCGGCAAAGCCCTTGAGTCTTGCAGCTGGTCTTTGGCATTGACGTGAGGAAGACAGACC   4370
           |||||||||||| ||||| || ||||| ||||||||||||||||||||||||||||||
Qy   1139 CACCAGCAACACTACACCCTTGTCACCTGCCTTGGGCCTTCTATGATGGCCTGCTGG 1198

Db   4371 CCACCGGCCACTCCTATGTCTTGTCACCTGCCTTGGGCCTTCTCTGATGGCCGTGCTGGT   4430
           | ||| |||||| |||| || ||||||||||||||||||||||| ||||||| ||||||||
Qy   1199 GTAATAATCAGATCTTTCCAAGACAGGCCTTCTGTATATCGTCCTGGCACAATTGCAA 1258

Db   4431 GTGATAATCAGATCAGTGCCAAGACAGCTTCCTGTAATTGTCCTGATGATTGCAA   4490
           ||||||||||||| ||| ||||||||||||||||| ||||||||| | |||||||||
Qy   1259 TGGAGGGCACAGCGCCTCTGAGGGGCGAAATCTGGAGGAGAATCTGGAGGAGGTGT 1318

Db   4491 TGGAGGGCGGCCGGCCCATGGGCCCTGAGGGAGCCCAGGAGGAGCGCCCAAGAGGTGT   4550
           ||||||| | |||||||||||| ||||||||||| | || |||||| ||||||||||||
Qy   1319 ATGATGGCAGTCACACTGCTGAGGGTGCTATGGGAGCCAGGAAACTGCTCACCCAAGATTGGG 1378

Db   4551 ATGATGGAGGGGGGACCACAGTGCCCTGCCATGGGAGCCCAGGAGGCCGCAGGGAAGATG   4610
           || |||||| ||||||| |||| | ||| |||||||||| |||||| | | ||||||||||
Qy   1379 TGCAGGAAAACTACCTGGAGTACCGGCAGGTACCGGCCAGTAATCCTGCCCGCGCATGAGT 1438

Db   4611 TGCAGGAAAGTACCTGGACGTCGGAGTAC-GGCAGGTGCCGGACGCTTTGAGAG   4669
           |||||||| |||||||| | | ||||||| |||||| ||||| ||||||||||
Qy   1439 TCCTGTGGGTCAATGCAAGAGTTCCATTGCCATTGGGAAGTCCTGAGCAGTGTGG 1498

Db   4670 TCCTGTGGGTCAGTGCAGATGTGCAGTTCGCTTTCTTCCCATCCCCGTGGTCAAGCAGCTTTGAGA   4729
           ||| ||||||||| ||||| |||||||||| ||| ||||| ||| |||||| ||||||||| ||||
Qy   1499 TCAGGTCAATGCAAGAGTTCCATTGCCATTCCTCCTGCTGGGGTGTGGGGCAGGGCT 1558

Db   4730 TCAGGTCAGTGCAAGAGTTCGCTTTCTTCCCATCCCCGTGGTCAAGCGCTTTGAGAG   4789
           |||||||| ||||||||||| |||||||||| ||| | | ||||||||||||||||
Qy   1559 AGGAGGAAGAGAGGAGTCTGAGCATGAGTTGCAGCTGAGGGGAGCAGGGCT 1618

Db   4790 AGGAGGAAGAGAGGAGTCTGAGCATGAGTTGCAGCAGTGAGGTGGGAGGGGGACTGGGC   4849
           |||||||||||||||||||||||||||| ||||||| |||| ||||||| ||||||||
Qy   1619 GGGCCAGTGCATCTAACAGCCCTGCCTTTGCCTGTAACATGAGGCC 1678

Db   4850 CAGTGCAC-CTTCCAGG-GCCGGGTCCAGCAGTTCCCCGCCTCGTGTGACATGAGGCC   4907
           ||| |||| |||||| ||||| ||||||||||||| || |||||| ||||||||||
Qy   1679 CATTCTTCACTCTGTTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGTTTCTATTTGT 1738

Db   4908 CATTCTTCACTCTG---AAGAGAGCGGTCAGTGTTCTTCAGTAGTAGTTTCTGTGTTCTAT   4963
           ||||||||||||| |||||| | |||||||||||| ||||| |||||||| || |||
Qy   1739 TGGATGACTTGGAGATTTATCTCTGTTTTCCTTTTACAATTGTTGAAATGTTCCTTTT-AA 1797

Db   4964 TGGGTGACTTGGAGATTTATTCTGTTCCTTTTTGGAATTGTTCAAATGTTTTTTTTTTAA   5023
           ||| |||||||||||||||| ||||| ||||||| |||||||| ||||||| |||||||||
Qy   1798 TGGATGGTGAATTAACTTCAGCATCCAAGTTATGAATCGTAGTTAACCGTATATTGCTG 1857

Db   5024 GGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGATTGACAGCAGTACACAGTTCTG   5083
           ||||||| |||||| || ||||||||||||| | ||| |||| |||||||| |||||||
Qy   1858 TTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTCAGATTGGGAAATCCGTTCTATT 1917

Matches 2068; Conservative 0; Mismatches 327; Indels 57; Gaps 27;

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Db      1 GGATCCAGGCCCTGCCTCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGATCATCC    60
          |||||||||||||||| ||| |||| ||| ||||||||||||||||  |||||||
Qy   3256 GGATCCAGGCCCTGCCAGAGAAAAATATAAGGGCCCTGCGTGAGACAGAGGGGGTCATCC   3315

Db     61 ACTCCATGAGAGTGGGACCTCACAGAGTCCAGCTGCAGCCCTACCCTCCTTGATGGCACTGAGGGAC   120
          ||| |||||||||||||| |||||||||||  ||  ||||||||| ||  ||||||||||||||
Qy   3316 ACTGCATGAGAGTGGGATGGATGGCACAGAGTCCAGCTGCAGCCCTCCAGCTGTAGCACTGAGAAGC   3375

Db    121 CGGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGGGATTCCTCTCCTAGGAGTCCA   180
          |||||||||||||||||||  ||||||||| || |||||||||||| ||||| ||||
Qy   3376 CAGGGCTGTGCTTCCGGTCTCCACCCTGAGGGCCCGGATTCCTCTCCTGGAGCTCCA   3435

Db    181 GGAACAAGGCCAGTGAGGCCTTGGTCTGAGACAGTGGTCGCTCCAGGTGCTACAGAGCAGAGGATG   240
          |||| ||||||||||||||||||||  |||| |||||||||||||||||||| |||||||||||||
Qy   3436 GGAACCAGGCCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTGCACAGAGCAGAGGATG   3495

Db    241 CACAGGCTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCACCTGCCA   300
          ||| |||||||||||||||||||||  ||||||| |||||||||||||||||||||||
Qy   3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA   3555

Db    301 CAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCATCAATCCTGCAGAAT   360
          |||||||||| || ||| || ||||||||||||| ||||||||||||||||
Qy   3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCACTCCTACTGTCAGTCCTGTAGAAT   3615

Db    361 CGACCTCGCTGGCCGGCTATACCGTGAGGTGCTCTCACTTCCTCCTTCCTCAGGTTCTGA   420
          |||||||||||||||||| ||| |||||||||||  | |||||||| |||||||||  |
Qy   3616 CGACCTCGCTGGCCGGCTACCCTGAGG-TACCCTGTG-TACCCTCTCACTTCCTCCTTCAGGTTTTCA   3674

Db    421 GCAGACAGGCCAACCG-GAG-ACAGGATTCCCTGGAGCCACAGGAGCACCAAGGAGA   478
          |  ||||||| ||| || ||| |||||||||||||||||||||||||||||||||||
Qy   3675 GGGGGCAGGGCCAACCCAGGACAGGATTCCCTGGAGGAGCAGAGGAGCACCAAGGAGA   3734

Db    479 AGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGTTCTCAGCTGAGGTCTCTC   538
          ||||||||||||||||||||||||||||   |||||||||  ||  ||||||||||||||
Qy   3735 AGATCTGTAAGTAAGCCTTTGTTAGAGTCTCCAAGGTCAGTTCTCAGCTCAGTGAGGCCTCTC   3794

Db    539 ACATGTCCCTCTCCGTGGAGGCTGTGGGTCCCATTGCCCAGCTTTGCCTCACTCT   598
          || ||||||||||||||||||||||||||||||  ||||||||  ||||| |||||||
Qy   3795 ACACACTCCCTCTCTCCCCCAGGCCTGTGGGTCTTCAATTGCCCAGCTCCTGCCCACACTCC   3854

Db    599 TGCCTGCTGCCTGTGAGTCAGCAGGTTT||||CATCATGTCTTCTGAGCAGAGAGTCAGCACTGCAAGC   658
          |||||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||||
Qy   3855 TGCCTGCTGCCTGTGACGAGTCATCATGTCTTCTGACGAGAGAGTCTGCACTGCAAGC   3914

Db    659 CTGAGGAAGGCGTTGAGGCCCAAGAGAGAGGCCCTGGGCTGTGGGTGCACAGGCTCCTA   718
          |||||||||| ||||| |||||||| || |||||||||||||  || |||||||| ||
Qy   3915 CTGAGGAAGGCCTGGGCCCAACAAGAGGGCCCTGGGCTGTGTGTGCACAGGCTGC--   3972

Db    719 CTACTGAGGAGCAGGAGGCTGCTGTCGTCTCCTCCTCCTCCTGTCCTCGGCCTGGCCACCCTGG   778
          |||||||||||||||||||   |||| |       |  |  |||||||||||||||||||||||
Qy   3973 --------------CA-------C---CTCCTCCTCCTCTGCTCTGGGCACCCTGG   4010

Db    779 AGGAAGTGCCTCTGCTGAGTCAGCAGGTCTCCCCAGAGTCCTCAGGGAGCCTCTGCCT   838
          |||| |||||||||||||||||  |||| ||| ||||||||||||||||||||||||||
Qy   4011 AGGAGGTGCCCTGGTTGCCCTGAGTCAGCAGGTCTCCCCAGAGTCCTCAGGGAGCCTCCGCCT   4070

Db    839 TACCCACTACCATCAGCTTCACTTCACTGCTGCAGGCACCCTGCTGAGGTTCCAGCAGCAAG   898
          | ||||||||||||||||| |||| || |||||||||||||||||||||||||||||||||
Qy   4071 TTCCCACTACCATCACCAACTTCACTGCAGCAGGCAACCCAGCCAGGTTCCAGCAGCAAG   4130

Db    899 AAGAGGAGGGGCCAAGCACCCTGCGTCATTTTCTGCTCCGCAAGTATCGGCCAGGACACTCAGTA   958
          ||||||||||| |||||||||  |  |||||||||||||||||||  || |||||||||||||||
Qy   4131 AAGAGGAGGGGCCAAGCACCTCTTGTATCCTTGTCCGGAGTCCTGAGAAGAGCTGGTCA   4190

Db    959 ACAAGGTGGATGAGTTGGCTGCTCATTTTCGTCCGCAAGTATGCGACCAAGTATCGGCCTGGCAGTGGTCA   1018
          ||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy   4191 AGAAGGTGGCTGCTCGATTTGGTTGTTTTCGTCCTCCTCAAATATCGGCCAGGGCCAGTCA   4250

Db   1019 CAAAGGCCAGAAATGTGGAGAGAGTCATCAAAAAATTACAAGCCGTGCTTTCCTGTGATCT   1078
          ||||||||||||||||||||||||||||||||||   |||||  |||||||||||||||||
Qy   4251 CAAAGGCAGAAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCT   4310
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Db   1918 TTGTGAATTGGACAATAATAACAGACAGTGGA-GTA---AGTATT-T-AGAAGTGTGAAT   1971
          ||||||||| || |||| |||| || ||||| |||    |  ||| | | |   | |||
Qy   5144 TTGTGAATTGGGATAATAACAGACAGTGGAATAGTGGTAGTACTTAGAAATGTGAAAATGAGACAG   5203

Db   1972 TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATACTTAATTCCCGGCCTTATGCC   2025
          ||     |       || ||   |  || ||| | |||| |||| ||||| |||| |||||
Qy   5204 TAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGAGATAGTGTCAATTCTTGCCTTATACC   5263

Db   2026 TCAGTCTATTCTGTAAAATTTAAAAATATATATGCATACCTGATTTCCTTGGCTTCGT-   2084
          ||||||||||||||||| ||| |||| |||||||  ||||||| |||| |||||||| |
Qy   5264 TCAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCTGATTTCCTTGGCTTCTT   5323

Db   2085 --GAATGTAAGACAGAAATTAAATCTGAATAAATAATTCTTTCTGTTAACTAGCTCATTTCT   2142
          |  |||||||| ||||||||||| |||||||||||||  |  | ||||||||||||||||||
Qy   5324 GAGAAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTTCTTCACTGGCTCTTTTCT   5383

Db   2143 TCTCTATGCACTGAGCATCTGCTCTGCTGGGAAGGCCCCAGGATTAGTAGTAGTGGAGATACTAGG   2202
          | |||||||| ||||| |||| || ||||  |||||||| |||| |||| ||||||||||||||||
Qy   5384 TCTCCATGCACTGAGCATCTGCTTTTGGAAGGCCCCTGGGTGGTTAGTAGTGGAGATGCTAAG   5443

Db   2203 GTAAGCCAGACACACACCTACCCGATAGGGTATTTAAGAGTCTAGGAGC-GCGGTCATATAA   2261
          |||||||||| |  |||| |  || ||||||| |||| | |  |  || |||||||||||||
Qy   5444 GTAAGCCAGACTCATACCCACCCATAGGGTCGTA-GAGTCGAGCTGCAGTCAGTCACGTAA   5502

Db   2262 TTAAGGTGACAAGAGTGTCCTCTAA-GATGTAGGGGAAAA-GT-A-ACGAGTGTTGGGTATG   2317
          |||||||||||| |  |  |||| | ||| |||||||||| || | ||||||||||||||||
Qy   5503 TCGAGGTGGCAAGATGTCTCTCTAAGATGTGGGGAAAAGTGAGAGAGGGGTGTG   5562

Db   2318 GGGCTCCAGGTGAGAGTGGTCGGGTGAAATTCCCTGTG-TGGGGCCTTTGGCTTTGG   2376
          ||||| ||||| ||||||||||  ||||||||||||| ||||||||||||||||||||
Qy   5563 GGGCTCCGGGTGAGTGGTGGAGTGTCAATGCCCGAGCTCGGGGCCATTTTGGGCTTTGG   5622

Db   2377 GAAACTCCATTTTCTTCTGAGGGATCCGATTCTAATGAAGCTGGGTGGGTCC   2428
          ||||| || ||||| || ||||| ||||| |||||||||| ||||||||| |
Qy   5623 GAAACTGCAGTTCCTTCCTTCGGGGGAGCTGATTCTGAATGATCTTGGGTGGATCC   5674
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RESULT 12
ID   Q72482 standard; DNA; 2531 BP.
AC   Q72482;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-4 gene.
KW   Tumour rejection antigen; melanoma antigen-4; MAGE-4; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   625..1578
FT   /*tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B,   Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Example 30; Page 66; 105pp; English.
CC   Q72482 is the gene which contains the coding sequence for melanoma
CC   antigen-4 (MAGE-4). Another melanoma antigen precursor MAGE-3 is encoded by
CC   Q72470, this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence 2531 BP;   608 A;   593 C;   700 G;   630 T;

Query Match   24.7%; Score 1399; DB 1; Length 2531;
Best Local Similarity   84.3%; Pred. No. 0.00e+00;

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Db 1079 TCGGCAAAGCCTCCGAGTCCTCGAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACC 1138
        ||||||||||||||| || || ||||||| |||||||||||||||||||| || |||||
Qy 4311 TCGGCAAAGCCTCTGCAGTCCTTGCAGCTGTCGTCTTTGGCATTGACGTGAAGGAGACC 4370

Db 1139 CCGCCAACACTACACCCTTGTCACCTGGCCTTCTATGATGGCCTGCTGG 1198
        || || ||  ||||||||| |||||||| ||| ||||||||||||||||
Qy 4371 CCACCGGCCACTCCTATGTCCTGTCTCCTAGGTCTCTATGATGGCCTGCTGG 4430

Db 1199 GTAATAATCAGATCTTTCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAA 1258
        ||  ||||||||||||  || || ||||||| | |||||| |||  ||||| |||| ||
Qy 4431 GTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAA 4490

Db 1259 TGGAGGGGCACAGCCGCCCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGT 1318
        |||| |||||  ||||  | ||||||||||| ||||||||||| ||||||||||| |||
Qy 4491 TGGGGGGGCCCATCTCCTCCGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT 4550

Db 1319 ATGATGGAGGAGCACACTGTCTATGGGAGGCCAGGAAACTGCTCACCCAAGATTGGG 1378
        |||||||||||||||||||| || ||||||||| || | ||||| |||||||| |||
Qy 4551 ATGATGGAGGAGCACAGTGCCCATGGGAGGCCAGGAAACTGCTCACCCAAGATTTGG 4610

Db 1379 TGCAGGAAACTACCTGGAGTACCGGCCAGTACCCCGCCAGTAATCCTGCGCGCTATGAGT 1438
        |||||||||| ||||||||||| |||| |||  |||| || || || |||| ||||||
Qy 4611 TGCAGGAAAAGTACCTGGAGTAC-GGCCAGTGCCGGACGACGCCGCACGCTATGAGT 4669

Db 1439 TCCTGTGGGGTCCAAGGCCTCTGCTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGG 1498
        ||||||||||| |||||| |||||||||||  |||| |||||||||||||| |||  ||||
Qy 4670 TCCTGTGGGGTCCAAGGCCCTCGCTGCTGAAACCAGTTATGTGAAAGTCCTTGAGTATGTGA 4729

Db 1499 TCAGGGTCAATGCAGCAAGAGTTCGCATTGCGCATTCCCGCGTGAAGCAGCTTTGTTAG 1558
        ||| |||||||||| || || || | || ||  |||| |||||||||||||| |||
Qy 4730 TCAAGGTCAGTGCAAGAGTTCGCATTCGGCTTTTCTTCCATCCCGCGTGAAGCAGCTTTGAGAG 4789

Db 1559 AGGAGGAAGAGGGAGTCTCAGACATGAGTTGCAGCAGGGCTGTGTGGAGAGGGGCAGGGCT 1618
        ||||||||||||||||| || || ||||||||||||||||| |||| ||||||| ||| |
Qy 4790 AGGAGGAAGAGGGAGTCTGAGCATGATGGCAGCATGGCAGGGCCAGTGGGAGGGGGACTGGGC 4849

Db 1619 GGGCCCAGTGCATCTAACAGCCCGTGCAGCAGCTTCCCTGCCGTCGTGTAACATGAGGCC 1678
        ||| || ||||||  |  ||||  |||| ||||||||| || || |  |  || ||||||
Qy 4850 GGGCCCAGTGCATCATGAGCCCTGTGCAGCAGCTTCCCCGTGTAACATGAGGCC 4907

Db 1679 CATTCTTCACTCGTGTTGAAGAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTTGT 1738
        ||||| | ||||||||||  ||||||||| ||||||| |||||||| |||  |||| ||
Qy 4908 CATTCTTCACTCTG----AAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTAT 4963

Db 1739 TGGATGACTTGGAGATTATCTCTGTTCCTTTTACAAGTTGTGAAATGTTCCTTTT-AA 1797
        ||||| | |||||||| || ||||||  ||||| |||||||| ||||| |||||  ||
Qy 4964 TGGGTGACTTGGAGATTTATCTTTGTTCTTTTGGAATTGTTCAAATGTTTTTTTTTAA 5023

Db 1798 TGGATGGTTGAATTAACTTCAGCATCCAAGTTTATGAATCCTAGTTAACCTATATTGCTG 1857
        |||||||||||||| ||||||||||| |||||||| || ||||||  |  | ||||
Qy 5024 GGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGCAGTCACAGCAGTCACAGTTCTG 5083

Db 1858 TTAATATAGTTAGGAGTAAGAGTCTTGTTTTTATTCAGATTGGGAAATCCGTTCTATT 1917
        | ||||||||| |||||||| ||||||||  |  ||||| |||||  | ||| || ||
Qy 5084 TGTATATAGTTTAAGGGTAAGAGTTTGTTTTTCAGTTTTATTCAGATTGGGAAATCCATTCTATT 5143

Db 1918 TTGTGAATTGGGACATAATAAACAGCAGTGGA---AGTATT-T-AGAAGTGTGAAT 1971
        ||||||||||||| ||  ||| ||  |||| ||   | ||  |   |||||||||
Qy 5144 TTGTGAATTGGGATAATAAATAACAGCAGTAGTACTTAGAATAAGTACTTAGAAAATGAGACAG 5203

Db 1972 TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATACTTAATTCCCGCCCTTATGCC 2025
        | |||    |  |  ||  |   |||||||||||| ||||| || |||| |||  | ||||
Qy 5204 TAAAATAGATGAGATAGAAGAACTAAAGAAATTAAGAGATAAGTAGTCAATTCTGCCTTATACC 5263

Db 2026 TCAGTCTATTCTGTAAAATTTAAAAATTATATATGCATACCTGGATTTCCTTGGCTTCGT- 2084
        |||||||||||  |  |  || | ||||    |||| | ||||| |||||| ||| |||
Qy 5264 TCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTT 5323

Db 2085 --GAATGTAAGAGAAATTAAATCTGAATAAAATTTCTTTCTGTTAACTGGCTCATTCT 2142
          || ||||| |||||||| ||||||| |  ||||| ||||||||||  |||| ||||||
Qy 5324 GAGAATGTAAGAGAAAATTAAATCTGAATAAAATTCTTTCCTGTTCACTGGCACTGAGAAGC 5383
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Db 2143 TCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATACTAGG 2202
        ||| ||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Qy 5384 TCTCCATGCACTGAGCATCTGCTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAG 5443

Db 2203 GTAAGCCAGACACACCTACCCATAGGGTATTAAGAGTCTAGGAGC-GCGGTCATATAA 2261
        ||||||||||| | ||||| |||||| ||  || ||||| | ||  |  || | |||||
Qy 5444 GTAAGCCAGACTCATACCCACCCATAGGTCGTA-GAGTCTAGGAGACTGCAGTCACGTAA 5502

Db 2262 TTAAGGTGACAAGATGTCCTCTAA-GATGTAGGGGGAAA-GT-A-ACGAGTGTGGGTATG 2317
        |  ||||| |||| |||||||||  |  ||| || |||| || | || |||||||||| |
Qy 5503 TCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGGAAAGTGAGGGTGAGGGTGTG 5562

Db 2318 GGGCTCCAGGTGAGAGTGTGCGGGTGTAAATTCCCTG-TGGGGCCTTTTGGGCTTTGG 2376
        ||||  |||||||||| || |  ||||  ||  || ||  | |  ||  ||||||||||
Qy 5563 GGGCTCCGGGTGAGAGTGGTGGGAGGTGTCAATGCCCTGAGCTGGGGGCCATTTTGGGCTTTG 5622

Db 2377 GAAACTGCCATTTTCTTCTGAGGGATCGATTCTGATTCTAATGAAGCTTGGTGGGTCC 2428
        ||| | | |   ||||||  |   | |||||| |||||| | || |||  |||||| ||
Qy 5623 GAAACTGCAGTTCCTTCTCGGGGGAGCTGATTGAGTGGTGATCTTGGTAATGATCTTGGGTGGGATCC 5674
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RESULT 13
ID   Q32357 standard; cDNA; 2531 BP.
AC   Q32357;
DT   22-APR-1993 (first entry)
DE   MAGE-4 gene.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   625..1578
FT   /*tag= a
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992; US-705702.
PR   23-MAY-1991; US-705702.
PR   09-JUL-1991; US-728838.
PR   23-SEP-1991; US-764364.
PR   12-DEC-1991; US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure; Page 79-80; 142pp; English.
CC   The sequences given in Q32352-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence. The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors. MAGE expression is not
CC   restricted to melanomas. MAGE refers to a family of tumor rejection
CC   antigen precursors. The antigens resulting from these genes are
CC   referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence 2531 BP;   608 A;   592 C;   701 G;   630 T;

Query Match   24.6%; Score 1397; DB 1; Length 2531;
Best Local Similarity 84.3%; Pred. No. 0.00e+00;
Matches 2067; Conservative 0; Mismatches 328; Indels 57; Gaps 27;

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Db    1 GGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGATCATCC 60
         |||||||||||||||| | |||||||  |  ||||||| ||||||| | |||| |||||
Qy 3256 GGATCCAGGCCCCGCCGCCAGAGAAAATATAAGCGCCCTGCGAGAACATATAAGGCGTCATCC 3315

Db   61 ACTCCATGAGAGTGGGGACCTGCAGACTTCACAGAGTCCTCGATGATGCGAGGGAC 120
         ||||||||| ||||||| || ||||||||||||||||  |  |||||||||||||
Qy 3316 ACTGCATGAGAGTGGGGATGATCTGCACAGAGTCACAGAGTCCACCGCCACCTCTGGTAGCACTGAGAAGC 3375
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Db   121 CGGGCTGTCTTACAGTCTGCACCCTAAGGGCCCATGGATTCCTCCTAGGAGCTCCA   180
         ||||||||||||| |||||||||||||||||| |||||||| ||| ||||||||||||
Qy  3376 CAGGGCTGTCTTGCGGGTCTGCACCCGGGATTCCTCTTCCTGGAGCTCCA       3435

Db   181 GGAACAAGGCAGTGAGGCCTGGTCTGAGACAGTGTCCTCAGGTTACAGAGCAGAGGATG   240
         |||| ||||||| |||||||||||||||||||||| ||| ||| || ||| ||||||||
Qy  3436 GGAACCAGGCAGTGAGGCCGTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495

Db   241 CACACAGGCTGCCCAGCAGCAGTGAATGTTGCCCTAAGGGCCCCCACCTGCCA       300
         |||| |||||||||||||||||||||||| ||||||||||||||||||||||||
Qy  3496 CACAGGGTGTGCCAGCAGCAGTGAATGCCCTATGGGAGGCCCCCACCTGCCA      3555

Db   301 CAAGACAATAGGACTCCAAAGAGTCTGGCCTCACCTGCCTCCACCTCCACCATCAATCCTGCAGAAT   360
         || |||| ||| | ||| ||||||||||||||||  ||||||||||||||| | || |||| |||||
Qy  3556 CAGGACAATAGGACTCCAGAGTCTGGGCCTCACCTACTCCCCCTGTCAGTCCTGTAGAAT         3615

Db   361 CGACCTCTGGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACTTCCTCCTTCAGGTTCTGA   420
         |||||||||||| ||||| |||||||||||||| |||||||||||||||||||||||| |
Qy  3616 CGACCTCTGGCTGGGCCGGCTGAG-TACCCCCTGGCTTCTCCTTCCTTCAGGTTTTCA    3674

Db   421 GCGACAGGCCAACCG-GAG-ACAGGATTCCCTGGAGGAGCCACAGAGGAGCACCAAGGAGA   478
         |  ||||||||||||  |||  ||||||||||||||||||||||||||||||||||||||
Qy  3675 GGGACAGGCCAACCGAGTACCCCTGGAGGACCAGGATTCCCTGGAGGAGCTCCACTGAGGAGA 3734

Db   479 AGATCTGTAAGTAAGCCTTTGTTAGAGCCTTAAGACCTGGAGGTCTCTC       538
         |||||||||||||||||||  ||| || | || |||| ||||||||||||
Qy  3735 AGATCTGTAAGTAAGCCTTTGTTTGTAGAGTTCAGTTCTCCAAGGTACAGGGCCTGTGTCTC 3794

Db   539 ACATGCTCCCTCTCCGTAGGCCTGTGGGTCCCATTGCCCAGCTTTGCCTGCACTCT   598
         |||   |||||||||  ||||||||||||||  ||||||||||||||||||| |||
Qy  3795 ACACACCCCTCTCCCCCAGGCCTGTGGGTCTTCAGTGCAC-CTTCCAGG-GCCGCGGTCC  3854

Db   599 TGCCTGTGCTGCCCGACCAGAGTCATCATGTGTCTGGAGGAGAGTCAGCACTGCAAGC   658
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3855 TGCCTGCTGCCCGACCAGAGTCATCATGTGTCTGGAGGAGAGTCTGCACTGCACTGCCAAGC 3914

Db   659 CTGAGGAAGGCGTTGAGGCCCAAGAGAGGCCCTGGGCCTGTGGGTGCACAGGCTCCTA   718
         |||||||||||| | |||||||||||||||||||||||| ||| || | | ||||||
Qy  3915 CTGAGGAAGGCCTTGGGGCCCAACAAGAGGCCCTGGGCGTGTGTGTGTCTCGCAGGCCTGC-- 3972

Db   719 CTACTGAGGAGCCAGGAGGCTGCTGTCTCCTCTCCGTGCCTCGGGTCCCATCGCCCCTGG   778
         ||||||||||||||||||||||||| |  ||||||||||||||||||||||||||||||
Qy  3973 ------------CA------C---CTCCTCCTCCCCGTCCCTCGGGCCACCCCTGG       4010

Db   779 AGGAGGTGCTCTGCGGCTGCAGCAGTGCCTCCAGGTCCTGAGCAGCCCTGCCT   838
         ||| |||||||||| ||||||||||||||||||||| ||||||||||||||||
Qy  4011 AGGAGGAGGTGCTCTGCGGCTGCAGCAGTGCCTCCAGGAGCCTGAGCAGCCCTCCGCCT  4070

Db   839 TACCCACTACCATCAGCTTCACTTGCTGGAGGCCCAATGAGAGGTTCCAGCGCAAG   898
         |||| |||||||||||||||||||||||||| | |||| ||||||||||||||| |
Qy  4071 TTCCCACTACCATCAGCTTCACTTGCTGGAGGCCAGAGTCAGTGAGGGTTCCAGCGCCGTG 4130

Db   899 AAGAGGAGGGCCAAGAGCCTCGGCCTGACGCAGAGTCCTGTTCCGAGAAGCACTCAGTA   958
         ||||||||||||||||||||  ||||||| ||||||  ||||||||||||||| ||||
Qy  4131 AAGAGGAGGGCCAAGAGCCTCGGTATCCTGGAGTCCTGGTCCGAGCAGCAGTAATCACTA   4190

Db   959 ACAAGGTGGATGAGTTGGCTCATTTCTGCTTCGGCAAGTATCGAGCCAAGGAGCTCGTGTCA   1018
         ||||||||||| | ||||||||||||| ||||||| ||||| |||||||||||| |||||
Qy  4191 AGAAGGTGGCTCGATTCGGTCTTGCGCTCCTGGCTTGCGTCTTTCAAATATCGAGGACCAGGCCAGTCA 4250

Db  1019 CAAAGGCAGAAATGCTGGAGAGTCATCAAAAAAATTACAAGCCGCTTTTCCTGTGATCT   1078
         |||||||||||||||||| |||||||| |||||||||||| |||||||||||||| |||
Qy  4251 CAAAGGCAGAAATGCTGGAGAGTCATCAAAAAATTACAAGCCACTGTTTCCTGTGAGATCT   4310

Db  1079 TCGGCCAAAGCCTCCGAGTCCTCGCAAGTGATCTTTGGCATTCGGCAAGTGAAGGAAGTGGACC   1138
         |||||| | || |||||||||||||||||||||| || ||||| |||||||||||||| ||||
Qy  4311 TCGGCCAAAGCCTCCGAGTCCTCGCAGCTGATTGGCATTTGGCATTTGCGACGTGAAGGAAGTGGAGATGGCTAAG 4370

Db  1139 CCGCCAGCAACACTACACCCTTGTCACCCTGCCTGGCCTTTTCCTATGATGGCCTGCTGG   1198
         ||||||||||||||||||||  |||| |||||| | |||| ||| ||||||||||||||||
Qy  4371 CCACCCGCCAGCAACACTACACCCCCCCCCATCATGGCCTGCTCTCTCCTATGCCTGCTGG   4430

Db  1199 GTAATAATCAGATCTTTCCCAAGACAGGCCTTCGATAATCGTCCTGGGCCACAATTGCAA   1258
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       GTAATAATCAGATCAGATCATGCCCAAGACAGGCCTTCCTGTATAATTGTCCTGGTGCTGCATGATTGCAA
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Qy  4431 GTGATAATCAGATCATGCCCAAGACAGGCCTTCCTGTATAATTGTCCTGGTGCTGCATGATTGCAA    4490
         || ||||||||||| | |||||||||||||||||||| |||||||||||||||||||||||||||
Db  1259 TGGAGGGGCACAGCGCCTCTGCGGTCTCCTGAGGAGAGAAATCTGGAGGAGGAGAATC          1318
         |||||||| |  | ||||||||||||||||||||||||||||||||||||||||||||||
Qy  4491 TGGAGGGGCCGCCATGCCTCCTGAGGAGAAATCTGGAGGAGGAGAATCTGGAGGAGGAGGATGT   4550

Db  1319 ATGATGGAGGGAGCACACTGTCTATGGGAGCCCAGGAAACTGCTCACCCAGAGTTGGG          1378
         ||| ||||| || || || || ||| |||||||||||||||||||||||||||| |||
Qy  4551 ATGATGGGAGGGAGCCACACTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG      4610

Db  1379 TGCAGGAAAACTACCTGGAGTAGAGTCCGGCCAGTAATCCTGCCGCGCTATGAGT          1438
         |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Qy  4611 TGCAGGAAAAGTACCTGGAGTAC--GGCAGGTGCCGGCCAGTGATCCCGGACGCGCTATGAGT  4669

Db  1439 TCCTGTGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGAGCATGTGG          1498
         ||||||||||||||||||||||||  |||||||||||||| |||||| |||||| ||||||
Qy  4670 TCCTGTGGGGTCCAAGGGCCCCTGAAAACCAGCTATGTGAAAGTGAAAGTCCTTGAGTATGTGA  4729

Db  1499 TCAGGGTCAATGCAAGAGTTGGCATTGCCTACCCATCCCGCGTGAAGCAGCTTTGTTAG          1558
         ||||||| |  |||||||| || ||| |||| |||||||  |||||||||||||||| |||
Qy  4730 TCAAGGTCAGTGCAAGAGTTCGCAAGAGTTGCAAGAGTCTCAGATGTTGAGAGCAGCTTTGAGAG  4789

Db  1559 AGGAGGAAGGAGGAGTCTGAGCATGAGTGAGTGCAGCAGCCCTGCAGAGCTCTC          1618
         ||||||||||||||||||||||||||||||||||||||||| |||||||||||| |||
Qy  4790 AGGAGGAAGGAGGAGTCTGAGCATGAGTGAGTGCAGCAGCCCAAGGCCAAGGGGGACTGGGC    4849

Db  1619 GGGCCAGTGCATCTAACAGCCCTGTGCAGCAGCCCTGTGCCTGCCCAGCTTTTGCCTGCACTCT          1678
         |||||| || |||   || || ||||  ||||  ||||||||||  || | ||| |||||
Qy  4850 CAGTGCAC-CTTCCAGG-GCCGCGCCAGCAGCTCCAGCTTCCCGTGCCTCGTGTGACATGGAGGCC  4907

Db  1679 CATTCTTCACTCTGTTGAAGAAATAGTCAGTGTTCTATTTTGT          1738
         |||||||||||| |||  |  ||| ||| ||||||||||| |||
Qy  4908 CATTCTTCACTCTG----AAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTAT   4963

Db  1739 TGGATGACTTGGACATAATAAACAGCAGTGGA-T-AGTATT--T-AGAAGTGTGAAT          1797
         ||| ||||||||||||||||||||||||||| |   || || |  |||||||||||||
Qy  4964 TGGGTGACTTGGATTATCTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTAA       5023

Db  1798 TGGATGGTTGAATTAAACTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTG          1857
         ||  ||||||||||||||||||||||| ||||||||||||||||| |||||||||||||
Qy  5024 GGGATAGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACACAGCAGTCACACAGTTCTG   5083

Db  1858 TTAATATAGTTTAGGAGTAAGAGCTTGTTTTTTATTCAGATTGGGAAATCCGTTCTATT          1917
         ||||||||||| ||||||||||||||||  || |||||||||||||||||||||||||||
Qy  5084 TGTATATAGTTTTAAGGGTAAGGATGTTTGTGTTTATTCAGATTGGGAAATCCATTCTATT    5143

Db  1918 TTGTGAATTTGGGACATAATAAACAGTGGA-GTA---AGTATT-T-AGAAGTGTGAAT          1971
         |||| |||||||||| ||||||||||| || ||  |||| |||  |  |||||||||||
Qy  5144 TTGTGAATTTGGGATAATAACAGCAGTGAATAAGTAAGTACTTAGAAAATGTGAAAAATGAGCAG  5203

Db  1972 TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATACTTAATTCCCGCCTATGCC          2025
         | |    |  ||  ||| | |  | |||| ||||||||||||||||||||||||||||||
Qy  5204 TAAAATAGATGAGATAAAGGATAAAGAACTAAGGAGAGTAGTCAATTCTGCCTTATACC      5263

Db  2026 TCAGTCTATTCTGTAAAATTTAAAAAATATATATGCCATACCTGGATTTCCTTGGCTTCGT-          2084
         ||||||||||| |||| ||||| |||||||||| ||||||||||||||| ||||||||||
Qy  5264 TCTCCATGCACTGAGCATCTGCTTTTTGGAGGCCCGTGGGTAGTGGAGATGCTAAG        5323

Db  2085 --GAATGTAAGAGAATTAAATCTGAATAATAATCTTGAATAACTCTTCGTCATTTCT          2142
           |||| ||||||||| |||| |||||  ||||||| | |||| ||||| || || |||
Qy  5324 GAGAATGTAAGAGAATTAAATCTGAATAACTCTAGGAGCTGTCACTGCTCTTTTTCT       5383

Db  2143 TCTCTATGCACTGAGCATCTGCTTCTGTCGAAGGAAGTGGACC          2202
         ||||||||| | || |||||  || || | |||| |||||||  |||
Qy  5384 TCTCCATGCACTGAGCATCTGCTTTGTGGAGGTAGTAGTGGAGATGCTAAG      5443

Db  2203 GTAAGCCAGACACACACCTACCGATAGGTATTAAGAGTCTAGAGAC-GCGGTCATATAA          2261
         |||||||||||||||||  ||||||||||  |||||||||   |||||| || |||||
Qy  5444 GTAAGCCAGACTCAGTCATACCCCACCCATAGGGTCGTA-GAGTCTAGGAGCTCACGTAA     5502

Db  2262 TTAAGGTGACAAGATGTCCTCTAA-GATGTAGGGGAAAA-GT-A-ACGAGTGTGGGTATG   2317
         | ||||||||||||||||||  |||| | |||||||||||  |
Qy       
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Qy  5503 TCGAGGTGGCCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGGAGAGGGGTGAGGGTGTG 5562
         ||||||   ||||||||||||||||||||||||
Db  2318 GGGCTCCAGGTGAGAGTGTCGGGTGAGTGGTGA-TGGGGCTTGCTTTGG 2376
         ||||||  ||||||||| ||| |||||||| |||||||| | |||| ||||
Qy  5563 GGGCTCCCGGTGGAGAGTGTGGAGTGGTGTCAATGCCCTGAGCTGGGGCATTTGGGCTTTGG 5622

Db  2377 GAAACTGCATTTCTTCTGAGGGATCGATTCTAATGAGAGCTTGGTGGGTCC 2428
         ||||||  |||||||  ||||| |||  |||||| |||||  | ||||| |||
Qy  5623 GAAACTGCAGTTCCTTCGGGGGGGATGGGAGGCTGATTGTAATGATCTTGGGTGGATCC 5674
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RESULT 14

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ID  Q32358    standard; cDNA; 2531 BP.
AC  Q32358;
DT  22-APR-1993 (first entry)
DE  MAGE-41 gene.
KW  melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW  tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS  Homo sapiens.
FH  Key             Location/Qualifiers
FT  CDS             625. .1578
FT  /*tag=          a
PN  WO9220356-A.
PD  26-NOV-1992.
PF  22-MAY-1992;  U04354.
PR  23-MAY-1991;  US-705702.
PR  09-JUL-1991;  US-728838.
PR  23-SEP-1991;  US-764364.
PR  12-DEC-1991;  US-807043.
PA  (LUDW-) LUDWIG INST CANCER RES.
PI  Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI  Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR  WPI; 92-415460/50.
PT  Nucleic acid mol. encoding a human tumour rejection antigen
PT  precursor - useful as an immunostimulant in a vaccine for
PT  treating and preventing cancers, also useful in diagnosis
PS  Disclosure; Page 81-82; 142pp; English.
CC  The sequences given in Q32352-69 represent a new family of genes
CC  refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC  family were identified during the isolation of the antigen E gene.
CC  The MAGE cDNAs, when tested, did not transfer expression of antigen
CC  E, but they did show substantial homology to the antigen E cDNA
CC  sequence. The MAGE DNAs share a certain degree of homology with each
CC  other and are expressed in tumour cells including several types of
CC  human tumor cells as well as in human tumors. MAGE expression is not
CC  restricted to melanomas. The antigens resulting from these genes are
CC  antigen precursors. The antigens are referred to as MAGE tumor rejection
CC  referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC  See also Q32351.
SQ  Sequence 2531 BP;    607 A;    593 C;    701 G;    630 T;

Query Match             24.6%;  Score 1395;  DB 1;  Length 2531;
Best Local Similarity   84.3%;  Pred. No. 0.00e+00;
Matches 2066;  Conservative    0;  Mismatches 329;  Indels  57;  Gaps  27;
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Db     1 GGATCCAGGCCCTGCCTGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCC 60
         ||||||||||||| ||||| ||||||| |||||||| |||| |||||||||  ||||
Qy  3256 GGATCCAGGCCCCCCCAGGAGAAAAATATAAGGGCCCTGCTGAGAGAGGGGGTCATCC 3315

Db    61 ACTCCATGAGAGTGGGGGACCTCACAGAGTCCAGCTACCCCTCTTGATGCGCACTGAGGGAC 120
         ||||||||||||  |||||||||| ||||||||| ||||||||| | |||||||||| ||||
Qy  3316 ACTGCATGAGAGTGGGGGATGGGTGCTGCACCAGAGTCCAGCAGCTCCTGGTAGCACTGAGAAGC 3375

Db   121 CGGGGCTGCTGCTTACAGTGGCCTGCACCTGAGACAGTGCCTCCTAGGAGCTCCA 180
         | ||| | |||||| ||||||||| | ||||| ||||||||||||||| |||||||
Qy  3376 CAGGGCTGTGCTGCTTGCGGTCTGCACCCTGACAGTATCCTCAGGTCACAGAGAGCTCCA 3435

Db   181 GGAACCAGGCAGTGAGGCCTGGCTGTGCTGACACTGTCCTCAGGTACAGAGCAGAGGATG 240
         ||||| ||||| ||||||||||| ||||| |||||||||||||||||| |||||||||||
Qy  3436 GGAACCAGGCAGTGAGGCCTGGCTGTCGGTCTGACACGTATCCTCAGGTCACAGAGCAGAGGATG 3495

Db   241 CACAGGGCTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300
         ||||||  |||||||||||||||||||
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Qy  3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
         ||||||  |||||||||||||  |||||||||| |||||| |||||| |||||  |||||
Db   301 CAAGACACATAGGACTCCAAAGAGTCTGGCCTTCACCTCCTACCATCAATCCTGCAGAAT 360
         || |||||||||||| ||||||||  ||| || || |||| |||||||  | | |||||
Qy  3556 CAGGACACATAGGACTCCACAGATCTGGCCTGCAATGCCCTGAGCTGGGGCATTTGGGCTTTGG 3615

Db   361 CGACCTCGCTGCGGCCGTATACCCTGAGGGTGCTCTCACTTCCTCCTCCTTCAGGTCTGA 420
         |||||||||||| |||| |||||||||  |||||||| | |||  ||||  ||||  |
Qy  3616 CGACCTCGCTGCGGCCGTGACCCTGAG-TACCCTCCTCACTTCCTCCTTCCTTCAGGTTTTCA 3674

Db   421 GCAGACAGGCCAACCG-GAG-ACAGGATTCCTGGAGGCCACAGAGGAGCACAAGGAGA 478
         ||||  ||||| |||  | | | |||| |||| ||||||| |||||||| ||||||||
Qy  3675 GGGGACAGGCCAACCCAGGAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 3734

Db   479 AGATCTGTAAGTAAGCCTTTGTTAGAGCCTTG |||||||||
         ||||||||||||||| ||||  |||||||| |
Qy  3735 AGATCTGTAAGTAAGTAGGCCTTTGTTAGAGTCTCAAGGTTCTCAGCTGAGTGTCTC 3794

Db   539 ACATGCTCCCTCTCCCAGGCCTGGGTCCCAGCTTTGCCTGCACTCT 598
         ||| |||||||||||||||||| || |||||||||||||||||
Qy  3795 ACACACTCCCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCCTCTGCCCACACTCC 3854

Db   599 TGCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTGAGCAGAGAGTCAGCACTGCAAGC 658
         |||||||||||| |||||||| ||| |||||| ||| |||||||||| ||||||||||
Qy  3855 TGCCTGCTGCCCTGACGAGAGTCATCATGTCTTGAGCAGAGAGTCTGCACTGCAAGC 3914

Db   659 CTGAGGAAGGCGGTTGAGGCCCCAAGAGAGGCCCTGGGCCTGTGGGTGGTGGGTGCCTCCTA 718
         ||||||||||| | ||||||||||||||||||||||| |||||||||||| | ||||
Qy  3915 CTGAGGAAGGCCCCTTGAGGCCTGGGCCTGGGCCTGGTGTGTGGCAGGCTGC-- 3972

Db   719 CTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTGGTCCTCTGGTCCTGCCACCCTGG 778
         |                 ||      |      | ||||| ||| |||||||| |||||
Qy  3973 ------------------CA-------C-----CTCCTCCTCCTCCTCCTGGGCACCCTGG 4010

Db   779 AGGAAGTGCCTGCTGCTGAGTCAGCAGTCCTCCCAGAGTCCTCAGGGAGCCTCGCCT 838
         ||| |||||||||||||||| |||| ||||||||||| |||||||||||||||||||
Qy  4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCCCAGGGAGCCTCCGCCT 4070

Db   839 TACCCACTACCATCAGTTGCTGGAGCGCAACCCAATGAGGGTTCCAGCAGCCAAG 898
         | ||| ||| ||||  || |||||| | |||||||||||||| |||||||||
Qy  4071 TTCCCACTACCATCAACTTCACTGCGACAGAGCAACCCAGTGAGGGTTCCAGCAGCCGTG 4130

Db   899 AAGAGGAGGGGCCAAGCACCTGCGCTGACGCCGACAGTCCTTGTTCGAGAAGCACTCAGTA 958
         |||||||||| |    |    ||    |     || |||| ||||| |||||||||||||
Qy  4131 AAGAGGAGGGGGGCCAAGCACCTTGTGTATCCTGAGTCCTTGGTCCGAGCAGTAATCACTA 4190

Db   959 ACAAGTTGGATGAGTTGGCTCCATTTTCTGCTGCTCCTCCTCAAATATCAGCCCAGGSTCA 1018
         ||||||||| || |||  ||||  | |||| |||| |||| ||||||| |||| ||||
Qy  4191 AGAAGGTGGCTGATTGGTGTTGGTTTTCTGCTTCTCCTCCTCAAATATCAGCCCAGGCCAGTCA 4250

Db  1019 CAAAGGCCAGAAAATGCTGGAGAGAGTGCATCAAAATTACAAGCCGCTGCTTCCTGGATCT 1078
         |||||||||||||||||||||||||||||| |||||||||||| |||||||||||||||||
Qy  4251 CAAAGGCAGAAAATGCTGGAGAGAGTGCTCATCAAAATTACAAGCCACTGTTTTCCTGAGATCT 4310

Db  1079 TCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACC 1138
         |||||||||||||| ||||||||||| || | |||||| ||||| |||||||||||||||
Qy  4311 TCGGCAAAGCCTCCTGAGTCCCTGAAGTCCTTGCAGCTGGTCTTTGGCGTCTTTGGCGTGAAGGAGAGCCAGACC 4370

Db  1139 CCACCAGCAACAACCTACACCCTTGTTCAGCTGCCTGGGCCCTTCAGCGGCACTGAGGTGG 1198
         || |  |||  ||  ||||| ||  | | ||  |||| |||| || || ||||||| ||||
Qy  4371 CCACCGGCCACTGTCCTATGTCCTCACTGCGCCTAGGTGTCTCCTCAGGTACTGATGGGCACTGTG 4430

Db  1199 GTAATAATCAGATCTTTCCCAAGACACAGGCCTTCTATTCGTCTGATAATGCA 1258
         |     |   | | |    |||| || ||||| | |  |   ||| |||||||
Qy  4431 GTGATAATCAGATCATGCCCAAGACAGGCTTCCTGAATTCGTGTGATAATTGCCA 4490

Db  1259 TGGAGGGCGACAGCGCCTGCTGACAGTGTCCTGAGCAGTTACAGCAGAGGATG 1318
         |||||||||| |||||||||| |||||||| ||| ||||||||| |||||||
Qy  4491 TGGAGGGCGGCGGCCATGCTCCTGAGGAGGAAAATCGGGAGGAGCTGGGGGGTGT 4550

Db  1319 ATGATGGGGAGGAGGAGTGCTATGGGAGGACCCAGGAGAAAACTGCTCACCCAAGATTTGG 1378
         |||||||||||||||||||| || || ||||||||||||||||||||| || ||||||||
Qy  4551 ATGATGGGGAGGAGGAGGAGTGCTATGGGAGGACCCAGGAGAAGAGCTGCTCACCCAAGATTTTGG 4610
```

RESULT 15
ID   Q72486 standard; DNA; 2305 BP.
AC   Q72486;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-51 genomic DNA.
KW   Tumour rejection antigen; melanoma antigen-51; MAGE-51; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   645..992
FT   /*tag=   a
PN   WO9423031-A.
PD   13-OCT-1994;
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Disclosure; Page 72; 105pp; English.
CC   Q72486 is the genomic DNA which contains the coding sequence for
CC   melanoma antigen-51 (MAGE-51). Another melanoma antigen MAGE-3 is
CC   encoded by Q72470, this is a tumour rejection antigen precursor.
CC   Melanomas characterised by the expression of MAGE-3 can be detected,
CC   or monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence 2305 BP;   549 A;   568 C;   611 G;   577 T;

Query Match   21.6%; Score 1225; DB 1; Length 2305;
Best Local Similarity   84.1%; Pred. No. 0.00e+00;
Matches 1956; Conservative   0; Mismatches 299; Indels 72; Gaps 32;

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Db     1 GGATCCAGGCCTTGCCAGGAGAAGAAAGGTGAGGGCCCTGTGTGAGCAGAGGGGACCATTC    60
         |||||||||||||||||  |||| || |||||||| | ||| || |||||||||  |||||
Qy  3256 GGATCCAGGCCCTGCCAGGAGAAAAATATAAGGGCCCTGCGTGAGAACAGAGAGGGGTCATCC  3315

Db    61 ACCCCAAGAGGGTGAGACCTCAGAGATTCAGCAGTCCCTATGCC   120
         || ||| ||  ||||| | |||||| ||||| |||||||||||||
Qy  3316 ACTGCATGAGAGTGGGATGTCACAGAGTCCAGCAGTCCCACCCTCCGGTAGCACTGGAGAAGC  3375

Db   121 TGAGGCTGTGCTTGCAGTCTGCCACCCTGAGGGGCCATGCAATTCCTCCTTCCAGGAGCTCCA   180
         ||||||||||||||| || ||||||||||||||| |||||||||||||||||||||||||||
Qy  3376 CAGGGCTGTGCTTGCAGTCTGCCACCCTGAGGGGCCCGTGAGTTCCTCCTTCCTGGAGCTCCA  3435

Db   181 GGAAACAGACACTGAGGCCTTGGTCTCAGAGGCCGTGCCCTCAGGTCACAGACAGGAGGAGA   240
         ||| ||| ||| |||||||||||||| |||| | |||||||||||| ||||||||||||||||
Qy  3436 GGAACCAGGCAGTGAGGGCCCTTGGTCTGCGACAGCAGTATCCTCAGGTCACAGACAGCAGGA--  3493

Db   241 TGCAGACGTCTGAGTGCTCCAGCAGTGAACGTTTGCCTGAATGCACACTAATGCCCCATC   300
         |||| | |||| ||| | ||||| |||||| |  | | ||||| |||| ||||||||||| |
Qy  3494 TGCACAGG-T-GTGCCAGCAGTGAATGTTGCCCTGAATGCACACCTCGTCAGTCGTCAGTCCT  3551

Db   301 GCCCCAGAACATATGGGACTCCAGAGACGCACCTGGCCTCACTGTACCTGTCAGTCCTGC   360
         ||| |||| ||  ||||||| |  | ||| |  |||||||||| |||||||||||||||| |
Qy  3552 GCCCAGAGACACACATAGGACTCCACGAGTCTCCAGAGGTCTGCCTCACC-TCCCTACTGTCAGTCCTGT  3610

Db   361 AGAATCAGCCTCGCTTGCTTG-TGTACCCCTGAGGTGCCCTCTCACTTTTTTCCTTCAGGT   419
         |||||| || |||| |||| ||  |  | || || ||||||||||||||||||| ||||| |
Qy  3611 AGAATCGACCTCTGCTGCGGCCTCTGGGTCAATGGTAGGCTTAGCCTTGTTCCTTCAGGT  3669

Db   420 TCTCAGGTGGACAGGCTGACCTGGATCAGCATCACCAGGAGCTCCAGAGGGCCCT   479
         || ||| ||| ||||||||| || ||| || |  |  | |||| |||||||||||
Qy  3670 TTTCAGGGGACCAGGC-----CA--A-C-CCAG--AGGAC---AGGATTCCCTGGAGCCAC  3716

Db   480 AGAGGAGCACCAAAGGAGAGAGATCTGTAAGTAAGCCTTGTTGAGAGCCTCCAAGGTTCAG   539
         ||||||||||||||| |||||||||| || |||||| ||||||||||||||||||||||||
Qy  3717 AGAGGAGCACCACCAA-GGAGAAGAGATCTGTAATGAGCTGGGACTGAATCTTGGGTGCCTGT  3775
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Db  1379 TGCAGGAAAACTACCTGAGTGAGACCCGGCAGTAATCCTGCGCGCGTATGAGT  1438
         |||||||||||||||||||||||||  |||||| |||||||  |||||||||||
Qy  4611 TGCAGGAAAGTACCTGGGAGTAC-GGCAGGTGCCGACACAGTGATCCCGACGCGTATGAGT  4669

Db  1439 TCCTGTGGGGTCCAAGGGCTGGCTGAAACCAGCAGTCCTGGAGCATGTGG  1498
         ||||| |||||||| ||||||||||| |||||| ||||||||||||| ||||
Qy  4670 TCCTGTGGGGTCCAAGGGCCCTGCTGAAACCAGCCTTGAGTATGTGA  4729

Db  1499 TCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAG  1558
         ||| ||||| ||||||||| || ||||||||   |||||||||| || |||||||  | ||
Qy  4730 TCAAGGTGCAGAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG  4789

Db  1559 AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGCTGTGGGGAAGGGGCAGGGCT  1618
         |||||||||||||||||||||||||  ||| |||| || ||||||   ||||||||||||
Qy  4790 AGGAGGAAGAGGGAGTCTGCAGCATGCAGTTGCAGCCAGGGCCAAGGGCAGTGGGGAGGGGACTGGGC  4849

Db  1619 GGGCCAGTGCATCTAACAGCCCTGTGCAGCAGCTTCCCTGCTCTCGTTGTAACATGAGGCC  1678
         ||||||  | |||||||||||   | |||  | |||| ||| ||||||| ||||||||||||
Qy  4850 CAGTGCAC-CTTCCAGG-GCCGCGTCCAGCAGCTTCCCCGTGTCCCCCTGCTCTCCCTGTGTGACATGAGGCC  4907

Db  1679 CATTCTTCACTCGTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTTGT  1738
         |||||||||||    |       | |  ||||||  ||||| |||||| || |||| |
Qy  4908 CATTCTTCACTCTG---AAGGAGCGGTCAGTGTTCTCAGTGTTCTTCAGTAGTAGGTTTCTGTTCTAT  4963

Db  1739 TGGATGACTTGGAGATTTAТCTCTGTTTCCTTTACAATTGTTGAAATGTTCCTTTT-AA  1797
         ||| |||||||||| | |||| ||||||||| || ||||||||||||||||| ||| ||
Qy  4964 TGGGTGACTTGGAGAТTTAТCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTTTAA  5023

Db  1798 TGGAGGTTGAATTAACTTCAGCATCCAAGTTGATGAATCGTAGTTAACGTTAACTATTGCTG  1857
         |||||||||||||||||||||||||||||   || |    |||||||  | |  |  | |||
Qy  5024 GGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACCACAGTTCTG  5083

Db  1858 TTAATATAGTTAGGAGTAAGAGTCTTGTTTTTTATTCAGATTGGGAAATCCGTTCTATT  1917
         | |||||||||  ||||||||||||||  |||| ||||||||||||||||   |||||||
Qy  5084 TGTATATAGTTTAAGGGTAAGGTAAGAGTCTTGTTGTGTTTTATTCAGATTGGGAAATCCATTCTATT  5143

Db  1918 TTGTGAATTTGGGACATAATAACAGCAGTGGA-GTA---AGTATT-T-AGAAGTGTGAAT  1971
         |||| ||||| ||| ||| |||||||||||| || |  | |  |  ||||  |||||||
Qy  5144 TTGTGAATTGGGATATAATAACAGCAGTGGATAAGTACTTAGAAATGTGAAAAATGAGCAG  5203

Db  1972 TCACC--G-TGAAATAG-GTG--AGATAACAGATACTTAATTCCCCGCCCTATGCC  2025
         |||||  |  ||| ||| |||   |||| |||||||| |  | | | | ||||||||
Qy  5204 TAAAATAGATGAGATAAAGAACTAAAGAACTTAAGAATATAAGAAAATCTTGCCTTATACC  5263

Db  2026 TCAGTCTATTCTGTAAAATTTAAAAATATATATGCATACCCTGGATTTCCTTGGCTTCGT-  2084
         ||| | |||||||||| |    ||| ||||   |||||||||||  ||||||||||||||
Qy  5264 TCAGTCTATTCTGTAAAATTTTTAAAGATATGCATACCTGGATTTCCTTGGCTTCTTT  5323

Db  2085 --GAATGTAAGAGAAATTAAAATCTGAATAAAATAAATAATTCTTCTGTTAACTGGCTCATTTCT  2142
         | |||||| |||  |||||||| || |||||||||||||||||||||||||||||   |||
Qy  5324 GAGAATGTAAGAGAAATTAAAATCTGAATAAAGAATTCTTCTGTTAACTGGCTCTCTTTTTCT  5383

Db  2143 TCTCTATGCACTGAGCATCTGCTTCTGCCAGGATTAGTAGTGGAGATACTAGG  2202
         ||| ||| | ||| |||||  ||||||||||||||||||| ||||||||||||
Qy  5384 TCTCCATGCACTGAGCATCTGCTTTTGGGGAGGCCCAGGATTAGTAGTGGGTTAGTAGTGGGCTAAG  5443

Db  2203 GTAAGCCAGAACACACCACCTACCGATAGGGTATTAAGAGTCTAGGAGC-GCGGTCATATAA  2261
         ||||||| |||||||| ||||| ||| ||| ||||||| |||||||||| | ||| |||||
Qy  5444 GTAAGCCAGACACACACCATACCCCATAGGGTCGTA-GAGTCTTAGGAGCTGCAGTCACGTAA  5502

Db  2262 TTAAGGTGACAAGATGTCCTCTAA-GATGTAGGGGAAA-GT-A-ACGAGTGTGGGGTATG  2317
         |||| ||||| ||||||| |||||   |||| ||  |  || | ||| ||||||||||||
Qy  5503 TCGAGGTGGCAAGATGTGGTCGGGTGAGTGTCAAAGATGTAGGGAAGGGTGAGGGTGTG  5562

Db  2318 GGGCTCCAGGTGAGAGTGAGTGGTCGGGTTGAAATTCCCTGTG-TGGGGGCCTTTTGGG  2376
         ||||| |||||||||||||||||||| ||||||||| ||| ||| |||||||||||||||
Qy  5563 GGGCTCCGGGTGAGGGTGAGTGGTCGGGTCAATGCCCGAGCTGGGGCATTTGGGCTTTGG  5622

Db  2377 GAAACTGCCATTTTCCTTCTCTGAGGGGATCTGATTCTAATGAAGCTTGGTGGGTCC  2428
         |||||| | ||||||||||| || ||||||| ||||||||  ||||||||||||||
Qy  5623 GAAACTGCAGTTCCTTCTCTGGGGGGACCTGATTCTGGGTTGGGTTGGGTGGATCC  5674
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Db   540 TTTTTAGCTGAGGCTTTCTCACATGCTCCCTCTCTCTCCAGGCCAGTGGGTCTCCATTGCC 599
         ||  ||||||||||  ||| ||||||||||||||||||||||||||  ||||  ||| |||||
Qy  3776 TTCTCAGCTGAGGCCTTCACACACTCCCTCTCTCTCCAGGCCAGGCCTGGGTCTCATTGCC 3835

Db   600 CAGCTCCTGCCCACACTCCTGTCGGTGACCAGAGTCGTCATGTCTCTTGAGCAG 659
         |||||||||||||||||||| ||| |||| ||||||||||||||||||||||||
Qy  3836 CAGCTCCTGCCCACACTCCTGCCTGCCCGTGACGAGTCATCATGTCTCTTGAGCAG 3895

Db   660 AAGAGTCAGCACTGCAAGCCTGAGGAAGGCCTTGACACCCAGAAGAG-CCCTGGGCCTG 718
         | |||||  |||||||||||||||||||  |||| || |||||  ||| ||||||||||||
Qy  3896 AGGAGTCGCACTGCCAAGCCTGAGGAAGGCCCTGAGGCCCAACAAGAGCCCTGGGCCTG 3955

Db   719 GTGGGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTGTCCTCTCCTCTCCTCTG 778
         ||  ||  || |||||||      ||  |||  ||   ||         ||||||||||
Qy  3956 GTGTGTGCAGGCTGCCAC------------CT----CCTCTCCTCTCCTCTG 3994

Db   779 GTCCCAGGCACCCTGGGGGAGTGGCTGCTGCTGGGTCACCAGGTCCTCTCAAGAGTCCT 838
         |||| ||||||||||||  ||||||||||||   |||||   || || ||| |||||||
Qy  3995 GTCCTGGGCACCCTGGAGGAGTGGCTGCTGGGTCACTGGGTCAAGATCCTCCCAGAGTCCT 4054

Db   839 CAGGGAGCCCTCGCCATCCCACTGCCATGCCATGGAGGCAATCCATTAAG 898
         |||||||||||||| | ||| |||||||| || ||||| |  |||| | |
Qy  4055 CAGGGAGCCCTCGCCTTCCCACTACCATCAACTTCACTCGACAGAGCCAGTCAGTGAG 4114

Db   899 GGCTCCAGCAACCAGCAGGAGGAGGGCCAAGCACCTCCCCTGACCCCAGAGTCTGTGTTC 958
         ||||||||| | |||||| ||||| ||| |||||  || |||| ||||||  || || ||
Qy  4115 GGTTCCAGCAGCCGCGTGAAGAGGAGGGCCCAAGCACCACCCCTTGTATCCTGAGTCCTTGTTC 4174

Db   959 CGAGCAGCACTCAGTAGTAAGAAGGTGGCTGGCTACTTGATTCATTTCTGCTCCTCCTCAAGTATTAA 1018
         |  ||||||| |||||||||||||||||||||||  ||||||| |  |   |  ||| ||||||||
Qy  4175 CGAGCAGTAATCACTAAGAAGGTGGCTGGCTGATTGGTTGGTTTTCTGCTTTCTGCTCCTCAAATATCGA 4234

Db  1019 GTCAAGGAGCCGGTCACAAGGCAGAAATGCTGGAGAGCGTCATCAAAAATTACAAGCGC 1078
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Qy  4235 GCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCAC 4294

Db  1079 TGCTTCCTGAGAATCTTCGGCAAAGCCTCGGAGTCCTTGCAGCTGGTCTTTGGCATTGAC 1138
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Qy  4295 TGTTTTCTGAGAATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGAC 4354

Db  1139 GTGAAGGAAGCGGACCCCACCACAGCAACACCTTGTCACCTGCCTGCGGGACTC--C 1196
         ||||||||||| || |||| | |||| || ||||||||| |||| |||| ||||| |
Qy  4355 GTGAAGGAAGCAGACCCCACCGCCATGTGGGAGCCCATGGGGGAGCCCAGGAAGCTG 4414

Db  1197 TATGATGGCCTGGTGTT--TAATCAGATCATGCCCAAGACGGGCCCTGATAATCGTC 1254
         |||||||||| | ||| ||  |||||| |||||| ||||||| | || |||||||||
Qy  4415 TATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACGGGAGGAAATCTGGGAGGACTG 4474

Db  1255 TTGGGCATGATTGCAATGGAGGGGCAAAATGCTCCCTGAGGAGGAAAATCTGGGAGGAGCTG 1314
         ||||||||| |  |||  |||||| ||||| |||| ||||||||||||||||||||||||||
Qy  4475 CTGGGCATGATTGCAATGGAGGGGCCGCCATCTCCTGAGGAGGAAAATCTGGGAGGAGCTG 4534

Db  1315 GGTGTCGATGAAGGTGTATGTTGGGAGAGGAGGCACAGTGTCGTGGGAGCCCAGGAAGCTG 1374
         ||||| || ||||||||||||||| |||||||  |||| |||||||||||||||||||||
Qy  4535 AGTGTGGATGAAGGTGTATGATGGGAGGGGGAGGCACAGTTGTGGGAGGAGCCCAGGAAGCTG 4594

Db  1375 CTCACCCAAGATTTGGTGCAGGAAAACTACCTGGAGTACCGCAGTGCCCAGTGATC 1434
         |||||||||||| ||||||||| ||| |||||||||||||| |||||||||||||
Qy  4595 CTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGCCGGACAGTGATC 4654

Db  1435 CCATATGCTATGAGTTACTGTGGGGTCCAAGGGTCACTCGCTG------CT---TGAAAG 1484
         |||| ||||| ||||| || |||||| |||| || |||  ||        |   ||||||
Qy  4655 CCGCACGCTATGAGTTCCTGTGGGGTCGGGGTGTCAAAGGGCCCATGTGAAACCAGCTATGTGAAAG 4714

Db  1485 TACTCGAGCACGTGGTCAGGGTCAATGCAGTCTCAATGCCTACCCATCCCTGCATG 1544
         |||| |||||||||||||||||| || || |||| ||| |||  ||| |||||||
Qy  4715 TCCTTGAGTATGTGATCAAGGTCAGTGATCAAGTCTCGTTTCGTTTCTTCCCATCCCTGCGTG 4774

Db  1545 AAGCAGCTTTGAGAGAGGAAGAGGGAGTCCTGAGCCATGCGCAGCCGCGGCCACTG 1604
         |||||||||| |||||||||||||||||||| ||||| ||| |||| |||||||||
Qy  4775 AAGCAGCTTTGAGAGAGGAAGAGGGAGTCCTGAGCCATGGTCCATGAGTGTGCGCAGGCCAGTG 4834
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Db  1605 CGAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCCGTCCAGTAGTTCCCTGCCTTAA 1664
         ||||||||| ||||||||||||||||||||||||||||  ||||||||||||||||||||||
Qy  4835 GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCGCCAGCAGCTTCCCCTGCCTCG- 4893

Db  1665 TGTGACATGAGGCCATTCTTCTCTTTGAAGAGAGCAGTCAACATTCTTAGTAGTTGGG 1724
         |||||||||||||||||||||||  ||||||  ||  || |||| ||| ||||||||||
Qy  4894 TGTGACATGAGGCCCATTCTCACTCT--GAAGAGCGGTCAGTGTGTCTCCAGTAGTAGG 4951

Db  1725 TTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGTTCCTTTGGAATTGTTCAAAT 1784
         ||||||||||||||||||||||||| ||||||||  |||||||||||||||| |||||
Qy  4952 TTTCTGTTCTATTGGGTGACTTTGGGATTTATCTTTGTTCCTTTTGGAATTGTTCAAAT 5011

Db  1785 GTTCCTTTAATGGG-TGGTTGAATGAACTTCAGCATTCAAATTATGAATGACAGTAGT 1843
         ||| |||  ||| |  | ||||||||||||||| ||  |||  ||||||||| |||||
Qy  5012 GTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAGT 5071

Db  1844 CACACATAGTGCTGTTTTATATAGTTTAGGAGTAAGAGTCTTGTTTTATTCAGATTGGG 1903
         |||||        |||||||||||| | ||||||||||||  ||||| ||||||||||||
Qy  5072 CACACA--GTTCTGTGTATATAGTTTAAGGTAGTTAGGGTAAGAGTCTTGTTTTATTCAGATTGGG 5129

Db  1904 AAATCCATTCCATTTTGTGAATTGGGACA-TAGTTACAGCAGTGGAA-TAAGTATTCATT 1961
         |||||||  |||||| |||||||||| ||  | ||| |||| ||||||  || |||   |
Qy  5130 AAATCCATTTCATTTCTGTGAATTGGGGATAATAACAGCAGTGGAATAAGTACTTAGAAATG 5189

Db  1962 T-AGAAATGTGAA-TGAGC-AGTAAAACTGATGAGATAAAGAAATTAAAGATATTAAT 2018
         | | |||| | |  | | |  | | | |||| || ||| | || ||||| | |||
Qy  5190 TGAAAAATGAGCAGTAAAATAGATGAGATAAAGAAGAACTAAAGAAATTAAGAGATAGTCAAT 5249

Db  2019 TCTTGCCTATAC-TCAGTCTATTCGGTAAAATTTTTTTTAAAAATGTGCATAACCTGGA 2077
         |||||||  ||  |||| ||| |||||||  |||||| |||  | ||||| |||||||||
Qy  5250 TCTTGCCTTATACCTCAGTCTTATTCGTAAAAATTTTAA--AGATATGCATAACCTGGA 5307

Db  2078 TTTCCTTGGCTTCTTGAGAATGTAAGCAGACAAATTAAAATCTGAATAAATCATTCTCCCTGT 2137
         ||||||||||||||||||||||| |||||| ||||| || ||||||||||| |||||||||||
Qy  5308 TTTCCTTGGCTTCTTGAGAATGTGAGCAGACACACTACTCTGAATAAATCATTCTTCCTGT 5367

Db  2138 TCACTGGCTCATTTATTCTTCCTGAGCATTTGCTCTGTGGAAGGCCCCTGGGTTAA 2197
         ||||||||||| ||||| |||| |||||||||||||||||||||||||||||||| |
Qy  5368 TCACTGGCTCTTTTCTCTCCCATGCAGCATCTGCGACTCTGCCTTTTTGGAAGGCCCTGGGTTAG 5427

Db  2198 TAGTGGAGATGCTAAGGTAAGCCAGAGTCACCCCTACCCACAGGGTAGTAAAGTCTAGGA 2257
         ||||||||||||||||||||| |||||||||||||| | ||||||||||||||||||||
Qy  5428 TAGTGGAGATGGCTAAGGTAAGCCAGGACTCATCACCCCACCCATAGGGGTCGTAGAGTCTAGGA 5487

Db  2258 GCACAGTCATATAATTAAGGTGAGAGATGCCCTCTAA-GATGTAG 2303
         ||  |||||| |  |||| ||||||||| |||| ||| |||||||
Qy  5488 GCTCGAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
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Search completed: Tue Apr 7 20:51:08 1998
Job time : 508 secs.

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***    M   P   S   R   C   H                  ***  (TM)
***                                           ***
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MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

Run on:          Tue Apr 7 20:51:27 1998;   MasPar time 301.84 Seconds
                                             943.881 Million cell updates/sec
Tabular output not generated.

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Perfect Score:  5674
N.A. Sequence   1 CCCGGGGCACCACTGGCATC.........TAATGATCTTGGTGGATCC 5674
Comp:             GGGCCCCGTGGTGACCGTAG.........ATTACTAGAACCCACCTAGG

Scoring table:  TABLE default
                Gap 6

Nmatch  STD :   Dbase 0;  Query 0

Searched:       96465 seqs, 25105746 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       n-issued
                1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics:     Mean 10.059;  Variance 5.500;  scale 1.829

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	%Query Match	Length	DB		ID	Description	Pred. No.
1	5674	100.0	5674	7		US-08-299-	Sequence 8, Applicatio	0.00e+00
2	5674	100.0	5674	6		US-08-190-	Sequence 1, Applicatio	0.00e+00
3	5674	100.0	5674	4		US-07-807-	Sequence 8, Applicatio	0.00e+00
4	2419	42.6	2419	4		US-07-807-	Sequence 7, Applicatio	0.00e+00
5	2419	42.6	2419	7		US-08-299-	Sequence 7, Applicatio	0.00e+00
6	1483	26.1	4157	7		US-08-299-	Sequence 9, Applicatio	0.00e+00
7	1483	26.1	4157	4		US-07-807-	Sequence 9, Applicatio	0.00e+00
8	1399	24.7	2531	7		US-08-299-	Sequence 13, Applicati	0.00e+00
9	1399	24.7	2531	7		US-08-299-	Sequence 14, Applicati	0.00e+00
10	1225	21.6	2305	7		US-08-299-	Sequence 17, Applicati	0.00e+00
11	943	16.6	2226	7		US-08-299-	Sequence 16, Applicati	0.00e+00
12	811	14.3	1640	7		US-08-299-	Sequence 11, Applicati	0.00e+00
13	811	14.3	1640	4		US-07-807-	Sequence 11, Applicati	0.00e+00
14	682	12.0	1067	4		US-07-807-	Sequence 15, Applicati	0.00e+00
15	683	12.0	1068	7		US-08-299-	Sequence 15, Applicati	0.00e+00
16	645	11.4	1412	7		US-08-299-	Sequence 21, Applicati	0.00e+00
17	611	10.8	1947	7		US-08-299-	Sequence 19, Applicati	0.00e+00
18	562	9.9	1810	7		US-08-299-	Sequence 20, Applicati	0.00e+00
19	392	6.9	1107	7		US-08-299-	Sequence 23, Applicati	3.65e-272
20	350	6.2	943	7		US-08-299-	Sequence 12, Applicati	1.17e-239
21	350	6.2	943	4		US-07-807-	Sequence 12, Applicati	1.17e-239
22	207	3.6	1866	6		US-08-403-	Sequence 1, Applicatio	4.92e-130
23	199	3.5	920	7		US-08-299-	Sequence 22, Applicati	5.62e-124
24	177	3.1	226	4		US-07-807-	Sequence 14, Applicati	2.20e-107
25	149	2.6	225	4		US-07-807-	Sequence 15, Applicati	1.93e-86
26	149	2.6	225	7		US-08-299-	Sequence 18, Applicati	1.93e-86
27	136	2.4	2099	7		US-08-299-	Sequence 25, Applicati	8.40e-77
28	137	2.4	2150	7		US-08-299-	Sequence 24, Applicati	1.53e-77
29	130	2.3	662	4		US-07-807-	Sequence 10, Applicati	2.24e-72
30	130	2.3	662	7		US-08-299-	Sequence 10, Applicati	2.24e-72
31	127	2.2	7218	7		US-08-232-	Sequence 16, Applicati	3.61e-70
32	93	1.6	166	4		US-07-807-	Sequence 14, Applicati	1.67e-45
33	87	1.5	687	6	c	US-08-403-	Sequence 4, Applicatio	3.08e-41
34	78	1.4	7218	7		US-08-232-	Sequence 14, Applicatio	6.57e-35
35	62	1.1	461	6		US-08-403-	Sequence 2, Applicatio	6.42e-24
36	53	0.9	476	6		US-08-403-	Sequence 3, Applicatio	6.09e-18
37	47	0.8	215	6	c	US-08-238-	Sequence 5, Applicatio	4.51e-14
38	41	0.7	215	6		US-08-238-	Sequence 5, Applicatio	2.54e-10
39	33	0.6	780	15	c	PCT-US96-0	Sequence 1, Applicatio	1.41e-05
40	27	0.5	27	7		US-07-807-	Sequence 1, Applicatio	2.74e-02
41	29	0.5	105	5	c	US-07-865-	Sequence 13, Applicatio	2.37e-03
42	29	0.5	2732	8	c	US-08-476-	Sequence 60, Applicati	2.37e-03
43	29	0.5	4325	13		PCT-US94-0	Sequence 21, Applicati	2.37e-03
44	28	0.5	11236	4	c	US-07-853-	Sequence 1, Applicatio	8.13e-03
45	29	0.5	11558	12	c	PCT-US93-0	Sequence 23, Applicati	2.37e-03

ALIGNMENTS

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RESULT   1
ID    US-08-299-849B-8 STANDARD; DNA; UNC; 5674 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 8, Application US/08299849B.
CC    Sequence 8, Application US/08299849B
CC    Patent No. 5612201
CC    GENERAL INFORMATION:
CC    APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
CC    APPLICANT:  Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC    APPLICANT:  Chomez, Patrick
CC    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
CC    TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precurso
r
CC    NUMBER OF SEQUENCES:  48
CC    CORRESPONDENCE ADDRESS:
CC    ADDRESSEE:  Felfe & Lynch
CC    STREET:  805 Third Avenue
CC    CITY:  New York City
CC    STATE:  New York
CC    ZIP:  10022
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC    COMPUTER:  IBM
CC    OPERATING SYSTEM:  PC-DOS
CC    SOFTWARE:  Wordperfect
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER:  US/08/299,849B.
CC    FILING DATE:  1-SEPTEMBER-1994
CC    CLASSIFICATION:  435
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER:  08/037,230
CC    FILING DATE:  26-MARCH-1993
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER:  PCT/US92/04354
CC    FILING DATE:  22-MAY-1992
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER:  07/807,043
CC    FILING DATE:  12-DECEMBER-1991
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER:  07/764,364
CC    FILING DATE:  23-SEPTEMBER-1991
CC    PRIOR APPLICATION DATA:
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CC       APPLICATION NUMBER:   07/728,838
CC       APPLICATION NUMBER:   9-JULY-1991
CC       PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER:   07/705,702
CC       FILING DATE:   23-May-1991
CC       ATTORNEY/AGENT INFORMATION:
CC       NAME: Hanson, No. 561220Iman D.
CC       REGISTRATION NUMBER:   30,946
CC       REFERENCE/DOCKET NUMBER: LUD 5355
CC       TELECOMMUNICATION INFORMATION:
CC       TELEPHONE:   (212) 688-9200
CC       TELEFAX:   (212) 838-3884
CC  INFORMATION FOR SEQ ID NO:   8:
CC       SEQUENCE CHARACTERISTICS:
CC       LENGTH:   5674 base pairs
CC       TYPE:   nucleic acid
CC       STRANDEDNESS:   single
CC       TOPOLOGY:   linear
CC       MOLECULE TYPE:   genomic DNA
CC       FEATURE:
CC       NAME/KEY: MAGE-1 gene
SQ  Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match      100.0%;   Score 5674;   DB 7;   Length 5674;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 5674;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
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(Sequence alignment between Db and Qy strands, positions 1–1800, 100% identity.)

Db 2881 GACCAGAACACTGAGGGAGGACTGCACAGAAATCAGCCTGCCCTGCTGTCACCCAGAG 2940
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Qy 2881 GACCAGAACACTGAGGGAGGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG 2940

Db 2941 AGCATGGGCTGGGCCGTCTGCCGAGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000
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Qy 2941 AGCATGGGCTGGGCCGTCTGCCGAGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000

Db 3001 ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGGAGGAGCCTCCCAGGCC 3060
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Qy 3001 ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGGAGGAGCCTCCCAGGCC 3060

Db 3061 CTGCCAGGAGTCAAGTGAGGACCAAGCGGCACCCACCTCACCCAGGCACGTGTGCCAGAT TAATTCCAAT 3120
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Qy 3061 CTGCCAGGAGTCAAGTGAGGACCAAGCGGCACCCACCTCACCCAGGCACGTGTGCCAGAT TAATTCCAAT 3120

Db 3121 GAATTTGATATCTCTTGCTCGCCCTTCCCCAGGACCTAGGCACGTGGCCAGATGTTT 3180
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Qy 3121 GAATTTGATATCTCTTGCTCGCCCTTCCCCAGGACCTAGGCACGTGGCCAGATGTTT 3180

Db 3181 GTCCCCTCCTCGTCTGTCCTTCCATTCTTATCATGATTGAACTCTTGATTTGGATTTCTCAG 3240
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Qy 3181 GTCCCCTCCTCGTCTGTCCTTCCATTCTTATCATGATTGAACTCTTGATTTGGATTTCTCAG 3240

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Qy 3241 ACCAGCAAAAGGGCAGGATCCAGGCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300

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Qy 3301 CAGAGGGGTCATCCACTGCATGACCACTCCATGAGAGTGTCACAGAGTCCACCCTCCTG 3360

Db 3361 GTAGCACTGAGAGCCAGGGCTGTCGTCTGCGTCTGCACCCTGAGGGCCCGTGATTCCT 3420
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Qy 3361 GTAGCACTGAGAGCCAGGGCTGTCGTCTGCGTCTGCACCCTGAGGGCCCGTGATTCCT 3420

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Qy 3421 CTTCCTGGAGCTCCAGGAACCAGCAGTGAGGCCTTGGTCTGACAGTATCCTCAGGTC 3480

Db 3481 ACAGAGCAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACCACCAA 3540
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Qy 3481 ACAGAGCAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACCACCAA 3540

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Qy 3541 GGGCCCACCTGCCACAGACACATAGGACGTCTGGCCTCACCTCCTACTG 3600

Db 3601 TCAGTCCTGTAGAATGCACCTCTGCTGCCGGCTGAGTCAGTACCCTGAGTCACTTCCT 3660
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Db 3661 CCTTCAGGTTTCAGGGGACAGGCAGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG 3720
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Qy 3661 CCTTCAGGTTTCAGGGGACAGGCAGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG 3720

Db 3721 GAGCACCAAGGAGAGATCGTAAGTCTGTTAGAGTCTTTAGAGTCTCCAAGTTCAGTTCTC 3780
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Qy 3721 GAGCACCAAGGAGAGATCGTAAGTCTGTTAGAGTCTTTAGAGTCTCCAAGTTCAGTTCTC 3780

Db 3781 AGCTGAGGCCTCTCACACTCCCTCTCCCCAGGCGCTTCATTGCCGTGGGGTCTTCATTGCCCAGCT 3840
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Db 3901 TCTGCACTGCAAGCCTGAGGAAGCCTTGAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTG 3960
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Qy 3901 TCTGCACTGCAAGCCTGAGGAAGCCTTGAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTG 3960

Db 3961 TGTGCAGGCTGCACCCTCCACCCTGTCCTCTGGTCCTTGGCACCCTGGAGGAGGTGCC 4020

Db 1801 ACCCTGGGAGGGAACTGAGGGTTCCCACCCACACACTGTTCCTCATCTCCACCGCCACC 1860
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Qy 1861 CCACTCACAATTCCCATACCTACCCCCCTACCCCCAACCTCACTCTTGTCAGAATCCCTGCTG 1920

Db 1921 TCAACCCACGGAAGCCACGGGAATGCGGCCAGGCACTCGGATCTTGACGTCCCATCCA 1980
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Qy 1921 TCAACCCACGGAAGCCACGGGAATGCGGCCAGGCACTCGGATCTTGACGTCCCATCCA 1980

Db 1981 GGGTCTGATGGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCCAGAGGGAGGGGCCCTAC 2040
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Qy 1981 GGGTCTGATGGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCCAGAGGGAGGGGCCCTAC 2040

Db 2041 TGCGAGATGAGGGAGGAGGCCTCAGAGGACACCCGCACCCTGTCTGAG 2100
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Qy 2041 TGCGAGATGAGGGAGGAGGCCTCAGAGGACACCCGCACCCTGTCTGAG 2100

Db 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160
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Qy 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160

Db 2161 GTGGGACCCAGGCCTGCCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220
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Qy 2161 GTGGGACCCAGGCCTGCCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220

Db 2221 GGAATCCAGATCAGTGTGGAACTCGGCCTCGAGAGTTCCAGGGCCCCTGAGGGCACGTGGTCCAGGCACATATG 2280
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Qy 2221 GGAATCCAGATCAGTGTGGAACTCGGCCTCGAGAGTTCCAGGGCCCCTGAGGGCACGTGGTCCAGGCACATATG 2280

Db 2281 GCCCATATTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340
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Qy 2281 GCCCATATTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340

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Qy 2341 TCAGTTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCTTCATG 2400

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Qy 2401 AGGACTGGGGATATCCCCGGCTCAGACAGAAAGAGGGACTCCACACAGTCTGGCTGTCCCCTT 2460

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Qy 2461 TTAGTAGCTCTAGGGGACCAGATCAGGGATGGCCGGTATGTTCCATTCTCACTTGTACCA 2520

Db 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGAGTGGGTCTTGGGGTAAAGGGGGATGTCT 2580
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Qy 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGAGTGGGTCTTGGGGTAAAGGGGGATGTCT 2580

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Db 2641 GAGACAGACAAGGCTATTGGAATCCACACACCCAGAACCAAAGGGGTCAGCCCTGGACACC 2700
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Qy 2641 GAGACAGACAAGGCTATTGGAATCCACACACCCAGAACCAAAGGGGTCAGCCCTGGACACC 2700

Db 2701 TCACCCAGGATGTGGCTTCTTCTTTCACTCGTTTCTTCACTCGTTTCTTCACTCGGAGGGTGAGGACCT 2760
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Qy 2701 TCACCCAGGATGTGGCTTCTTCTTTCACTCGTTTCTTCACTCGTTTCTTCACTCGGAGGGTGAGGACCT 2760

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Qy 2761 CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTTCTAAAGACAGAGCG 2820

Db 2821 GTCCCAGGATCTGCCATGGCGTTCGGGTGAGGAGGAACATGAGGGTGAGGGACTACCCCAG 2880
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Qy 2821 GTCCCAGGATCTGCCATGGCGTTCGGGTGAGGAGGAACATGAGGGTGAGGGACTACCCCAG 2880

Left column:

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Qy        |||||||||||||||||||||||||||||||||||||||||||||||||||||
     3961 TGTGCAGGCTGCCACCTCCTCCTCCTCGTCCTGGCACCCTGAGGAGGGTGCC 4020
Db   4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTTCCGCCTTTCCCACTAC 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTTCCGCCTTTCCCACTAC 4080

Db   4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAGGAGGAGGG 4140
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Qy   4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAGGAGGAGGG 4140

Db   4141 GCCAAGCACCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTCAAGAAGGTGGC 4200
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Qy   4141 GCCAAGCACCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTCAAGAAGGTGGC 4200

Db   4201 TGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260
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Qy   4201 TGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260

Db   4261 AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGC 4320
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Qy   4261 AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGC 4320

Db   4321 CTCTGAGTCCTTGCAGCTGGTCTTTGCATTGACGTGAAGAAGCAGCAGACCCCACCCGCCA 4380
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Qy   4321 CTCTGAGTCCTTGCAGCTGGTCTTTGCATTGACGTGAAGAAGCAGCAGACCCCACCCGCCA 4380

Db   4381 CTCCTATGTCCTGTCCTAGGTCTCTCCTAGTGATGGCCTGCTGGGTGATAATCA 4440
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Qy   4381 CTCCTATGTCCTGTCCTAGGTCTCTCCTAGTGATGGCCTGCTGGGTGATAATCA 4440

Db   4441 GATCATGCCCAAGACAGAGCTTCTGTTCCTGATAATTGTCCTGGTCATGATTGCAATGAGGGGCCG 4500
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Qy   4441 GATCATGCCCAAGACAGAGCTTCTGTTCCTGATAATTGTCCTGGTCATGATTGCAATGAGGGGCCG 4500

Db   4501 CCATGCTTCCTGAGGAGGAAATCTGGAGGAGGAGCTGAGTGTGATGGAGTGTATGATGGAG 4560
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Qy   4501 CCATGCTTCCTGAGGAGGAAATCTGGAGGAGGAGCTGAGTGTGATGGAGTGTATGATGGAG 4560

Db   4561 GGAGCACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCGAGGAAAA 4620
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Qy   4561 GGAGCACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCGAGGAAAA 4620

Db   4621 GTACCTGGAGTACGGCAGGTGCCGGACACGTGAGTCCTATGAGTTCCTGTGTGGGGT 4680
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Qy   4621 GTACCTGGAGTACGGCAGGTGCCGGACACGTGAGTCCTATGAGTTCCTGTGTGGGGT 4680

Db   4681 CCAAGGGCCCTCCTGCTGAAAACCAGCAGCTCCTTGAGTATGTGAAAGTCAGGTCAGT 4740
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Qy   4681 CCAAGGGCCCTCCTGCTGAAAACCAGCAGCTCCTTGAGTATGTGAAAGTCAGGTCAGT 4740

Db   4741 GCAAGAGTTCGCTTTTTCTCCCATCCCTGCGTGAGACAGCTTTGAGAGGAGGAAGAG 4800
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Qy   4741 GCAAGAGTTCGCTTTTTCTCCCATCCCTGCGTGAGACAGCTTTGAGAGGAGGAAGAG 4800

Db   4801 GGAGTCTGAGCATGAGTTGCAGCCAAGCCAAGGCCAGTGGGAGGGGGACTGGGCCCAGTT 4860
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Qy   4801 GGAGTCTGAGCATGAGTTGCAGCCAAGCCAAGGCCAGTGGGAGGGGGACTGGGCCCAGTT 4860

Db   4861 CCAGGGGCCGTCCAGCAGCTTCCCCTGCCTCCCGCTCCCCGCTATGAGGCCCATTCTTCACTCT 4920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4861 CCAGGGGCCGTCCAGCAGCTTCCCCTGCCTCCCGCTCCCCGCTATGAGGCCCATTCTTCACTCT 4920

Db   4921 GAAGAGCGGCGGTCAGTGTCGGTCAGTGTTCTCAGTAGGTTTCTGTTCTCTATTGGGTGACTTGGAGATT 4980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4921 GAAGAGCGGCGGTCAGTGTCGGTCAGTGTTCTCAGTAGGTTTCTGTTCTCTATTGGGTGACTTGGAGATT 4980

Db   4981 TATCTTTGTTCTCTTTGGAATGTTCAAATGTTTTTTTTAAGGATGGTTGAATGAAC 5040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4981 TATCTTTGTTCTCTTTGGAATGTTCAAATGTTTTTTTTAAGGATGGTTGAATGAAC 5040

Db   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTAAGGG 5100
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Right column:

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Qy   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTAAGGG 5100
Db   5101 TAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCATTTTTTTTGTGAATTGGGATAAT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5101 TAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCATTTTGTGAATTGGGATAAT 5160

Db   5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAGAAATAGATGAGATAA 5220
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Qy   5161 AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAGAAATAGATGAGATAA 5220

Db   5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
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Qy   5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280

Db   5281 ATTTTTAAAGATATATGCATACCTGATTCCTTCGTTCTTTGAGAATGTAAGAGAAAAT 5340
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Qy   5281 ATTTTTAAAGATATATGCATACCTGATTCCTTCGTTCTTTGAGAATGTAAGAGAAAAT 5340

Db   5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTCTTCCATGCCACTGAGCA 5400
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Qy   5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTCTTCCATGCCACTGAGCA 5400

Db   5401 TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
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Qy   5401 TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460

Db   5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTCGAGTCACGTAATCGAGGTGGCAAGAGATGTC 5520
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Qy   5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTCGAGTCACGTAATCGAGGTGGCAAGAGATGTC 5520

Db   5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGGTGAGGGTGGAGAGTG 5580
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Qy   5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGGTGAGGGTGGAGAGTG 5580

Db   5581 GTGGAGTGTCAATGCCCTGAGCTGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
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Qy   5581 GTGGAGTGTCAATGCCCTGAGCTGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Db   5641 GGGGGAGCTGATTGTAATGAATCTTGGGTGGATCC 5674
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Qy   5641 GGGGGAGCTGATTGTAATGAATCTTGGGTGGATCC 5674
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CC          FILING DATE:  01-FEBRUARY-1994
CC        CLASSIFICATION:  436
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  037,230
CC        FILING DATE:  26-MARCH-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/04354
CC        FILING DATE:  22-MAY-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/807,043
CC        FILING DATE:  12-DECEMBER-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/764,364
CC        FILING DATE:  23-SEPTEMBER-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/728,838
CC        FILING DATE:  9-JULY-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/705,702
CC        FILING DATE:  23-MAY-1991
CC    ATTORNEY/AGENT INFORMATION:
CC        NAME:  Hanson, No. 5541104man D.
CC        REGISTRATION NUMBER:  30,946
CC        REFERENCE/DOCKET NUMBER:  LUD 5354
CC    TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (212) 688-9200
CC        TELEFAX:  (212) 838-3884
CC  INFORMATION FOR SEQ ID NO: 1:
CC    SEQUENCE CHARACTERISTICS:
CC        LENGTH:  5674 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC    MOLECULE TYPE:  genomic DNA
CC    FEATURE:
CC        NAME/KEY:  MAGE-1 gene
SQ  Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match     100.0%;
Best Local Similarity  100.0%;
Score 5674;  DB 6;  Length 5674;
Matches   5674;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;
Pred. No. 0.00e+00;

Db      1 CCCGGGCACCACTGGCATCCCTCCCCCCAATCCCTACCACCCCCTTACGCCACCC 60
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Qy      1 CCCGGGCACCACTGGCATCCCTCCCCCCAATCCCTACCACCCCCTTACGCCACCC 60

Db     61 ATCCAAACATCTTCACGCTCACGCTCACCCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
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Qy     61 ATCCAAACATCTTCACGCTCACGCTCACCCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Db    121 CTCTCAACCCAGGGAAGCGAGGTTTTCGGTTCGGGGCGGCTTGAGGGGCGGCTGAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
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Qy    121 CTCTCAACCCAGGGAAGCGAGGTTTTCGGTTCGGGGCGGCTTGAGGGGCGGCTGAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Db    181 TTAGAGAGAAGCGAGGTTTTCGGTTCGGGGCGGCTTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTTCGGGGCGGCTTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGG 240

Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCCGGTGAGGGAGGACTGAGGGAGGACCCACTTACCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCCGGTGAGGGAGGACTGAGGGAGGACCCACTTACCCC 300

Db    301 AGATAGAGGACCCCAAATAATCCCTCATGCCAGTCCTGGACCATCTGGTTGGTGGCTTC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 AGATAGAGGACCCCAAATAATCCCTCATGCCAGTCCTGGACCATCTGGTTGGTGGCTTC 360

Db    361 TCAGGCTGGCCGGCCACCCCCAGCCCCTTGCTCTTAAACCCACTGGGGACTCGAAGTCAGAG 420
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Qy    361 TCAGGCTGGCCGGCCACCCCCAGCCCCTTGCTCTTAAACCCACTGGGGACTCGAAGTCAGAG 420

Db    421 CTCCGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCCAGGCGTCCAGACAT 480
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Qy    421 CTCCGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCCAGGCGTCCAGACAT 480

Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCACTCCCGTGACCCAAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCACTCCCGTGACCCAAC 540

Db    541 CCCCACTCCAATGCTCACTCCCGTGACCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
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Qy    541 CCCCACTCCAATGCTCACTCCCGTGACCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Db    601 CCCACACATCCCCACCCTCAACCTGATGCCCATCCCGTGACCCATTCCACCCT 660
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Db    661 CACCCCCACCCCCACCCCCAGCGCCACCCCCACCCCCAGGCAGGATCCGGTTCCCG 720
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Qy    661 CACCCCCACCCCCACCCCCAGCGCCACCCCCACCCCCAGGCAGGATCCGGTTCCCG 720

Db    721 CCAGGAAACATCCGGTGACGCCGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 780
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Qy    721 CCAGGAAACATCCGGTGACGCCGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 780

Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCTGAGGGAGGACTGAGGAGCCCGCCACTCCAAATA 840
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Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCTGAGGGAGGACTGAGGAGCCCGCCACTCCAAATA 840

Db    841 CTCTGTGAGGAGGCAAGGTGAGAGGTGAGAGGTGAGAGGCGGCCACCACCCGCGGGAAGA 900
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Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGTGAGAGGTGAGAGGCGGCCACCACCCGCGGGAAGA 900

Db    901 GAGAGCCCAAATATTCCAGCCCCGCCCTTGCTGCCCAGCCCCTGCCCAGCCCTGCGGGAAGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 GAGAGCCCAAATATTCCAGCCCCGCCCTTGCTGCCCAGCCCCTGCCCAGCCCTGCGGGAAGA 960

Db    961 CGTCTCAGCCTGGGCGTGCCCCCAGACCCCTGCTCAAAAGCCTTGAGAGACACCAGGTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 CGTCTCAGCCTGGGCGTGCCCCCAGACCCCTGCTCAAAAGCCTTGAGAGACACCAGGTTC 1020

Db   1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGCAGCACCAGGTTAGGAGAGG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGCAGCACCAGGTTAGGAGAGG 1080

Db   1081 GCAGGGCACCAGGTCTCGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGGCTGTGGCCC 1140
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Qy   1081 GCAGGGCACCAGGTCTCGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGGCTGTGGCCC 1140

Db   1141 CCAAGACTGCACTCCAATCCCACCTCCACCCCCCATTCGCATTCCCACTCCTACTCCGTCACCTGGTTCCCACCCAACC 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 CCAAGACTGCACTCCAATCCCACCTCCACCCCCCATTCGCATTCCCACTCCTACTCCGTCACCTGGTTCCCACCCAACC 1200

Db   1201 CCCATCTCCTCAGCTACACCTCACACCTCCACCCCCCAACCCTTCTGCCACCTCACCCTGCCCCCAAC 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201 CCCATCTCCTCAGCTACACCTCACACCTCCACCCCCCAACCCTTCTGCCACCTCACCCTGCCCCCAAC 1260

Db   1261 ACCCTCAGCCCCAGCCCCAACCCTTCTGCCACCTCACCCTCTGCCCCCCAAC 1320
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Qy   1261 ACCCTCAGCCCCAGCCCCAACCCTTCTGCCACCTCACCCTCTGCCCCCCAAC 1320

Db   1321 CCCACCCTCATCTCTCATGTGCCCCACTCGCCTCCCCCATTCTGGCAGAATCC 1380
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Qy   1321 CCCACCCTCATCTCTCATGTGCCCCACTCGCCTCCCCCATTCTGGCAGAATCC 1380

Db   1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAAACCACTGACT 1440
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Qy   1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAAACCACTGACT 1440

Db   1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGGTTCTGAGGGGTTGAG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGGTTCTGAGGGGTTGAG 1500

Db   1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560
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Qy   1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560
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Db  1561 ACTGAGGAGGCACACCCCAGGTAGATGGCCCAAAATGATCCAGTACCACCCTGCTG 1620
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Qy  1561 ACTGAGGAGGCACACCCCAGGTAGATGGCCCAAAATGATCCAGTACCACCCTGCTG 1620

Db  1621 CCAGCCCTGGACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTGCCCGTCC 1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1621 CCAGCCCTGGACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTGCCCGTCC 1680

Db  1681 CACTGCCACTTAACCCACCACAGAGGCCAATCTGTAGTCATAGCTATAGTGATGGGG 1740
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Qy  1681 CACTGCCACTTAACCCACCACAGAGGCCAATCTGTAGTCATAGCTATAGTGATGGGG 1740

Db  1741 GGTCAGGAGAGCAGGGCCCAGGCATCAAGGTCCAGCATCCGGCCGGCATTAGGGTCAGG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741 GGTCAGGAGAGCAGGGCCCAGGCATCAAGGTCCAGCATCCGGCCGGCATTAGGGTCAGG 1800

Db  1801 ACCCTGGGGAACTGAGGGTTCCCACCCACCTGTCTCCTCATCTCCACCGCCACC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801 ACCCTGGGGAACTGAGGGTTCCCACCCACCTGTCTCCTCATCTCCACCGCCACC 1860

Db  1861 CCACTCACATTCCCATACCTACCCCCCCAACCTCATCTGTCAGAATCCCTGCTG 1920
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Qy  1861 CCACTCACATTCCCATACCTACCCCCCCAACCTCATCTGTCAGAATCCCTGCTG 1920

Db  1921 TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980

Db  1981 GGGTCTGATGAGGAGGAGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGAGGGGCCCTAC 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 GGGTCTGATGAGGAGGAGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGAGGGGCCCTAC 2040

Db  2041 TGCCGAGATGAGGAGGAGGGCTTGAACAGGGGCCTCAGGGGACTCAGGGGACCTGTGAG 2100
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Qy  2041 TGCCGAGATGAGGAGGAGGGCTTGAACAGGGGCCTCAGGGGACTCAGGGGACCTGTGAG 2100

Db  2101 ACTGAGGCTGCCACTTCTGCATCTTTGAGGTGACAGGAGACAGAGCTGTGTCTGAGTGGGG 2160
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Qy  2101 ACTGAGGCTGCCACTTCTGCATCTTTGAGGTGACAGGAGACAGAGCTGTGTCTGAGTGGGG 2160

Db  2161 GTGGGAGACCCAGGCCTGCAAGGCTTACCGCGGAGGAGGGAGGAGGACTCAGGGGACCTT 2220
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Qy  2161 GTGGGAGACCCAGGCCTGCAAGGCTTACCGCGGAGGAGGGAGGAGGACTCAGGGGACCTT 2220

Db  2221 GAATCCAGATCAGTGGGGATATCCCGGCTCGGCCCTGAGAGGTGGCCACACGGTGGCCACATATG 2280
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Qy  2221 GAATCCAGATCAGTGGGGATATCCCGGCTCGGCCCTGAGAGGTGGCCACACGGTGGCCACATATG 2280

Db  2281 GCCCATATTTCCTGCATCTTTGAGGTGACAGAGCTGTGTCTGAGAAGTGGGGC 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 GCCCATATTTCCTGCATCTTTGAGGTGACAGAGCTGTGTCTGAGAAGTGGGGC 2340

Db  2341 TCAGGTCAACAGAGGAGGAGTTCAGGGACTCATATGCCCAAGATGTGCCCCTTCATG 2400
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Qy  2341 TCAGGTCAACAGAGGAGGAGTTCAGGGACTCATATGCCCAAGATGTGCCCCTTCATG 2400

Db  2401 AGGACTCAACAGAGGGGATATCCCGGCTCAGGGGAGTCTGGGGTCTTGGGGTCTTCACCACAA 2460
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Qy  2401 AGGACTCAACAGAGGGGATATCCCGGCTCAGGGGAGTCTGGGGTCTTGGGGTCTTCACCACAA 2460

Db  2461 TTAGTAGCTCTAGGGGATTGGGGTGGGGGAATTGGGGTCTTAGTGTTCCATTCTCACTTGTACCA 2520
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Qy  2461 TTAGTAGCTCTAGGGGATTGGGGTGGGGGAATTGGGGTCTTAGTGTTCCATTCTCACTTGTACCA 2520

Db  2521 CAGGCAGGAAGTTGGGGGTCTTGGGGTCTTTGGGGTAAAGGGGGATGTCT 2580
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Qy  2521 CAGGCAGGAAGTTGGGGGTCTTGGGGTCTTTGGGGTAAAGGGGGATGTCT 2580

Db  2581 ACTCATGTCAGGGGTTGGGGTGGGGTTGGGGGTTGGGGTTGGGGAAGCACAGGGGAATAAAGATGAGT 2640
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Qy  2581 ACTCATGTCAGGGGTTGGGGTGGGGTTGGGGGTTGGGGTTGGGGAAGCACAGGGGAATAAAGATGAGT 2640

Db  2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCCAAAGGGGTCAGCCCTGGACACC 2700
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Qy  2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCCAAAGGGGTCAGCCCTGGACACC 2700
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Db  2701 TCACCCAGGATGTGGCTTCTTCTTTCTCACTCCTGTTTCCTGTTTCTTTCACTCCTGTCC 2760
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Db  2761 CATTCTCAGAGGTGACTCAGGTCAACGTCAGGTCAACGTCTGTCTCAAGACAGAGACGCG 2820
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Qy  2761 CATTCTCAGAGGTGACTCAGGTCAACGTCAGGTCAACGTCTGTCTAAAGACAGAGACG 2820

Db  2821 GTCCCAGGATCTGCCATGCCATGCCATGCCTGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880
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Qy  2821 GTCCCAGGATCTGCCATGCCATGCCATGCCTGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880

Db  2881 GACCAGAACACTGAGGGAGGACTGCACAGAAATCAGCCCTGCCCTGTGTCACCCCAGAG 2940
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Qy  2881 GACCAGAACACTGAGGGAGGACTGCACAGAAATCAGCCCTGCCCTGTGTCACCCCAGAG 2940

Db  2941 AGCATGGGCTTGGGCCGTCTGGCCGTCAGGTCAGGCTGCGAGAAGGCTCAGTGAGAGGGAGGTCCCAGGGG 3000
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Qy  2941 AGCATGGGCTTGGGCCGTCTGGCCGTCAGGTCAGGCTGCGAGAAGGCTCAGTGAGAGGGAGGTCCCAGGGG 3000

Db  3001 ACGGGGAGGCCTTGGTCTCAGAAGAGGGTCGCGCCTCAGGTCAGTAGAGGGAGGCGTCCCAGGCC 3060
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Qy  3001 ACGGGGAGGCCTTGGTCTCAGAAGAGGGTCGCGCCTCAGGTCAGTAGAGGGAGGCGTCCCAGGCC 3060

Db  3061 CTGCCAGGAGTCAAGTGAGGACTGAGGAGTGAGGAGGACACCAGGACCTCACCCAGGCACGTGTGGCCAGCAATTCCAAT 3120
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Qy  3061 CTGCCAGGAGTCAAGTGAGGACTGAGGAGTGAGGAGGACACCAGGACCTCACCCAGGCACGTGTGGCCAGCAATTCCAAT 3120

Db  3121 GAATTTGATATCTCTTGCTGCCCCTTCCATTCCATTCCTTATCATGATGTGAACTCTTGATTTGATTTCTCAG 3180
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Qy  3121 GAATTTGATATCTCTTGCTGCCCCTTCCATTCCATTCCTTATCATGATGTGAACTCTTGATTTGATTTCTCAG 3180

Db  3181 GTCCCCTCCTGTCCTTCCATTCCTTATCATGATGGCTCTTGATTTGATTTCTCAG 3240
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Qy  3181 GTCCCCTCCTGTCCTTCCATTCCTTATCATGATGGCTCTTGATTTGATTTCTCAG 3240

Db  3241 ACCAGCAAAAGGCAGGATCCAGGACCCCTGCCAGATCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300
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Qy  3241 ACCAGCAAAAGGCAGGATCCAGGACCCCTGCCAGATCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300

Db  3301 CAGAGGGGTCATCCACTGCATGAGAGTGGGATGTCACAGAGTCCAGCACCCTGTGCCCAGCTCTG 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301 CAGAGGGGTCATCCACTGCATGAGAGTGGGATGTCACAGAGTCCAGCACCCTCTG 3360

Db  3361 GTAGCACTGAGAAGCCAGGCTGTGCTTGCGGTCTGCGGTCTGGGATTCCT 3420
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Qy  3361 GTAGCACTGAGAAGCCAGGCTGTGCTTGCGGTCTGCGGTCTGGGATTCCT 3420

Db  3421 CTTCCTGGAGCTCCAGGACAGCCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGTGTC 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421 CTTCCTGGAGCTCCAGGACAGCCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGTGTC 3480

Db  3481 ACAGAGCAGGATGCCACCAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA 3540
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Qy  3481 ACAGAGCAGGATGCCACCAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA 3540

Db  3541 GGGCCCCACCTGCTGTGTGCTTGCCGTCTGGCCTCCTGGATTCCT 3600
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Qy  3541 GGGCCCCACCTGCTGTGTGCTTGCCGTCTGGCCTCGGCCCGTGGATTCCT 3600

Db  3601 TCAGTCCTGTAGAATGCCCTGCTCCTGAGTCACCCGTACCCTGAGTCACTTGTG 3660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601 TCAGTCCTGTAGAATGCCCTGCTCCTGAGTCACCCGTACCCTGAGTCACTTGTG 3660

Db  3661 CCTTCAGTTTTCAGGGGACCAGGCCTGCCAGGACCAACCCAAGGACAGGAGAGAG 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661 CCTTCAGTTTTCAGGGGACCAGGCCAACCCAACCCAAGGACAGCAACAGAG 3720

Db  3721 GAGCACCAAGGAGAAGAATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3721  GAGCACCAAGGAGGAGAGATCGTAAGTAGGCCTTTGTTAGAGTCTTCCAAGGTTCAGTTCTC  3780
Db  3781  AGCTGAGGGCCTCTCACACACTCCCTCTCCCCCAGGCCTGTGGGTCTTCATTGCCCCAGCT  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3781  AGCTGAGGGCCTCTCACACACTCCCTCTCCCCCAGGCCTGTGGGTCTTCATTGCCCCAGCT  3840

Db  3841  CCTGCCCACACTCCTGCCTGCCCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3841  CCTGCCCACACTCCTGCCTGCCCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG  3900

Db  3901  TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG  3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3901  TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG  3960

Db  3961  TGTGCAGGCTGCCACCTCCTGGGTCCTGGGCACCCTGGGGAGGAGGTGCC  4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3961  TGTGCAGGCTGCCACCTCCTGGGTCCTGGGCACCCTGGGGAGGAGGTGCC  4020

Db  4021  CACTGCTGGGTCAACAGATCTCTCCCAGAGTCCTCAGGGAGCCTTCGCCCTTCCCACTAC  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4021  CACTGCTGGGTCAACAGATCTCTCCCAGAGTCCTCAGGGAGCCTTCGCCCTTCCCACTAC  4080

Db  4081  CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG  4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4081  CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG  4140

Db  4141  GCCAAGCACCTCTTGTATCCTGTTGTTCCGAGTCCTTCCGAGCAGTAATCACTAAGAGGTGGC  4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4141  GCCAAGCACCTCTTGTATCCTGTTGTTCCGAGTCCTTCCGAGCAGTAATCACTAAGAGGTGGC  4200

Db  4201  TGATTTGGTTGGTTTTCTGCTCTCCTCAAATATTACAGACCAGTCACAAGGCAGA  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4201  TGATTTGGTTGGTTTTCTGCTCTCCTCAAATATTACAGACCAGTCACAAGGCAGA  4260

Db  4261  AATGCTGAGAGTGTCATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCCAAAGC  4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4261  AATGCTGAGAGTGTCATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCCAAAGC  4320

Db  4321  CTCTGAGTCCTTGCAGTCTGTTCTTGGCATTGCAGTCTCTCCTATGATGGCCTGCTGGTGATAATCA  4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4321  CTCTGAGTCCTTGCAGTCTGTTCTTGGCATTGCAGTCTCTCCTATGATGGCCTGCTGGTGATAATCA  4380

Db  4381  CTCCTATGATGCCTTGTGTCACCTGCTAGGTCTCTCCTATGATGCCTGCTGCTGGTGATGAGGGGCGG  4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4381  CTCCTATGATGCCTTGTGTCACCTGCTAGGTCTCTCCTATGATGCCTGCTGCTGGTGATGAGGGGCGG  4440

Db  4441  GATCATGCCCAAGACAGCAGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGAGGGGCGG  4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4441  GATCATGCCCAAGACAGCAGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGAGGGGCGG  4500

Db  4501  CCATGCTCCTGGAGGAGAAATCTGGGAGGAGCTGAGTGTATGAGGTGTATGATGGGAG  4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4501  CCATGCTCCTGGAGGAGAAATCTGGGAGGAGCTGAGTGTATGAGGTGTATGATGGGAG  4560

Db  4561  GGAGCACAGCTGCCTATGGGAGGCCCAGGAAGCTGCTCACCCAGAGATTTGGTGCAGGAAAA  4620
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Qy  4561  GGAGCACAGCTGCCTATGGGAGGCCCAGGAAGCTGCTCACCCAGAGATTTGGTGCAGGAAAA  4620

Db  4621  GTACCTGGAGTACGGCAGGTGCCGGACGATCCCGCACGCGCTATGAGTTCCTGTGGGGT  4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4621  GTACCTGGAGTACGGCAGGTGCCGGACGATCCCGCACGCGCTATGAGTTCCTGTGGGGT  4680

Db  4681  CCAAGGGCCCTGCCTGGAAAACCAGCTAGGTGAAAGTCCTTGAGTATGTGAATCAAGGTCAGT  4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4681  CCAAGGGCCCTGCCTGGAAAACCAGCTAGGTGAAAGTCCTTGAGTATGTGAATCAAGGTCAGT  4740

Db  4741  GCAAGAGTTCGCTTTTCTTTCTTCCCATCCTGCTTTTGAGAGCAGCAGTTTTGAGAGGAGGAAGAG  4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4741  GCAAGAGTTCGCTTTTCTTTCTTCCCATCCTGCTTTTGAGAGCAGCAGTTTTGAGAGGAGGAAGAG  4800

Db  4801  GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGCGGAGGGGACTGGGCCAGTGCCACCTT  4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4801  GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGCGGAGGGGACTGGGCCAGTGCCACCTT  4860
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Db  4861  CCAGGGGCCGTCCAGCAGCTTCCCGTGCCTGCCTCGTGTGACATGAGCCCATTCTTCACTCT  4920
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Qy  4861  CCAGGGGCCGTCCAGCAGCTTCCCGTGCCTGCCTCGTGTGACATGAGCCCATTCTTCACTCT  4920

Db  4921  GAAGAGAGCGGTCAGTGTTCTCAGTAGGTTTCTGTTCTATTGGTGACTTGGAGATT  4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4921  GAAGAGAGCGGTCAGTGTTCTCAGTAGGTTTCTGTTCTATTGGTGACTTGGAGATT  4980

Db  4981  TATCTTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTAAGGATGGTTGAATGAAC  5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4981  TATCTTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTAAGGATGGTTGAATGAAC  5040

Db  5041  TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG  5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5041  TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG  5100

Db  5101  TAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT  5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5101  TAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT  5160

Db  5161  AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGCAGTAAAATAGAGATAA  5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5161  AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGCAGTAAAATAGAGATAA  5220

Db  5221  AGAACTAAAGAAATTAAGACAGTAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA  5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5221  AGAACTAAAGAAATTAAGACAGTAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA  5280

Db  5281  ATTTTAAAGATATATGCATACCTGGAATTGAGAATGTAAGAGAAAT  5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5281  ATTTTAAAGATATATGCATACCTGGAATTGAGAATGTAAGAGAAAT  5340

Db  5341  TAAATCTGAATAAAGAATTCTTCCTGTTCACTGCCTCTTTTCTTCCCATGCACTGAGCA  5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5341  TAAATCTGAATAAAGAATTCTTCCTGTTCACTGCCTCTTTTCTTCCCATGCACTGAGCA  5400

Db  5401  TCTGCTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC  5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5401  TCTGCTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC  5460

Db  5461  CCACCCATAGGGTCGTAGAGCTGCAGTCAGTCAATCGAGTGTGGCAAGATGTC  5520
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Qy  5461  CCACCCATAGGGTCGTAGAGCTGCAGTCAGTCAATCGAGTGTGGCAAGATGTC  5520

Db  5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGCTCCGGGTGAGAGTG  5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGCTCCGGGTGAGAGTG  5580

Db  5581  GTGGAGTGTCAATGCCCTGAGCTGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCT  5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5581  GTGGAGTGTCAATGCCCTGAGCTGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCT  5640

Db  5641  GGGGGAGCTGATTGTAATGAGTCTTGGGTGGATCC  5674
          |||||||||||||||||||||||||||||||||||
Qy  5641  GGGGGAGCTGATTGTAATGAGTCTTGGGTGGATCC  5674
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CC   CITY:  New York City
CC   STATE:  New York
CC   ZIP:  10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER:  IBM
CC   OPERATING SYSTEM:  PC-DOS
CC   SOFTWARE:  Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/807,043B
CC   FILING DATE: 19911212
CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME:  Hanson, No. 542774man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 253.3
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 8:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 5674 base pairs
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: singular
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-1 gene
SQ   Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match      100.0%;  Score 5674;  DB 4;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 5674;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db      1 CCCGGGCACCACTGGCATCCCTCCCCTACCACCCCCAATCCTCCCTTACGCCACCC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 CCCGGGCACCACTGGCATCCCTCCCCTACCACCCCCAATCCTCCCTTTACGCCACCC   60

Db     61 ATCCAAACATCTTCACGCTCACGCGGAAGCCCAAGCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ATCCAAACATCTTCACGCTCACGCCCTCCCCCTACCACCCCCCAATCCTCCCTTTACGCCACCC  120

Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGGTGCCGGCCCAGCGATGTGACGCCACTGAGCATTAGTGG  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGGTGCCGGCCCAGCGATGTGACGCCACTGAGCATTAGTGG  180

Db    181 TTAGAGAAGCGAGGTTTCGGTCTGAGGGCGGCCGTCTGAGGGGCGGCGTCTGAGGGGAGGGAAGCGGGG  240
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Qy    181 TTAGAGAAGCGAGGTTTCGGTCTGAGGGCGGCCGTCTGAGGGGCGGCGTCTGAGGGGAGGGAAGCGGGG  240

Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCGGAGGGAGGGACCCACTTACCCC  300
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Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCGGAGGGAGGGACCCACTTACCCC  300

Db    301 AGATAGGAGGACCCCAAATAAATCCCTTCATGCCAGTTCCTTAAACCACTGGGGACTCGAAGTCAGAG  360
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Qy    301 AGATAGGAGGACCCCAAATAAATCCCTTCATGCCAGTTCCTTAAACCACTGGGGACTCGAAGTCAGAG  360

Db    361 TCAGGCTGGGCCACCCCCCAGCCCCCCCTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAGACAT  420
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Qy    361 TCAGGCTGGGCCACCCCCCAGCCCCCCCTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAGACAT  420

Db    421 CTCCGTGTGATCAGGAAGGGCTGCTTAGGAGAGAGGCAGCGTCCGAGGCTCTGCCAGACAT  480
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Qy    421 CTCCGTGTGATCAGGAAGGGCTGCTTAGGAGAGAGGCAGCGTCCGAGGCTCTGCCAGACAT  480

Db    481 CATGCTCAGGATTCTCAAGGAGGGTGAGGGTCCTAAGACCCCACTCCCGTGACCCAAC  540
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Qy    481 CATGCTCAGGATTCTCAAGGAGGGTGAGGGTCCTAAGACCCCACTCCCGTGACCCAAC  540

Db    541 CCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA  600
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Qy    541 CCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA  600

Db    601 CCCCACATCCCACCCACCCATCCTCAACCTGATGCCCATTCGGCCCAGCCATTCCACCCT  660
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Qy    601 CCCCACATCCCACCCACCCATCCTCAACCTGATGCCCATCGGCCCAGCCATTCCACCCT  660

Db    661 CACCCCCACACCCCACCCCCACCCCCACCCCCAGCGCCCCACTCCAGGCAGGATCGGTTCCCG  720
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Qy    661 CACCCCCACACCCCACCCCCACCCCCACCCCCAGCGCCCCACTCCAGGCAGGATCGGTTCCCG  720

Db    721 CCAGGAAACATCCGGTGCCGGATGTGACGCCACTGACTTGCGCCATTGTGGGCAGAGA  780
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Qy    721 CCAGGAAACATCCGGTGCCGGATGTGACGCCACTGACTTGCGCCATTGTGGGCAGAGA  780

Db    781 GAAGCGAGGTTCCATTCTGAGGACGGCGGTAGAGTTCGGCCGAAGAACCTGACCCAGG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 GAAGCGAGGTTCCATTCTGAGGACGGCGGTAGAGTTCGGCCGAAGAACCTGACCCAGG  840

Db    841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGGAGGACTGAGGACCCCGCCACTCCAAATA  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGGAGGACTGAGGACCCCGCCACTCCAAATA  900

Db    901 GAGAGCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 GAGAGCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA  960

Db    961 CGTCTCAGCCTGGGCTGCCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 CGTCTCAGCCTGGGCTGCCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020

Db   1021 TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGCAGGCAGGCAGAGGGAGGAGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021 TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGCAGGCAGGCAGAGGGAGGAGG 1080

Db   1081 GCAGGGCACAGGCTCTGCCAGCCATCAAGATCAGCACCCAAGAGGAGGAGGCGTGTGGCCCC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081 GCAGGGCACAGGCTCTGCCAGCCATCAAGATCAGCACCCAAGAGGAGGAGGCGTGTGGCCCC 1140

Db   1141 CCAAGACTGCACTCCCAATCCCACCCCACCCCATCCGATTCCCATTCCGTCCACCCAACC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 CCAAGACTGCACTCCCAATCCCACCCCACCCCATCCCAATCCGCATTCCCACCCAACC 1200

Db   1201 CCATCTCCTCAGTCTACAACCTCCACCTCCTACTCCGTCCGTCACCTGACCACC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201 CCATCTCCTCAGTCTACAACCTCCACCTCCTACTCCGTCCGTCACCTGACCACC 1260

Db   1261 ACCCTCCAGCCCCAGCACCAGCCCAACCCTTCTGCCACCTCACCCTACTGCCCCCCAAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261 ACCCTCCAGCCCCAGCACCAGCCCAACCCTTCTGCCACCTCACCCTACTGCCCCCCAAC 1320

Db   1321 CCACCCCATCTCTCTCATGTGCCCCCATCCGCTTCGGCAGAATCC 1380
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Qy   1321 CCACCCCATCTCTCTCATGTGCCCCCATCCGCTTCGGCAGAATCC 1380

Db   1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT 1440
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Qy   1381 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT 1440

Db   1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGGTTCTTCTGAGGGGCGGCTTGAG 1500
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Qy   1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCATTTAATGTTCTTCTGAGGGGCGGCTTGAG 1500

Db   1501 ATCCACTGAGGGGAGTGGTTTAGGCTCGTGAGGAGGCAAGGTGAGATGCGAGGAGG 1560
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Qy   1501 ATCCACTGAGGGGAGTGGTTTAGGCTCGTGAGGAGGCAAGGTGAGATGCGAGGGAGG 1560
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Db  2641  GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCCAGAAGGGTCAGCCCTGGACACC  2700
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Qy  2641  GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCCAGAAGGGTCAGCCCTGGACACC  2700

Db  2701  TCACCCAGGATGTGGCTTCTTTTTCACTCGTCTTTCCAGATCTGGGGCTCGGGCGTGAGGACCT  2760
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Qy  2701  TCACCCAGGATGTGGCTTCTTTTTCACTCGTCTTTCCAGATCTGGGGCTCGGGCGTGAGGACCT  2760

Db  2761  CATTCTCAGAGGGTGACTCAGGTCAACGTGGACCCCATCTGGTCTCAAAGACACAGAGCG  2820
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Qy  2761  CATTCTCAGAGGGTGACTCAGGTCAACGTGGACCCCATCTGGTCTCAAAGACACAGAGCG  2820

Db  2821  GTCCCAGGATCTGCCATGCGGTTCGGGTGAGGAACATGAGGAGGAACTGAGGGTACCCCAG  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2821  GTCCCAGGATCTGCCATGCGGTTCGGGTGAGGAACATGAGGAGGAACTGAGGGTACCCCAG  2880

Db  2881  GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCGTGTCACCCCAGAG  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2881  GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCGTGTCACCCCAGAG  2940

Db  2941  AGCATGGGCTGGGCCGTCTGCGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATTGTCAGGG  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2941  AGCATGGGCTGGGCCGTCTGCGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATTGTCAGGG  3000

Db  3001  ACGGGGAGGGCCTTGGTCTGAGAAGGCTGCGCTCAGTCAGTCAGTGGAAGGCGTCCCAGGCC  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001  ACGGGGAGGGCCTTGGTCTGAGAAGGCTGCGCTCAGTCAGTCAGTGGAAGGCGTCCCAGGCC  3060

Db  3061  CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCCACCCCAGGACACATTAATTCCAAT  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061  CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCCACCCCAGGACACATTAATTCCAAT  3120

Db  3121  GAATTTGATATCTCTTGCTGCCCTTCCATTCCTTATCATGGATGTGAACTCTTGATTGGATTTCTCAG  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121  GAATTTGATATCTCTTGCTGCCCTTCCATTCCTTATCATGGATGTGAACTCTTGATTGGATTTCTCAG  3180

Db  3181  GTCCCCCTCCGTCCTTCCATTCCTTATCATGGATGTGCCAGGAAAAAATAAGGGCCTGCGTGAGAA  3240
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Qy  3181  GTCCCCCTCCGTCCTTCCATTCCTTATCATGGATGTGCCAGGAAAAAATAAGGGCCTGCGTGAGAA  3240

Db  3241  ACCAGCAAAAGGGCAGGATCCAGGCCTGCGTGGGGATGGGGGATCCAGAGTCCAGCCTCCTG  3300
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Qy  3241  ACCAGCAAAAGGGCAGGATCCAGGCCTGCGTGGGGATGGGGGATCCAGAGTCCAGCCTCCTG  3300

Db  3301  CAGAGGGGGTCATCCAGCGTGTGTGCTTCTGCAGCAGTGTCCCTGGATTGTTGCCCAGCCCGGATTCCT  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3301  CAGAGGGGGTCATCCAGCGTGTGTGCTTCTGCAGCAGTGTCCCTGGATTGTTGCCCAGCCCGGATTCCT  3360

Db  3361  GTAGCACTGAGAAGCCAGGGTCGTGTCTGCCAGCAGTGAATGTTTGCCCTGGATCCTCAGGTC  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3361  GTAGCACTGAGAAGCCAGGGTCGTGTCTGCCAGCAGTGAATGTTTGCCCTGGATCCTCAGGTC  3420

Db  3421  CTTCCTGGAGTCTCCAGGAACCAGGACTCCACCCTCTGAATGCACACCAA  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3421  CTTCCTGGAGTCTCCAGGAACCAGGACTCCACCCTCTGAATGCACACCAA  3480

Db  3481  ACAGAGCAGGAGGATGCACAGGTGTGCCAGCAGTGGTCTGCCCTGGATTGTTGCCCAGCCCGGATTCCT  3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3481  ACAGAGCAGGAGGATGCACAGGTGTGCCAGCAGTGGTCTGCCCTGGATTGTTGCCCAGCCCGGATTCCT  3540

Db  3541  GGGCCCCACCTGCCACAGGACACATAGGACTCCACCAGAGTCTGGCCTCACCTCCCTACTG  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3541  GGGCCCCACCTGCCACAGGACACATAGGACTCCACCAGAGTCTGGCCTCACCTCCCTACTG  3600

Db  3601  TCAGTCCTGTAGAATCGACCTTCGTCGGCCGGCGTGTACCCTGAGTACCCTTCACTTCCT  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3601  TCAGTCCTGTAGAATCGACCTTCGTCGGCCGGCGTGTACCCTGAGTACCCTTCACTTCCT  3660

Db  3661  CCTTCAGTTTTCAGGGTTTCAGGGACGAAGCCAACCCAGGACACAGGAATTCCCTGGAGGCCACAGAG  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3661  CCTTCAGTTTTCAGGGTTTCAGGGACGAAGCCAACCCAGGACACAGGAATTCCCTGGAGGCCACAGAG  3720

Db  3721  GAGCACCAAGGAGAAGATCGTGTAAGTAGTAGGCCTTTGTTAGTCTCCAAGGTCTCAGTTGTCTCTC  3780
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Db  1561  ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCCACCCCTGCTG  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1561  ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCCACCCCTGCTG  1620

Db  1621  CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTCCCCGTCC  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1621  CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTCCCCGTCC  1680

Db  1681  CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681  CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT  1740

Db  1741  GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741  GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG  1800

Db  1801  ACCCTGGGAGGGAACTGAGGGTTCCCCACCACTGTCTCCTCATCTCCACCGCCACC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801  ACCCTGGGAGGGAACTGAGGGTTCCCCACCACTGTCTCCTCATCTCCACCGCCACC  1860

Db  1861  CCACTCACAATTCCCATACCTACCCCCACCCCAACCTCATCTTGTCAGAATCCCTGCTG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861  CCACTCACAATTCCCATACCTACCCCCACCCCAACCTCATCTTGTCAGAATCCCTGCTG  1920

Db  1921  TCAACCCACCGGAAGCCACGGGAATGCGGGCCAGGGCACTCGGATCTTGACGTCCCCATCCA  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921  TCAACCCACCGGAAGCCACGGGAATGCGGGCCAGGGCACTCGGATCTTGACGTCCCCATCCA  1980

Db  1981  GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCTGCAGAGGGCAGAGGGGAGGGCCCTAC  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981  GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCTGCAGAGGGCAGAGGGGAGGGCCCTAC  2040

Db  2041  TGCGAGATGAGGGAGGGCCTCAGAGGACACCCAGGACACCGGTCAGGCACCCCACCCGTCTGAG  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041  TGCGAGATGAGGGAGGGCCTCAGAGGACACCCAGGACACCGGTCAGGCACCCCACCCGTCTGAG  2100

Db  2101  ACTGAGGGCTGCCACTTCTCGGCCTCAGAATCAGAACGATGGGACTCAGATTGCATGGGG  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101  ACTGAGGGCTGCCACTTCTCGGCCTCAGAATCAGAACGATGGGACTCAGATTGCATGGGG  2160

Db  2161  GTGGGACCCAGGCTGCAAGGCTGCGGAGGAGGGGAGGAGGGCTCAGGGGACCTT  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161  GTGGGACCCAGGCTGCAAGGCTGCGGAGGAGGGGAGGAGGGCTCAGGGGACCTT  2220

Db  2221  GGAATCCAGATCAGTCAGTTGGGGGGCCCTCAGAGGTCCAGGGCACGGTGGCCACATATG  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221  GGAATCCAGATCAGTCAGTTGGGGGGCCCTCAGAGGTCCAGGGCACGGTGGCCACATATG  2280

Db  2281  GCCCATATTTCCTGACGTCTTTGAGGTGACAGGAGGGGACTCCACCAGTCTCGGCTGGGGGCC  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281  GCCCATATTTCCTGACGTCTTTGAGGTGACAGGAGGGGACTCCACCAGTCTCGGCTGGGGGCC  2340

Db  2341  TCAGGTCAACAGAGGGAGGAGTTCCAGGAGTCCGGTATGTTCCATTCTCACTTGTACCA  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341  TCAGGTCAACAGAGGGAGGAGTTCCAGGAGTCCGGTATGTTCCATTCTCACTTGTACCA  2400

Db  2401  AGGACTGGGGATATCCCCGGCTCAGAAAGAGAGGACTCCACCAGTCTCGGCTGCGTGTCCCCTT  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401  AGGACTGGGGATATCCCCGGCTCAGAAAGAGAGGACTCCACCAGTCTCGGCTGCGTGTCCCCTT  2460

Db  2461  TTAGTAGCTCTAGGGGACCCAGGGGGGGTATGTTCCATTCTCACTTGTTCATCATG  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461  TTAGTAGCTCTAGGGGACCCAGGGGGGGTATGTTCCATTCTCACTTGTTCATCATG  2520

Db  2521  CAGGCAGGAGTTGGGGGGCTCTTGGGGTAAAGGGGGGATGTCT  2580
          ||||||||||||||||||||||||||||||||||||||||||||
Qy  2521  CAGGCAGGAGTTGGGGGGCTCTTGGGGTAAAGGGGGGATGTCT  2580

Db  2581  ACTCATGTGTGCAGGGAATTGGGGTTGAGGAAGGCACAGGCGCTGGCCAGGCACCAGGCAATAAAGATGAGT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581  ACTCATGTGTGCAGGGAATTGGGGTTGAGGAAGGCACAGGCGCTGGCCAGGCACCAGGCAATAAAGATGAGT  2640
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Qy   3721 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GAGCACCAAGGAGAAGAGATCTGTAAGTAGGCCTTTGTTGTAGAGTCTCCAAGGTTCAGTTCTC 3780

Db   3781 AGCTGAGGCCTCACACTCCCTCTCTCCCCAGGCCGTCTTCATTGCCCAGCT 3840
Qy   3781 AGCTGAGGCCTCACACTCCCTCTCTCCCCAGGCCGTCTTCATTGCCCAGCT 3840

Db   3841 CCTGCCCACACTCCTGCGTCGCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG 3900
Qy   3841 CCTGCCCACACTCCTGCGTCGCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG 3900

Db   3901 TCTGCACTGCAAGCCTGAGGAAGCCCTGAGGCCCAACAAGAGCCCTGGGCCTGGTGTG 3960
Qy   3901 TCTGCACTGCAAGCCTGAGGAAGCCCTGAGGCCCAACAAGAGCCCTGGGCCTGGTGTG 3960

Db   3961 TGTGCAGCTGCCACCTCCTCTCGTCCTGGGCACCCTGGAGGAGGTGCC 4020
Qy   3961 TGTGCAGCTGCCACCTCCTCTCGTCCTGGGCACCCTGGAGGAGGTGCC 4020

Db   4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080
Qy   4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080

Db   4081 CATCAACTTCACTCAGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCAGGAGGG 4140
Qy   4081 CATCAACTTCACTCAGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCAGGAGGG 4140

Db   4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAGGTGGC 4200
Qy   4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAGGTGGC 4200

Db   4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260
Qy   4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260

Db   4261 AATGCTGGAGAGTGTCATCAAAAATTACAGAGCACTCGTTTCCTGAGATCTTCGGCAAAGC 4320
Qy   4261 AATGCTGGAGAGTGTCATCAAAAATTACAGAGCACTCGTTTCCTGAGATCTTCGGCAAAGC 4320

Db   4321 CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCA 4380
Qy   4321 CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCA 4380

Db   4381 CTCCTATGTCCTGTCACCTGCCTAGGTCTCTCCTATGATGAGGCTGCTGGGTGATAATCA 4440
Qy   4381 CTCCTATGTCCTGTCACCTGCCTAGGTCTCTCCTATGATGAGGCTGCTGGGTGATAATCA 4440

Db   4441 GATCATGCCCAAGACAGCAGGCTTCAGGGAAATCTGGAGGAGCGTATGATGGGGAG 4500
Qy   4441 GATCATGCCCAAGACAGCAGGCTTCAGGGAAATCTGGAGGAGCGTATGATGGGGAG 4500

Db   4501 CCATGTCCTGAGGAGAAATCTGGAGGAGCTGTATGGGGAG 4560
Qy   4501 CCATGTCCTGAGGAGAAATCTGGAGGAGCTGTATGGGGAG 4560

Db   4561 GGAGCACAGTACGGCCTATGGGGAGGCCCAAGAGCTGCTATCACCCAGAGATTTGGTGCAGGAAAA 4620
Qy   4561 GGAGCACAGTACGGCCTATGGGGAGGCCCAAGAGCTGCTATCACCCAGAGATTTGGTGCAGGAAAA 4620

Db   4621 GTACCTGGAGTACGGCCAGTGCCGCGACTGCCGGGACGTGATCCGCGACACGTATCCGG 4680
Qy   4621 GTACCTGGAGTACGGCCAGTGCCGCGACTGCCGGGACGTGATCCGCGACACGTATCCGG 4680

Db   4681 CCAAGGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740
Qy   4681 CCAAGGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740

Db   4741 GCAAGAGTTCGCTTTTCTTCCCCATCCCGCGTGAAGCAGCTTTGAGAGAGGAAGAG 4800
Qy   4741 GCAAGAGTTCGCTTTTCTTCCCCATCCCGCGTGAAGCAGCTTTGAGAGAGGAAGAG 4800

Db   4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCGAGGGGGACTGGGCCAGTGCCACCTT 4860
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Qy   4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCGAGGGGGACTGGGCCAGTGCCACCTT 4860

Db   4861 CCAGGGCCGCGGTCCCAGCAGCTTCCCCTGCGTGTGACACTGAGGCCCCATTCTTCACTCT 4920
Qy   4861 CCAGGGCCGCGGTCCCAGCAGCTTCCCCTGCGTGTGACACTGAGGCCCCATTCTTCACTCT 4920

Db   4921 GAAGAGACGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATT 4980
Qy   4921 GAAGAGACGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATT 4980

Db   4981 TATCTTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTTAAGGATGGTTGAATGAAC 5040
Qy   4981 TATCTTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTTAAGGATGGTTGAATGAAC 5040

Db   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100
Qy   5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100

Db   5101 TAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Qy   5101 TAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Db   5161 AACAGCAGTGGAATAAGTACTTAGAAAATGTGAAAAATGAGACAGTAAAATAGATGAGATAA 5220
Qy   5161 AACAGCAGTGGAATAAGTACTTAGAAAATGTGAAAAATGAGACAGTAAAATAGATGAGATAA 5220

Db   5221 AGAACTAAAGAAATTAAGAGAGTAGTAGTCAATTCTGCCTATACCTCAGTCTATTCTGTAAA 5280
Qy   5221 AGAACTAAAGAAATTAAGAGAGTAGTAGTCAATTCTGCCTATACCTCAGTCTATTCTGTAAA 5280

Db   5281 ATTTTTAAAGATATATGCATACCTGGATTCCTCTTTGGCCTTCTTTGAGAATGTAAGAGAAAT 5340
Qy   5281 ATTTTTAAAGATATATGCATACCTGGATTCCTCTTTGGCCTTCTTTGAGAATGTAAGAGAAAT 5340

Db   5341 TAAAATCTGAATAAAGAATTCTTCCTGTTCACTGCGCTCTTTTCTTCCTCTCCATGCACTGACCA 5400
Qy   5341 TAAAATCTGAATAAAGAATTCTTCCTGTTCACTGCGCTCTTTTCTTCCTCTCCATGCACTGACGA 5400

Db   5401 TCTGCTTTTTGGAAGGCCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATCATAC 5460
Qy   5401 TCTGCTTTTTGGAAGGCCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATCATAC 5460

Db   5461 CCACCCATAGGGTCGTAGAGTCGTAGAGTCGAGTCCAGTCGCAGTAATCGAGGTGGCAAGAGTC 5520
Qy   5461 CCACCCATAGGGTCGTAGAGTCGTAGAGTCGAGTCCAGTCGCAGTAATCGAGGTGGCAAGAGTC 5520

Db   5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGTGGGGTGTGGGGTTCCGGGTGGAGAGTG 5580
Qy   5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGTGGGGTGTGGGGTTCCGGGTGGAGAGTG 5580

Db   5581 GTGGAGTGTCAATGCCCTGATTGTAATGATCTTGGGTGGATCC 5640
Qy   5581 GTGGAGTGTCAATGCCCTGATTGTAATGATCTTGGGTGGATCC 5640

Db   5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Qy   5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
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CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/807,043B
CC   FILING DATE: 1911212
CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5342774man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 253.3
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 7:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2419 base pairs
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: singular
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
SQ   Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;

Query Match          42.6%;  Score 2419;  DB 4;  Length 2419;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 2419;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC      60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGTCATCC   3315

Db     61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC    120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC   3375

Db    121 CGAGGGCTGTGCTTGCGGCTCGCACCCTGGTCTGACAGTATCCTTCCTGGAGCTCCA     180
          ||||||||||||||||||||||||||||||||||||||||||||||
Qy   3376 CGACCTTCTGCTTGCGGCTCGCACCCTGGTCTGACAGTATCCTTCCTGGAGCTCCA    3435

Db    181 GGAACCAGGCAGTGCGCCAGCAGTGAGGCCTTGGTCTGACAGTATCCTCAGGTCACGAGAGGATG    240
          |||||||||||||||||||||||||||||||||||||||||||||
Qy   3436 GGAACCAGGCCAACCCAGGACAGGATTCCCTGGAGGCCACCAGAGAGCCACCAGAGGATG    3495

Db    241 CACAGGGTGTGCCAGCAGTGGGGATGTCACAGAGTCTTGCCTGAATGCACACCAGGGCCCCACCTGCCA    300
          ||||||||||||||||||||||||||||||||||||||||||
Qy   3496 CACAGGGTGTGCCAGCAGTGGGGATGTCACAGAGTCTTGCCTGAATGCACACCAGGGCCCCACCTGCCA    3555

Db    301 CAGGACACATAGGACTCCACAGAGTCTGGGCTACCCTGAGTCCTCACTGTCTCAGTCTGTAGAAT    360
          ||||||||||||||||||||||||||||||||||||
Qy   3556 CAGGACACATAGGACTCCACAGAGTCTGGGCTACCCTGAGTCCTCACTGTCTCAGTCTGTAGAAT    3615

Db    361 CGACCTTCTGCTGCGGCGGCTGTACCCTGAGGCCCACCAGAGGCCACCAGAGGAGGACCAAGGAGAA    420
          |||||||||||||||||||||||||||||||||||||||||
Qy   3616 CGACCTTCTGGCGCGGCTGTACCCTGAGTCCCTCAGTTTCAGGTTTTCAG    3675

Db    421 GGGACAGGCCAACCCAGGACAGGATTCCCTGGAGGCCACCAGAGAGCCACCAGAGGAGAA    480
          |||||||||||||||||||||||||||||||||||||||||
Qy   3676 GGGACAGGCCAACCCAGGACAGGACCACCAGAGGAGGACCAAGGAGAGA    3735

Db    481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTTCAAGTTCAGTTCGTC         540
          ||||||||||||||||||||||||||||||||||||||||
Qy   3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTTCAAGTTCAGTTCGTC      3795

Db    541 CACACTCCCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTGCTTGCCCACTCCT       600
          ||||||||||||||||||||||||||||||||||||||||
Qy   3796 CACACTCCCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTGCTTGCCCACTCCT    3855

Db    601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTTGACAGCAGAGAGTCTGCACTGCAAGCC      660
          |||||||||||||||||||||||||||||||||||||||||||
Qy   3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTTGACAGCAGAGAGTCTGCACTGCCAAGCC    3915

Db    661 TGAGGAAGCCCTTGAGCCCAACAAGAGACCCTGGCCTGGTGTGTGCAGGCTGCCAC       720
          ||||||||||||||||||||||||||||||||||||||||
Qy   3916 TGAGGAAGCCCTTGAGCCCAACAAGAGACCCTGGCCTGGTGTGTGCAGGCTGCCAC    3975

Db    721 CTCCTCCTCCTCTGTCCTGGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC       780
          ||||||||||||||||||||||||||||||||||||||
Qy   3976 CTCCTCCTCCTCTGTCCTGGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC    4035

Db    781 AGATCCTCCCAGAGTCCTCAGGGAGCCTTCGGGAGCCTTCCCACTACCATCAACTTCACTCG       840
          |||||||||||||||||||||||||||||||||||||||||
Qy   4036 AGATCCTCCCAGAGTCCTCAGGGAGCCTTCGGGAGCCTTCCCACTACCATCAACTTCACTCG    4095

Db    841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG       900
          |||||||||||||||||||||||||||||||||||||||||
Qy   4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG    4155

Db    901 TATCCTGGAGTCCTTGTTCCGACGAGCAGTAATCACTAAGAGAGGTGGCTGATTTGGTTGGTTT       960
          |||||||||||||||||||||||||||||||||||||||||
Qy   4156 TATCCTGGAGTCCTTGTTCCGACGAGCAGTAATCACTAAGAGAGGTGGCTGATTTGGTTGGTTT    4215

Db    961 TCTGCTCTCAAATATCGAGCCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGGAGAGTGT      1020
          |||||||||||||||||||||||||||||||||||||||||
Qy   4216 TCTGCTCTCAAATATCGAGCCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGGAGAGTGT    4275

Db   1021 CATCAAAAATTACAAGCACTGTTTTCCGGCAAAGCCTTCTGAGTCCTTGCA      1080
          ||||||||||||||||||||||||||||||||||||
Qy   4276 CATCAAAAATTACAAGCACTGTTTTCCGGCAAAGCCTTCTGAGTCCTTGCA   4335

Db   1081 GCTGGTCTTTGGCATTGACGTGAAGGAGGCAGACCCCACCGGCCACTCCTATGTCCTTGT      1140
          ||||||||||||||||||||||||||||||||||||||||
Qy   4336 GCTGGTCTTTGGCATTGACGTGAAGGAGGCAGACCCCACCGGCCACTCCTATGTCCTTGT   4395

Db   1141 CACCTGCCTAGGTCTCTCCTATATGATGCCCTCGGTGATAATCAGATCATGCCCAAGAC      1200
          |||||||||||||||||||||||||||||||||||
Qy   4396 CACCTGCCTAGGTCTCTCCTATATGATGCCCTCGGTGATAATCAGATCATGCCCAAGAC   4455

Db   1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGGCCATGCTCCTGAGGA      1260
          |||||||||||||||||||||||||||||||||||
Qy   4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGGCCATGCTCCTGAGGA   4515

Db   1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGGAGGGAAAAAGTACCTGGAGTACGG      1320
          |||||||||||||||||||||||||||||||||||||||||
Qy   4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGGAGGGAAAAAGTACCTGGAGTACGG   4575

Db   1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGAGTTCGTCAGGGGGCCCTGCCGCT      1380
          ||||||||||||||||||||||||||||||||||||||||
Qy   4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGAGTTCGTCAGGGGGCCCTGCCGCT   4635

Db   1381 CAGGTGCCGACAGTGATCCCGCCCTATGAGTTCGTCTGGGGTCCAAGGGGCCCTGCGCT      1440
          |||||||||||||||||||||||||||||||||||||||||
Qy   4636 CAGGTGCCGACAGTGATCCCGCCCTATGAGTTCGTCTGGGGTCCAAGGGGCCCTGCGCT   4695

Db   1441 GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT      1500
          |||||||||||||||||||||||||||||||||||||||||
Qy   4696 GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT   4755

Db   1501 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGCGCCACCAGAGGAGTCGAGCATGA      1560
          |||||||||||||||||||||||||||||||||||||||||
Qy   4756 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGCGCCACCAGAGGAGTCGAGCATGA   4815
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CC r  TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precurso

CC      NUMBER OF SEQUENCES: 48
CC      CORRESPONDENCE ADDRESS:
CC        ADDRESSEE:  Felfe & Lynch
CC        STREET:  805 Third Avenue
CC        CITY:  New York City
CC        STATE:  New York
CC        ZIP:  10022
CC      COMPUTER READABLE FORM:
CC        MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC        COMPUTER:  IBM
CC        OPERATING SYSTEM:  PC-DOS
CC        SOFTWARE:  Wordperfect
CC      CURRENT APPLICATION DATA:
CC        APPLICATION NUMBER:  US/08/299,849B
CC        FILING DATE:  1-SEPTEMBER-1994
CC        CLASSIFICATION:  435
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  08/037,230
CC        FILING DATE:  26-MARCH-1993
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  PCT/US92/04354
CC        FILING DATE:  22-MAY-1992
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/807,043
CC        FILING DATE:  12-DECEMBER-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/764,364
CC        FILING DATE:  23-SEPTEMBER-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/728,838
CC        FILING DATE:  9-JULY-1991
CC      PRIOR APPLICATION DATA:
CC        APPLICATION NUMBER:  07/705,702
CC        FILING DATE:  23-May-1991
CC      ATTORNEY/AGENT INFORMATION:
CC        NAME:  Hanson, No. 5612201man D.
CC        REGISTRATION NUMBER:  30,946
CC        REFERENCE/DOCKET NUMBER:  LUD 5355
CC      TELECOMMUNICATION INFORMATION:
CC        TELEPHONE:  (212) 688-9200
CC        TELEFAX:  (212) 838-3884
CC      INFORMATION FOR SEQ ID NO: 7:
CC      SEQUENCE CHARACTERISTICS:
CC        LENGTH:  2419 base pairs
CC        TYPE:  nucleic acid
CC        STRANDEDNESS:  single
CC        TOPOLOGY:  linear
CC      MOLECULE TYPE:  genomic DNA
SQ      Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;

Query Match             42.6%;  Score 2419;  DB 7;  Length 2419;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches 2419;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db          1 GGATCCAGGCCCTGCCAGGAGAAAATATAAGGGCCCTGCGTGGTGGAACAGAGGGGGTCATCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       3256 GGATCCAGGCCCTGCCAGGAGAAAATATAAGGGCCCTGCGTGGTGGAACAGAGGGGGTCATCC 3315

Db         61 ACTGCATGAGAGTGGGATGTCACAGAGTCAGAGGGGTCACCCTCCTGGTACTGAGAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       3316 ACTGCATGAGAGTGGGATGTCACAGAGTCAGAGGGGTCACCCTCCTGGTACTGAGAAGC 3375

Db        121 CAGGGCTGTGCTTGGGCTCTGCACCCTGAGGGCCCTGGGATTCCTCCTGGAGCTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       3376 CAGGGCTGTGCTTGGGCTCTGCACCCTGAGGGCCCTGGGATTCCTCCTGGAGCTCCA 3435

Db        181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACGAGCAGAGGATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACGAGCAGAGGATG 3495

Db        241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAGTCACACCAAGGGCCCCACCTGCCA 300
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Db       1561 GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGCCAGTGCACCTTCCAGGGCCGCGTCCA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       4816 GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGCCAGTGCACCTTCCAGGGCCGCGTCCA 4875

Db       1621 GCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGCGGTCAG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       4876 GCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCTGAAGAGAGCGGTCAG 4935

Db       1681 TGTTCTCAGTAGTAGTTCTCGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       4936 TGTTCTCAGTAGTAGTTCTCGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT 4995

Db       1741 TTGGAATTGTTCAAATGTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       4996 TTGGAATTGTTCAAATGTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT 5055

Db       1801 TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGTAAGAGTCTTGTGTT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5056 TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGTAAGAGTCTTGTGTT 5115

Db       1861 TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA 1920
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Qy       5116 TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA 5175

Db       1921 AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5176 AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT 5235

Db       1981 AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5236 AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATA 5295

Db       2041 TGCATACCTGGATTCCTGGCTTCCTTGGAGATGTAAGAGAAGAAATTAAAATCTGAATAAAG 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5296 TGCATACCTGGATTCCTGGCTTCCTTGGAGATGTAAGAGAAGAAATTAAAATCTGAATAAAG 5355

Db       2101 AATTCTTCCTGTTCACTGGCTCTTTTCTTCCTCCATGCACTGAGCACTGCTTTTTGGAAG 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5356 AATTCTTCCTGTTCACTGGCTCTTTTCTTCCTCCATGCACTGAGCACTGCTTTTTGGAAG 5415

Db       2161 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5416 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 5475

Db       2221 TAGAGTCTAGGAGAGCTGCCAGTCACGTGAGGCCTGGCAAGATGTCCTCTAAAGATGTAGG 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5476 TAGAGTCTAGGAGAGCTGCCAGTCACGTGAGGCCTGGCAAGATGTCCTCTAAAGATGTAGG 5535

Db       2281 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGTGGTCAATGC 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5536 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGTGGTCAATGC 5595

Db       2341 CCTGAGCTGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCCTCTGGGGGAGCTGATTGT 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       5596 CCTGAGCTGGGCATTTGGGCTTTGGGAAACTGCAGTTCCTTCCTCTGGGGGAGCTGATTGT 5655

Db       2401 AATGATCTTGGGTGGATCC 2419
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Qy       5656 AATGATCTTGGGTGGATCC 5674
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RESULT 5
ID   US-08-299-849B-7 STANDARD; DNA; UNC; 2419 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 7, Application US/08299849B.
CC   Sequence 7, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC     APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
CC     APPLICANT:  Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC     APPLICANT:  Chomez, Patrick
CC   .   TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
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Qy  3496  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  3555
Db   301  CAGGACACATAGGACTCCACAGAGTCGAATGTTGCCCTGAGAGTCGGCCTCCACCTCCCTACTGTCCTGTAGAAT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3556  CAGGACACATAGGACTCCACAGAGTCGAATGTTGCCCTGAGAGTCGGCCTCCACCTCCCTACTGTCCTGTAGAAT  3615

Db   361  CGACCTCTGCTTGGCCGGCTGTACCCTGAGTACCCTCACTTCCTCCTCACTTCCTCCTTCAGGTTTTCAG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3616  CGACCTCTGCTTGGCCGGCTGTACCCTGAGTACCCTCACTTCCTCCTCACTTCCTCCTTCAGGTTTTCAG  3675

Db   421  GGGACAGGCCAACCCAGAGGACACAGGATTCCCTGGAGGCCACAGAGAGGAGCACCAAGGAGAA  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3676  GGGACAGGCCAACCCAGAGGACACAGGATTCCCTGGAGGCCACAGAGAGGAGCACCAAGGAGAA  3735

Db   481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCTCAGCTGAGGCCTCTCA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3736  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCTCAGCTGAGGCCTCTCA  3795

Db   541  CACACTCCCTCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3796  CACACTCCCTCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT  3855

Db   601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCGCACTGCAGCC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3856  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCGCACTGCAGCC  3915

Db   661  TGAGGAAGCCCCTGAGGCCCCAACAAGAGGGCCCTGGGTCTGTGTGTCAGGCTGCCAC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3916  TGAGGAAGCCCCTGAGGCCCCAACAAGAGGGCCCTGGGTCTGTGTGTCAGGCTGCCAC  3975

Db   721  CTCCTCCTCCTCCTGGTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTACCACTCAACTCACTCG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3976  CTCCTCCTCCTCCTGGTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTACCACTCAACTCACTCG  4035

Db   781  AGATCTCCCCAGAGTCCTCAGGGACGGACCTTCCCGCCTTCCCACTACCATCAACATCACTCG  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4036  AGATCTCCCCAGAGTCCTCAGGGAGGACCTTCCCGCCTTCCCACTACCATCAACATCACTCG  4095

Db   841  ACAGAGGCAACCCAGTGAGGGTTCCAGCAGGGGCCAGTGAGAGGAGGGGCCAAGCACCTCTTG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4096  ACAGAGGCAACCCAGTGAGGGTTCCAGCAGGGGCCAGTGAGAGGAGGGGCCAAGCACCTCTTG  4155

Db   901  TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTGGTTT  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4156  TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTTGGTTGGTTT  4215

Db   961  TCTGCTCCTCAAATATCGAGCCAGGAGCCAGTGCACAAAGCAGAAATGCTGGAGAGTGT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4216  TCTGCTCCTCAAATATCGAGCCAGGAGCCAGTGCACAAAGCAGAAATGCTGGAGAGTGT  4275

Db  1021  CATCAAAAATTACAAGCACTGTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4276  CATCAAAAATTACAAGCACTGTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA  4335

Db  1081  GCTGGTCTTTGCGTTGACGTGAGGAAGGCAGAACCCAGCCACTCCTATGTCCTTGT  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4336  GCTGGTCTTTGCGTTGACGTGAGGAAGGCAGAACCCAGCCACTCCTATGTCCTTGT  4395

Db  1141  CACCTGCCTAGTCTCTCCTATGATGGCCCTGGGTGATAATCATGACTCCCAAGAC  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4396  CACCTGCCTAGTCTCTCCTATGATGGCCCTGGGTGATAATCATGACTCCCAAGAC  4455

Db  1201  AGGCTTCCTGATAATGTCCTGGTCATGATTGCAATGGAGGCGGCCATGGTCCTGAGGA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4456  AGGCTTCCTGATAATGTCCTGGTCATGATTGCAATGGAGGCGGCCATGGTCCTGAGGA  4515

Db  1261  GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGGAGGGCGGCCACAGTGCCTA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4516  GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGGAGGGCGGCCACAGTGCCTA  4575

Db  1321  TGGGGAGGCCAGGAAGCTGCTCACCCAAGATTTGGTTGCAGGAAAAGTACCTGGAGTACGG  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||


Qy  4576  TGGGGAGGCCAGGAAGCTGCTCACCCAAGATTTGGTTGCAGGAAAAGTACCTGGAGTACGG  4635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CAGGTGCCGGACAGTGATCCGCACGTATGAGTTCCTGTGGGTCCAAGGGCCTCGCT  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4636  CAGGTGCCGGACAGTGATCCGCACGTATGAGTTCCTGTGGGTCCAAGGGCCTCGCT  4695

Db  1441  GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTCGCAAGAGTTCGCTTT  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4696  GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTCGCAAGAGTTCGCTTT  4755

Db  1501  TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGGAGGAGGAGCTGAGCATGA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4756  TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGGAGGAGGAGCTGAGCATGA  4815

Db  1561  GTTGCAGCCAAGGCACCAGTGGAGGGGGACTGGGCCAGTGGACGCACCTTCCAGGGCCGCGCTCCA  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4816  GTTGCAGCCAAGGCACCAGTGGAGGGGGACTGGGCCAGTGGACGCACCTTCCAGGGCCGCGCTCCA  4875

Db  1621  GCAGCTTCCCCTGCCTCGTGTGACATGAGCGCCATTCTGAAGAGAGCGGTCAG  1680
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Qy  4876  GCAGCTTCCCCTGCCTCGTGTGACATGAGCGCCATTCTGAAGAGAGCGGTCAG  4935

Db  1681  TGTTCTCAGTAGTAGTTTCTGTTCTATTGGTGACTTGGAGATTTATCTTTGTCTCTT  1740
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Qy  4936  TGTTCTCAGTAGTAGTTTCTGTTCTATTGGTGACTTGGAGATTTATCTTTGTCTCTT  4995

Db  1741  TTGGAATTGTTCAAATGTTTTTTTTAAGGGATGTTGAATGAACTTCAGCCATCCAAGTT  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4996  TTGGAATTGTTCAAATGTTTTTTTTAAGGGATGTTGAATGAACTTCAGCCATCCAAGTT  5055

Db  1801  TATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGTAAGAGTCTGTGTT  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5056  TATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGTAAGAGTCTGTGTT  5115

Db  1861  TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAATA  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5116  TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAATA  5175

Db  1921  AGTACTTAGAAATGTGAAAATAGAGCAGTAAAAATAGAGATAAGAGAACTAAAGAAATT  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5176  AGTACTTAGAAATGTGAAAATAGAGCAGTAAAAATAGAGATAAGAGAACTAAAGAAATT  5235

Db  1981  AAGAGATAGTCAATTCTTGCCTATACCTCAGTCTCATTCGTGTAAAATTTTAAAGATATA  2040
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Qy  5236  AAGAGATAGTCAATTCTTGCCTATACCTCAGTCTCATTCGTGTAAAATTTTAAAGATATA  5295

Db  2041  TGCATACCTGGATTCCTTGGCCTTCTTGGCCTTCTTGGGAATGAATCTGAATAAAG  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5296  TGCATACCTGGATTCCTTGGCCTTCTTGGCCTTCTTGGGAATGAATCTGAATAAAG  5355

Db  2101  AATTCTTCCGTCCACTGGCCTCTTTCTTCTCCATGCCACTGAGCACTCGAGCAATGC  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5356  AATTCTTCCGTCCACTGGCCTCTTTCTTCTCCATGCCACTGAGCACTCGAGCAATGC  5415

Db  2161  GCCCTGGGTAGTAGTGGACATGCTAAGGTAAGCTGAATCGATAAGATGGTGG  2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5416  GCCCTGGGTAGTAGTGGACATGCTAAGGTAAGCTGAATCGATAAGATGGTCG  5475

Db  2221  TAGAGTCTAGGAGCTGCAGTCAATCGGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  5476  TAGAGTCTAGGAGCTGCAGTCAATCGGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG  5535

Db  2281  GAAAAGTGAGAGAGGGTGAGGGGTCCGGGCTCCGGGGTGGCTTGGGAGTGGTCAATGC  2340
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Qy  5536  GAAAAGTGAGAGAGGGTGAGGGGTCCGGGCTCCGGGGTGGCTTGGGAGTGGTCAATGC  5595

Db  2341  CCTGAGCTGGGGCATTTTGGGCATTTTGGGCTCCTTCTGGGAAACTGCGATTGT  2400
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Qy  5596  CCTGAGCTGGGGCATTTTGGGCATTTTGGGCTCCTTCTGGGAAACTGCGATTGT  5655

Db  2401  AATGATCTTGGGTGGATCC  2419
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Qy  5656  AATGATCTTGGGTGGATCC  5674
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RESULT 6

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ID   US-08-299-849B-9 STANDARD; DNA; UNC; 4157 BP.
AC   xxxxx
DT   01-JAN-1900
DE   Sequence 9, Application US/08299849B.
CC   Sequence 9, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC      APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC      APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC      APPLICANT: Chomez, Patrick
CC      TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
CC      TITLE OF INVENTION:  Determining Expression Of A Tumor Antigen Precurso
CC      NUMBER OF SEQUENCES: 48
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Felfe & Lynch
CC         STREET: 805 Third Avenue
CC         CITY: New York City
CC         STATE: New York
CC         ZIP: 10022
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC         COMPUTER: IBM
CC         OPERATING SYSTEM: PC-DOS
CC         SOFTWARE: Wordperfect
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/08/299,849B
CC         FILING DATE: 1-SEPTEMBER-1994
CC         CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 08/037,230
CC         FILING DATE: 26-MARCH-1993
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: PCT/US92/04354
CC         FILING DATE: 22-MAY-1992
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/807,043
CC         FILING DATE: 12-DECEMBER-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/728,838
CC         FILING DATE: 9-JULY-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/764,364
CC         FILING DATE: 23-SEPTEMBER-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/705,702
CC         FILING DATE: 23-May-1991
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Hanson, No. 561220 man D.
CC         REGISTRATION NUMBER: 30,946
CC         REFERENCE/DOCKET NUMBER: LUD 5355
CC      TELECOMMUNICATION INFORMATION:
CC         TELEPHONE: (212) 688-9200
CC         TELEFAX: (212) 838-3884
CC      INFORMATION FOR SEQ ID NO: 9:
CC         SEQUENCE CHARACTERISTICS:
CC            LENGTH: 4157 base pairs
CC            TYPE: nucleic acid
CC            STRANDEDNESS: single
CC            TOPOLOGY: linear
CC         MOLECULE TYPE: genomic DNA
CC         FEATURE:
CC            NAME/KEY: MAGE-2 gene
SQ   Sequence 4157 BP; 953 A; 1134 C; 1185 G; 885 T; 0 other;

Query Match             26.1%;  Score 1483;  DB 7;  Length 4157;
Best Local Similarity   78.7%;
Matches  2615;  Conservative    0;  Mismatches  622;  Indels   85;  Gaps   51;
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Db      858 CAGGGGGTTGGGCCCAGCCTCGCGGAGTCAAGGGGAGTCAAGGGGAGGGAAGAAGGAGGAGGGAGGACTGAGG 917

Qy     2154 CATGGGGGTGGGACCCCAGGCCTGCCAAGGCTTACGCGGAGGAAGAGAGGAGGAGGGACTCAGG 2213
                 ||||| |||| ||||||      |  |  |   | ||||||||||||||||  ||||||||||||
Db      918 GGACCTTGGAGTCCAGATCAGTGGCAACCTTGGGC-TGGGGGATCCTGGGCACAGTGGCC 976

Qy     2214 GGACCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCC 2273
                 ||||||||| |||||||||||||       |   ||||  | | |||||||| ||||||
Db      977 GAATGTGCCCCGTGCTCATTGCACCTTCAGGGTGCACAGAGAGTTGAGGGCTGTGGGTCTGA 1036

Qy     2274 ACATATAGGCCCATATTTCCTGCATCTTGAGGTGACAG-GACA-GAG--CTGTGGTCTGA 2329
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Db     1037 GGGCTGGGACTTCAGGTCAGCAGAGGAGGAATCCCAGGATCTGCCGGACCCAAGGTGTG 1096

Qy     2330 GAAGTGGGGCCTCAGGTCAACAGAGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTG 2389
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Db     1097 CCCCCTTCATGGAGGACTCCCATACCCCGGCCAGAAAGAAGGGATGCCACAGAGTCTG 1156

Qy     2390 CCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTG 2449
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Db     1157 GAAGTAAATTGTTCTTAGCTCTGGGGAACCTGATCAGGGATGGCCCTAAGTGACAATCT 1216

Qy     2450 GCTGTCCCCTTTTAGTAGCTGTAGGGGACCCAGATCAGGGATGGCGGGTATGTTCCATTCT 2509
                 | || |||| ||| |||| | ||||||||||||||||||||||| ||| ||||||||| ||
Db     1217 CATTTGTACCCAGGCAGGAGGTTGGGGAACCCTCAGGGAGTAAGGTGTTGGTGTAAAG 1276

Qy     2510 CACTTGTACCACCAGGCAGGAGTTGGGGGCCCTCAGGGAGTGGGTCTTGGGGTAAAAG 2569
                 || ||||||| ||||||||||| ||||| ||||||||||||  |||| ||| |||| ||
Db     1277 AGGAGCTGTCTGCTCATTCAGGGGGTTCCCCTTGAGAAAGGGCAGTCCCTTGGCCAGGAG 1336

Qy     2570 GGGGGATGGCTACTCATGTCAGGGAATTGGGGGTTGAGGAGGCACAGGCGCTGGCAGGAA 2629
                 ||| |  ||| | ||| ||||| ||  |||||| ||||| |||| ||| |||||||||||
Db     1337 TAAAGATGAGTAACCCACAGGAGGCCATCATAAGTTCACCCTAGAACCAAAGGGGTCAG 1396

Qy     2630 TAAAGATGAGTGAGCAGACAGCAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAG 2689
                 ||||||||||| ||||  |||| |||| | | ||| |||| ||| |||||||||||||||||
Db     1397 CCCTGGACAACGCACGTGGGTAACAGGATGTGGCCCCTCCTCACTGTGTCTTCCAGATC 1456

Qy     2690 CCCTGGACACCTCACCCAGGATGT--GGCT-T----CTTTTCACTCCTGTTTCCAGATC 2742
                 |||||||| |  || || |||||   |||  |    |  |||||| |||||||||||||
Db     1457 TCAGGGAGTTGATGACCTTGTTTTCAGAAGGTGACTCAG-TCAACACAGGGGCCC--TC 1513

Qy     2743 TGGGGCAGGTGAGGACCTCATTCTCAGAGGTGACTGCAGTGCCATGCGTTCGGGTGAGGAACATGAGGGA 2802
                 | ||| ||||||||||| ||||| |||||||||||| ||  ||| | | |||||| |||||||  ||||
Db     1514 TGGTGCACAGATGCAGTGGTTCTAGGATCTGCCAAGCATCCAGGTGGAGAGCCTGAGGTA 1573

Qy     2803 TGGTCTAAAGACAGAGCGGTCCCAGGATCTGCATGCGTTCGGGTGAGGAACATGAGGGA 2862
                 |||| |||||||||| | ||||||| | || |  |  |||| | |||||| | ||||||
Db     1574 GGATTGAGGTACCCCTGGCCAGATGCAGCAAGCAAGGGGCCCCATAGAAATCTGCCCTGC 1633

Qy     2863 GGACTGAGGGTACCCCAGGACCAGAACACTG-AGGGAGACTGCACAGAAATCAGCCCTGC 2921
                 ||| |||||  |||||||| | | || ||   ||||| ||||| ||| ||||||||||||
Db     1634 CCCTGCGGTTACTTCAGAGACCTGGCAGGGCTGTCAGCTGAAGCTGAAGGTCCTCCATTATC-T 1692

Qy     2922 CCCTGCTGTCACCCAGAGAGCATGGGGCCTGGGCGTCCGGTCCTTCCGTTATCCT 2981
                 |||||  |  | |||| | ||| |||  ||| |  || ||||  |||| | |||||
Db     1693 GGGATCTTGATGTGCAGGGGAGGGGCCTTGGCTCTGAAGGGGCTGGAGTCAGGTCAGT 1752

Qy     2982 GGGATCATTGATGTGTCAGGGGACGGGGAGGGCCCTGGTCGTCAGGAAGGTCGCTCAGGTCAGT 3041
                 |||||||| |||||| |||||| | ||| ||||| ||||| || ||||| |  | |||||||||
Db     1753 AGAGGAGGGTCAGGCCTGCCAGGGGTCAGGAGTCGAGGACTGAGGACCAAGGGACGGCTCGTCACCC 1812

Qy     3042 AGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACTCAAGGCGGCACCTCACCC 3101
                 |||| ||||| ||||||||| |||||||||| ||| ||||| |  ||| |  |||||||||
Db     1813 AGGACACCTGGACTCCAATGAATTT-GACATCTCTGTTGCTTCGGAGGACCTGGT 1871

Qy     3102 AGGACACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCAAGGACCTAGG 3161
                 |||| |  | ||  || |||||| |||  || |||||   ||| |||  || |||||| |
Db     1872 CACGTGGGCCAGATGGGTCCCCTCTATCCTTCGTACCCATATCAGGGATGTGAGT 1931

Qy     3162 CACGGTGTGGCCAGATGTTTGTCCCCTCC-TGTCCTTCCATTCCTTATCATGGATGTGAAC 3220
                 |||| |||| ||||||||| ||||||||| |   |  |||  ||  ||  ||||| ||||  ||
Db     1932 TCTTGACATGGAGAGATTCTCAAGCCAGCAAAAAGGGGTGGGATT-AGGCCCTACAAGGAGAA 1990
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Qy  3221 TCTTGATTG-GAT-TTCTCAGACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAA 3278
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Db  1991 AGGTGAGGGCCCTGAGTGAGCACAGAGGGGGACCTTCCACCTAGAGTGGGGACCTCA 2050

Qy  3279 ATATAAGGGCCCTGCGTGAGAACAGAGAGGGGGTCATCCACTGCATGAGAGTGGGATGTCA 3338
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Db  2051 CGGAGTCTGCTGCCAACCCTGCTGGAATCCTGGCTGTGGCTGTCAGTGCA 2110

Qy  3339 CAGAGTCCAGCCAGTCCAGAGAAGCCAGAGGCTGTGCTTGCCGGTCTGCA 3398
         |||  |||  |  ||  |||||| |||  |||||||||||
Db  2111 CACTGAAGGCCGTGCAATCCTCCTCCCAGGAATCAGGAGCTCCAGGAGGCCAGTGAG 2170

Qy  3399 CCCTGAGGGCCCCGTGGATTCCTCTCC-----T--GGAGTCCAGGAACCAGGCAGTGAG 3451
         |||  |||| |  |||||||||||||        |  ||||||||||||
Db  2171 GCCTTGGTCTGAGTCAGTG-CCTCAGGTCACAGGGACCGAGAGCCAGACAGTGCCAAC 2229

Qy  3452 GCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCCACAGGGGTGTGCCAGC 3511
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Db  2230 ACTGAAGGTTGCCTGGAATGCACACCAGGGCCCACCCGCC-CAGAACAAAATGGGACT 2288

Qy  3512 AGTGAATGTTTGCCCTGGATTCTCAGTTCCTGTCAGTGTA 3571
         ||||||||||||||   | |  | |  |  ||||| |
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Qy  3572 CCACAGAGTCTGGCCTCACC-TCCCTACTGTCACTTCCTCCTTCAGGTTTTCAGGGG-ACAGGCCCAAC 3630
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Db  2349 GGGTGTACCCGAGGGAGGGTGGCCCCACTTCTCAGGTCTTGAGGGGGGACAGGCTGAC 2408

Qy  3631 GGCTGTACCCGAG-TACCCCTCTCCACTTCCTCCTTCAGGTTTTCAGGGG-ACAGGCCCAAC 3688
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Db  2409 AAGTAGGACCCGAGCCACTGGGAGAG-CATTGAAGGAGAAGATCGTAAGTAAGCCTTTG 2467

Qy  3689 CCAGAGGACAGGATTCCCTGGAGGCCACACGAGGAGCAGGAGAAGAATGTCGTAAGTAG 3748
         ||||  | || ||| ||||||||  |  ||  |||| |||||| ||
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Qy  3749 GCCTTTGTTAGAGTCAGTTCAGTTGCTCAGCTGAGCCCCGAGGGCTGCCCAGCTCTC 3808
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Db  2526 TCCCCAGGCTGTGGGTCTTCATTGCCCAGGTTACCCTGGGAGTGCCTCCCCTG 2585

Qy  3809 TCCCCAGGCTGTGTGGGTCTTCATTGCCCAGGTCCTCGCCCACACTCCTGCCCTGCCCTG 3868
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Db  2586 ACCAGAGTCATCATGCCCTGAGGAGAGTCAGCACTGCAAGCCTGAGAGAGGCCTTT 2645

Qy  3869 ACCAGAGTCATCATGTCTCCTCCCAGAGGCCTGAGGAGTCTGCAGCTGCAAGCCTGAGGAGCCCTT 3928
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Db  2646 GAGGGCCCAGGAGAGCCCTGGTGCGCCAGGGCTCCTGCTACTGAGGAGCAG 2705

Qy  3929 GAGGGCCCAGGAGAGGGCCCTGGTGTGTGGCAGGCTGCCAC--CT-----C-- 3978
         |||||||||||||| | |||||| |  |  ||| ||||||   ||     |
Db  2706 CAGACCCAACAAGAGCCCACGCCAGCCGTGAAGAGAGGGGCCAAGA 2765

Qy  3979 CT--CCTCCTCT-CCTCGGT-C-CT---GG--GC-ACCCTGGAGGAGGTGCCCACTGCT 4027
         |        |     | |   |      ||  |  ||||||||||||||||
Db  2766 CAGACCGCTTCTCCTTCTTCCTCTAGTTGGAAGTTACCCTGGGAGTTCCAAGCAGCAGC 2825

Qy  4028 GACTCACCGAGTCCTCCCCACAGTCCTCCAGCTTCTGCAGAGGCCTTT 4087
         || |   |  |||  |||||||||||||||||
Db  2826 GGTCAACAGATCCTCCCAGAGTCCTCCGGCCTCCAGCAACCAAGGCCCAAGA 2885

Qy  4088 TACACTCTTTGGAGACAATCCGATGAGGGCCTCCAGCGAGGGCGAGGAGGAGGGGCCAAGA 4147
         |||||||    |||   |  | |||||| |   |||| || |||||||||||||||
Db  2886 TTCACTGACAGCAGGGGCCAACCCAGTGAGGGCTTCCAGAGCTACTCAGTGGTTGAGTTG 2945

Qy  4148 ACCTTGTATCCTGAGTCCTTGTTCCCGAGCCAGTCAGTAATCACTCAGGAAGGTGGCTGATTTG 4207
         || |   ||| || ||||    || |||  ||||||||||||||||||
Db  2946 GTTCATTTCTGCTCCTCTTCTGCGGTATGCAGACGGCCGAGGCCCGTGCCACAAGAGCTG 3005

Qy  4208 GTTGGTTTTCTGCTCCTCCAAAATATCGAGCACGAGGCCCGTGCCACAAATGCTG 4267
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Db  3006 GAGAGTGTCCTCAGAAAATTGCCAGGACTTCTTTCCGTGATCTGAGCACTGTTTTCGGCAGATCTTCGAGATC 3065

Qy  4268 GAGAGTGTCATCAAAATTACAAGCACACTGTTTTTCCTGAGATCTTCGGCAGATCTTCCTGAG 4327
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Db  3006 GAGAGTGTCCTCAGAAAATTGCCAGGACTTCTTTCCGTGATCTGAGCACTGTTTTCGGCAGATCTTCGAGATC 3065
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Db  3066 TACTTGCAGCTGGTCTTGGCATCGAGTGGTGGAAGTGGTCCCCATCAGCCACTGTGTAC 3125
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Qy  4328 TCCTTGCAGCTGTCTTGGCATTGGCATTGACGTGAAGCAGAGCAAGCCCACTGCCTCCTAT 4387

Db  3126 ATCCTTGTCACTGCCTCTGGGCCTCTACGATGGCCTCGTGGGTGCTGGGCGACAATGGTCATG 3185
         |||||||||||||| |||||||||||||| ||||| ||| |||||||||
Qy  4388 GTCCTTGTCACCTGCCTCAGTCTCTCCTATGATGGCCTGTGATAATCAGATCATG 4447

Db  3186 CCCAAGACAGGCCTCCTGTATAATCGTCTGGCCATAATGTCTGGTCATGATGGCGGCCATGCC 3245
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Qy  4448 CCCAAGACAGGCCTTCCTGTATAATTGTCTGGTCATGAGGGCGGCCATGCT 4507

Db  3246 CCTGAGGAGAAAATCTGGAGAGCTGAGTATGTTGAGGTGTTTGAGGGAGGGAGGAGGAC 3305
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Qy  4508 CCTGAGGAGAAATCTGGAGAGCTGAGTATGTTGAGGTGTGATGGGAGGGAGGGAGCAC 4567

Db  3306 AGTGTTCTCGCACATCCACATGGGGAGAGCTGCTCATCGCAAGATCTGGTGCAGAAATCTAGTG 3365
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Qy  4568 AGTGCCTATGGGAGGCCCAGGAAGCTGCTCACCCCAAGATTTGGTGCAGGAAAAGTACCTG 4627

Db  3366 GAGTACCGGCAGTGCCCGCGCAGTGATCCTGCAGCCTACGAGGTCCTGTGGGTCCAAGG 3425
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Qy  4628 GAGTAC-GGCAGTGCCGCGGACAGTGATCCGCTATGAGTTCCTGTGGGTCCAAGG 4686

Db  3426 GCCCTCATTGAAACCAGCTATGTGAAAGTCCTGCCACCATACACTAAAGATCGGTGGAGAA 3485
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Qy  4687 GCCCTCGCTGAAACCAGCACCCTTGAGTATGTGACATGAGGGTGCAGTCAGTCCAGTCGCAAGA 4746

Db  3486 CCTCACATTCCTACCCACCACCCCTCCCATCCCTGCGGTGAAGGGCTTTGAGAGAGTGAGTC 3545
         ||  |  || |    ||||||||||||||||||||||| |||||||||||
Qy  4747 GTTCGGCTTTCTTCTCGTTCCTCAGTTCTCAGTTTCTCATTGGGTGACTTTGGTGACTTTATC 4806

Db  3546 TCAGCACATGTTGCAGCCTGGGGTCTGGGCCCAGTGCAGAGGGGGGTCTGCACCTTCCAGGG 3605
         |  || | | |    | || ||||||||||||||||||  |||||||||||||
Qy  4807 TGAGCATGAGTTGCAGCCAGCCAGGTGGGGACTGGGCCAGTGCACCTGCACCTTCCAGGG 4866

Db  3606 CCCCATCCATTAGCTTCCACTGCTTCCTGTGATGAGGCCAATTCCTGCCTTTGAAG 3665
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Qy  4867 CCGCGTCCACCGCAGCGTCCCCGCCGTGTGTGACAGTGCCCATTCTTCACTCT--GAAG 4924

Db  3666 AGAGCAGTCAGCAGCATTCATTCAGATTCAGATTCTGTCTCGTGTTCGTGGTGATGACTTTATC 3725
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Qy  4925 AGAGCCGTCAGTGTCAGTAGTTCTCAGTAGTAGTTGGTGACTTGGACTTGGAGATTTATC 4984

Db  3726 TTTTCTTCCTGTGGGAATTGTTCAAATGTTCCTTTT-AACAAATGGTTGGATGAACTTCA 3784
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Qy  4985 TTTGTTTCTTTTGGAATTGTTTCAAATGTTTTTTTTAAGGGATGGTTGAATGAACTTCA 5044

Db  3785 GCATCCAAGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGGGTA 3844
         |  ||||||||||||||||||||||||||| |||||||| |  | ||||| |||||| ||
Qy  5045 CCGGTCCCAAGTTTATGAATGACAGCAGTCACACA--GTTCTGTGTGTATATAGTTTAAGGGTA 5102

Db  3845 AGAGTCCTGTTTTTTTATTCAGATTGGGAAATCCATTCCATTTGTGAGTTGTCACATAAT 3904
         |||||| ||||| |  | |||||   |||  |  |||||||   | | |||||||||  |
Qy  5103 AGAGTCTGTGTTTTTTATTCAGATTGGGAAATCCATTCTATTTGTGAGTTTGAATTGGGA--TAAT 5160

Db  3905 AACAGCAGTGGAATATGTATTTGCCTATATTGTGAACGAATTAGCAGTAAAAT-ACATGA 3963
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Qy  5161 AACAGCAGTGGAATAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGAGATAA 5220

Db  3964 T--AC-AAGGAACTCAAAAGATAGTTAATTCTTGCCTTATAACCTCAGTCTATTATGTAAA 4020
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Qy  5221 AGAACTAAAGAAATTAAGAAAATTAAGAGATATGCCTTATAACCTCAGTCTATTCTGTAAA 5280

Db  4021 ATTA--AAA-ATATGTG--TA--TG---TTT--TTG-CTTCTTTGAGAATGCAAAAGAAAT 4068
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Qy  5281 ATTTTTAAAGATATATGCATACCTGGATTTCTTTGAGAGATTAAGAGAAAT 5340

Db  4069 TAAAATCTGAATAAA---TTCTTCCTGTTCCATTGGCTCATTCTTTACCATTCACTCAGCA 4125
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Qy  5341 TAAATCTGAATAAAGAATTCTTCCTGTTCCACTGGCTCTTTCACTGGCTCTTTTCTTCCTGCATGCACTCGAGCA 5400
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Db  4126 TCTGCTCTGTGGAAGGCCCTGG 4147
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Qy  5401 TCTGCTTTTGGAAGGCCCTGG 5422

RESULT 7
ID   US-07-807-043B-9 STANDARD; DNA; UNC; 4157 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 9, Application US/07807043B.
CC   Sequence 9, Application US/07807043B
CC   Patent No. 5342774
CC   GENERAL INFORMATION:
CC     APPLICANT: Boon, Thierry, Van den Eynde, Beno t
CC     TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
CC     TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CC     NUMBER OF SEQUENCES: 16
CC     CORRESPONDENCE ADDRESS:
CC       ADDRESSEE: Felfe & Lynch
CC       STREET: 805 Third Avenue
CC       CITY: New York City
CC       STATE: New York
CC       ZIP: 10022
CC     COMPUTER READABLE FORM:
CC       MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC       COMPUTER: IBM
CC       OPERATING SYSTEM: PC-DOS
CC       SOFTWARE: Wordperfect
CC     CURRENT APPLICATION DATA:
CC       APPLICATION NUMBER: US/07/807,043B
CC       FILING DATE: 19911212
CC       CLASSIFICATION: 424
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/764,364
CC       FILING DATE: 23-SEPTEMBER-1991
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/728,838
CC       FILING DATE: 9-JULY-1991
CC     PRIOR APPLICATION DATA:
CC       APPLICATION NUMBER: 07/705,702
CC       FILING DATE: 23-May-1991
CC     ATTORNEY/AGENT INFORMATION:
CC       NAME: Hanson, No. 5342774man D.
CC       REGISTRATION NUMBER: 30,946
CC       REFERENCE/DOCKET NUMBER: LUD 253.3
CC     TELECOMMUNICATION INFORMATION:
CC       TELEPHONE: (212) 688-9200
CC       TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 9:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 4157 base pairs
CC       TYPE: NUCLEIC ACID
CC       STRANDEDNESS: singular
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: genomic DNA
CC     FEATURE:
CC       NAME/KEY: MAGE-2 gene
SQ   Sequence 4157 BP; 953 A; 1134 C; 1185 G; 885 T; 0 other;

Query Match         26.1%;  Score 1483;  DB 4;  Length 4157;
Best Local Similarity  78.7%;  Pred. No. 0.00e+00;
Matches 2615;  Conservative   0;  Mismatches 622;  Indels 85;  Gaps 51;

Db   858 CAGGGGGTTGGGCCAGCCTGCGACGGAGTCAAGGGAGGAGAAGAAGAGGAGGAGGACTGAGG 917
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Qy  2154 CATGGGGGTGGGACCCCAGGGCTTACGCGGAGGAAGAAGAGGAGGAGGACTCAGG 2213

Db   918 GGACCTTGGAGTCCAGATCAGTGGCAACCTTGGGC-TGGGGGATCCTGGGCACAGTGGCC 976
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Qy  2214 GGACCTTGGAATCCAGATCAGTAGTGTGGACCCTGCCTGGCCCCTGAGAGGTCCAGGTGCC 2273

Db   977 GAATGTGCCCCGTGCTCATTGCACCTTCAGGTGACCTTCAGGGTGACAGAGAGTTGAGGGTCTGA 1036
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Qy  2615

Qy  2274 ACATATGGCCCATATTCCTGCATCTTTGAGGTGACAG-GACA-GAG--CTGTGGTCTGA 2329
Db  1037 GGCTGGGACTTCAGTCAGCAGAGGAGGAGGAATCCCAGGATCTTGCCGGACCCAAGGTGTG 1096
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Qy  2330 GAGTGGGGGCCTCAGTCAACAGAGGAGGAGAGTTCCAGGATCCATATGGCCCAAGATGTG 2389
Db  1097 CCCCCTTCATGAGGACTCCCATACCCCGGCCCAGAAAGAAGGATGCCACAGAGTCTG 1156
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Qy  2390 CCCCCTTCATGAGGACTGGGGATATCCCGGCTCAGAAAGAAGAAGGACTCCACACAGTCTG 2449
Db  1157 GAGTAAATTGTTCTTAGCTCTGGGGAACCTGATCAGGGATGGCCCTAAGTGACAATCT 1216
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Qy  2450 GCTGTCCCCTTTTAGTAGTCTAGGGGACCAGATCAGGGATGGCGGGTATGTTCCATTCT 2509
Db  1217 CATTTGTACCACAGGCAGGAGGTGGGGAACCCTCAGGGAGATAAGGTGTGGTGGTGTAAAG 1276
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Qy  2510 CACTTGTACCACAGGCAGGAAGTTGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAG 2569
Db  1277 AGGAGCTGTCTGCTCATTTCAGGGGGTTCCCCCTTGAGAAAGGGCAGTCCCTGGCAGGAG 1336
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Qy  2570 GGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGGCGTGGCAGGAA 2629
Db  1337 TAAAGATGAGTAACCCACAGGAGGCCATCATAACGTTCACCCTAGAAACCAAAGGGGTCAG 1396
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Qy  2630 TAAAGATGAGTGAGCAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAG 2689
Db  1397 CCCTGGCAACGCACGTGGGGTAACAGATGTGGCCCCTCCTCACTTGTCTTCCAGATC 1456
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Qy  2690 CCCTGGACACCTCACCCAGGATGT-GGCT-T----CTTTTCACTCCTGTTTCCAGATC 2742
Db  1457 TCAGGGAGTTGATGACCTTGTTTCAGAAGTGACTCAG-TCAACACAGGGCCCC--TC 1513
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Qy  2743 TGGGGCAGTGAGGACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATC 2802
Db  1514 TGGTCGACAGATCAGTGGTTCTAGGATTCGCCAAGCATCCAGGTGGAGAGCCTGAGGTA 1573
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Qy  2803 TGGTCTAAAGACAGAGGCGGTCCCAGGATCTGCCATGCCGGTTCGGGTGAGGAACATGAGGGA 2862
Db  1574 GGATTGAGGGTACCCCTGGGCCAGAATGCAGCAGCAAAGGGGGCCCATAGAAAATCTGCCCTGC 1633
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Qy  2863 GGACTGAGGGTACCCCAGGACCCCCAGGAACACTG-AGGGAGACTGCCACAGAAATCAGCCCTGC 2921
Db  1634 CCCTGCGGTTACTTCAGAGACCCTGGGCAGGGCTGTCAGTGAAGTCCCTCCATTATC-T 1692
         |||||| || || |||||||| ||||| ||||| ||| ||| |  ||| ||| |||||| |
Qy  2922 CCCTGCGTCACCCCAGAGCATGGGCTGCGGCCTGGCCTTCGGTTATCCT 2981
Db  1693 GGGATCTTTGATGTCAGGGAAGGGGAGGGCCTTGGTCTGAAAGGGCTGGAGTCAGGTCAGT 1752
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Qy  2982 GGGATCATTGATGTCAGGACGGGGAGGGCCTTGGTCTGACAAGGCTGCGCTCAGGTCAGT 3041
Db  1753 AGAGGGAGGGTCTCAGCCCTGCCAGGAGTGGAGCTGAGGACCAAGCAGCCGTCGTCACCC 1812
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Qy  3042 AGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACAAGCGGGCACCTCACCC 3101
Db  1813 AGGACACCTGGACTCCAATGAATT-GACATCTCGTTGTCCTTCGCGGAGGACCTGGT 1871
         |||| |   |||| |||||| |||| |||| || | ||| |||  ||||||||| ||||
Qy  3102 AGGACACATTAATTCCAATGAATTTTGATATCTCTTCCTTCCTTCGTGCCCCTTCCCCAAGGACCTAGG 3161
Db  1872 CACGTATGCCCAGATGTGGGTCCCCTCCTCATCTCCTTCCTTCGTGTACCATATCAGGGATGTGAGT 1931
         ||||||||||||| ||||  ||||||| | |||||||  |||  ||||||||| |||||||| ||
Qy  3162 CACGTGTGCCCAGATGTTTTGTCCCCTCC--TGTCCTTCCATCCTTATCATGGATGGAAC 3220
Db  1932 TCTTGACATGGAGAGATTCTCAAGGCACGCAGCAAAAGGTGGGATT-AGGCCCTACAAGGAGAA 1990
         ||| ||| || ||| | ||  ||  ||| ||| ||||||  |||| |||||| |||||||||
Qy  3221 TCTTGATTTG-GAT-TTCTCAGACGCAGAGGAGGACCCTGCCCAGGAAAA 3278
Db  1991 AGGTGAGGGCCCTGAGTGACGACACGAGGGGATCCTGGGACCTTCA 2050
         || |||| |||||| ||| || ||||| |||||  || ||| |||| |||
Qy  3279 ATATAAGGGCCCTGCGTGAACAGAGGGGTCATCCACTGCATGAGAGTGGGATGTCA 3338
Db  2051 CGGAGTCTGCGCAACCCTGCTGAGCTTCTGGAATCCGTGGCTGCTCTGGCCTGCA 2110
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Qy  3339 CAGAGTCCAGCCCACCCCTCCTCGGTAGCACTGAGGACCAGGCCCTGGGTGTTGCGGTCTGCA 3398
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Db  2111  CACTGAGGCCCGTGCAATTCCTCTCCCCAGGAATCAGGAGCTCCAGGAACCAGGCAGTGAG  2170
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Qy  3399  CCCTGAGGCCCCTGGATTCCTTCTCC-----T--GGAGCTCCAGGAACCAGGCAGTGAG  3451

Db  2171  GCCTTGGTCTGAGTCAGTG-CCTCAGAGCAGAGGGACGCAGAGCAGTGCCAAC         2229
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Qy  3452  GCCTTGGTCTGAGACAGTATCCTCAGGTCACAGTGCACAGGGGTGTGCCAGC         3511

Db  2230  ACTGAAGGTTTGCTGGAATGCACACCAAGGGCCCCACCCGCC-CAGAACAAATGGGACT   2288
          | |||| |||||| |||||  ||||||||||||||||||||| ||  ||  ||| |||
Qy  3512  AGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCAGGGACACACTAGGACT     3571

Db  2289  CCAGAGGGCCTGGCCTCACCCTCCCTATTTCTCAGTCCTGCAGCCTGAGCGATGTGCTGCC  2348
          |||   ||  ||||||| ||||||| ||||  ||||| |||||||||||||| ||||||||
Qy  3572  CCACAGAGTCTGCGCCACC-TCCCTACTCTGCCAGTTCCTGTAGAATCGACCTCTGCTGCC  3630

Db  2349  GGCTGTACCCTGAGGTGCCTCCCACTTCCTCCTTCAGGTTCTGAGGGGACAGGCTGAC   2408
          |||||||||||| | |||||  ||||||| |||||| ||||||  |||||||||||||
Qy  3631  GGCTGTACCCTGAG-TACCCTCTCACTTCCTCCTTCAGGTTTTCAGGGG-ACAGGCCCAAC  3688

Db  2409  AAGTAGGACCCGAGGCACTGGAGAG-CATTGAAGGAGGAGATCTGTAAGTAAGCCTTTG   2467
               || ||||| |||| ||||| | ||| || | |  ||| | |  |  | |
Qy  3689  CCAGAGGACAGAGGCAGGATTCCCTGGAGGCACCAGAGGAAGAAGATCTGTAAGTAG    3748

Db  2468  TCAGAGGCCTCCAAGGTTCA--GTTCAGTTCTCACCTAAGGCCTCCACCACGCTCCTTCTC  2525
          || |||||  |      | |       || ||||| |||||||| |||| |  |||| |||
Qy  3749  GCCTTTGTAGAGTCTTCAGGTGTCAGTTCTCCAAGGCCTCTGAGGTTGTCCCTCTCC     3808

Db  2526  TCCCCAGGCCTGTGGGTTCATTGCCCAGCTCCTGCCCACTCCTGCCTGCTGCCCCTG   2585
           || ||||||||||| |||| || |||||| || |  ||||| || ||||| || |||
Qy  3809  TCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACTCCTGCCTGCTGCCCTG  3868

Db  2586  ACCAGAGTCATCATGCCTGAGCAGAGTCAGCACTGCAAGCCTGAAGAAGGCCTT     2645
          |  ||||| ||||||  |||||| |||||||| || |  || ||||||
Qy  3869  ACGAGAGTCAGTGTCTTCTCAGTAGTAGGATTCCTCATGCCTGGACTGG      3928

Db  2646  GAGGCCCAGGAGAGGAGCCCTGGGCCTGGTGGCCAAGGCGTCCTGCTACTGAGGAGCAG  2705
          |||||| |||| || | || |  | |   || |  ||  || |
Qy  3929  GAGGCCCAACAGAGAGGCCCTGGGCCTGGTGTGTGTGGTCGCAGGCCTGCC----------  3978

Db  2706  CAGACCGCTTCTTCCTTCTACTCTAGTGGAGTTACCCTCGGGGGAGTGCCTGCTGCC   2765
          |   |||  ||||| | | |||| |  |||  || ||||||
Qy  3979  CT--CCTCCTCT-CCTCTGGT-C-CT---GG--GC-ACCCTGGAGGGAGTGCCCACTGCT   4027

Db  2766  GACTCACCGAGTTCCTCCCCACAGCTCTCCGACTGCTCTCCGACTACCATCAAC     2825
          || | |||   |||||  |||||||||||| |  ||||| || |||||||||||
Qy  4028  GGTCAACAGATCCTCACCAGTGAGGGCTCCAGGAGCCCTCGCGTTTCCCACTACCATCAAC  4087

Db  2826  TACACTCTTTGGAGACAATCCGATGAGGGGCTCCAGCAACCAAGAGAGGAGGGCCAAGA  2885
          |||| | || | ||| |||  || |  | || ||||| || ||||||| |||||||||
Qy  4088  TTCACTGCAGAGGCCAACCCAGTGAGGGGTTCCAGCAGCAATCAGGCAGAAATGCTG   4147

Db  2886  ATGTTCCCGACCTGGAGTCCGAGTTCCAAGCAATCAGTAGGAAGAATGGTTGAGTTG    2945
          | |||||| | ||||||| | || |||||||||||||||| |||||| || || |
Qy  4148  ACCTCTTGTATCCTGGAGTCCTGTTCCGAGCAGCAGTAATCACTAAGAAGGTGGCTGAT   4207

Db  2946  GTTCATTTCTGCTCCTCAAGTATCGAGCCGGTCACAAGGTCAGAAATGCTG      3005
          ||  |||||||||  | |||||||||||| | | |  |||| |||||||  ||||||
Qy  4208  GTTGGTTTTCTGCTCTCCAAAATATGAGCCAGGCAATCAGAAATGCTG     4267

Db  3006  GAGAGTGTCCTCAGAAATTGCCAGGAGACTTCTTTCCCGTGATCTTCAGCAAGGCTCCGAG  3065
          |||||||||||||  |  | || ||  |  ||| || ||  | | || || ||||||  ||
Qy  4268  GAGAGTCATCAAAAATTACAGACACTGTTTCAGGATCTTCGGCAAAGCCCTCTGAG   4327

Db  3066  TACTTGCAGCTGGTCTTTGGCATCGAGGTGTGGAATGTCCCATCAGCCACTTGTAC    3125
          |||||| |||||| || ||||| ||||| ||||  ||||  || |  | || | ||||||
Qy  4328  TCCTTGCAGCTGTTTGGCGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCCTCTAT  4387

Db  3126  ATCCTTGTCACCTGCCTGGCCTTCTCCCTACGATGGGCCTGGTGGGCAATCAGTCATG  3185
          |||||||||||| |||| ||| |||  |||| |  ||  | |  | ||| | ||||||
Qy  4388  GTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGGCCTGCTGCTGGGTGATAATCATG  4447
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Db  3186  CCCAAGACAGGCCTCCTGATAATCGTCCTGGCCATAATCGGCAATAGAGGGCGACTGTGCC  3245
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Qy  4448  CCCAAGACAGGCCTTCCTGATAATTGTCCTGGTCATGATTGCCATGTGCAATGAGGGCGGCCCATGCT  4507

Db  3246  CCTGAGGAGAAAATCTGGGAGGAGCTGAGTATGTTGGAGGTGTTTGAGGGGAGGGAGGAC  3305
          || || ||||   | |||||||| | | ||  | | ||  | |  ||||||||||||||
Qy  4508  CCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGTATGGAGGTGTTATGGGGGAGGGAGCAC  4567

Db  3306  AGTGTCTTCGCACATCCCAGGAGAGCTGCTCATGCGAGCAGAGTCGTCGCAGGAAAACTACCTG  3365
          ||  | ||| | ||||  ||||||| ||    |||||| | |||||||||||||  ||||||||
Qy  4568  AGTGCCTATGGGAGCCCAGGAAGCTGCTCACCGGGTGCAGGATTGGTGCAGGAAAAGTACCTG  4627

Db  3366  GAGTACCGGCAGGTGCCCGGCCAGTGATCCTGCACGCTATGGGTCCTCCAAGG        3425
          |||| |  ||||| |||   |||||| ||||||| ||| ||  | ||||||||||
Qy  4628  GAGTAC-GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGTCCCAAGG  4686

Db  3426  GCCCTCATTGAAACCAGCTATGTGAAAGTCTGCACCACATACACTAAGATCGGTGGAGAA  3485
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Qy  4687  GCCCTGCTGCAAACAGCTATGTGAAAGTCCTGAGTATGTGATCAAGGTCAGTCAGTCAAGA  4746

Db  3486  CCTCACATTCCTACCCACCCCGCATGAACCCTGTTTGAGAGGAGGAGGAGAGTGAGTC  3545
           | |  |||   || |  |||||||  | ||| |     |||  ||||    ||||| ||
Qy  4747  GTTCGCTTTTCTTCCTCCATCCCTGCGTGAACCAGTGACGCTTTCACTCT---GAAG  4806

Db  3546  TCAGCACATGTTGCAGCCGTGGGAGGGGTCTGGGCACGTCCACCTTCCAGGG      3605
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Qy  4807  TGAGCATGAGTTGCAGCCAAGGCCAGTGGAGGGGACTGGGCACGTGCACCTTCCAGGG  4866

Db  3606  CCCCATCCATTAGCTTCCACTGCCTGCCTGGTGTGATATGAGGCCCATTCCTGCCTCTTGAAG  3665
          |||||| | | || ||   ||||| | ||  | | ||||||| || |||||||||||||||||
Qy  4867  CCGGTCCAGCACGTTCCCTGTGCCCCTTCTGACATGAGGCCATCCATTCTTCACTCT--GAAG  4924

Db  3666  AGAGCAGTCAGCATTCTTAGCAGTCAGTGAGTGGTTTCGTTCGTTGGATGATTTATC  3725
          ||||| ||||  |||| |  ||| |  || ||||||| |||||||| |||| ||||||
Qy  4925  AGAGCAGCGGTCAGTGTCTTCAGTAGTAGGTTTCGTTCGTTGGTTCATTGGTGAGATTTATC  4984

Db  3726  TTTCTTTCCTGTGGAATTGTGTCAAAATGTTCCTTTT-AACAAATGGTGGATGAACTTCA  3784
          |||| |||| |||  ||||| || |||| || ||||||      |||| |||| ||||||
Qy  4985  TTTGTTCTCTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGTTGAATGAACTTCA  5044

Db  3785  GCATCCAAGTTTATGAACTGACCAGTAGTCACACATAGTGCTGTTTTATATAGTTTAGGGGTA  3844
          |||||||||||| ||||| || |||| | || |||  |  |  |||||| |||||  |||||
Qy  5045  GCATCCAAGTTTATGAATGACCAGCAGCACACA--GTTCTGTGTGTATATAGTTTAAGGGTA  5102

Db  3845  AGAGTCCTGTTTTTATTCAGATTGGGAAATCCATTCCATTTGTGACTTGTCACATAAT    3904
          |||| | |||| | | || |  |  | |||||| | | ||||| |||||  |  |||
Qy  5103  AGAGTCTGTGTTTTATTCAGATTTGGGAAATCCATTCTATTTTGTGAATTGGGA--TAAT  5160

Db  3905  AACAGCAGTGGAATAGTGTATTTGCCTATATTGTGAACAGCGAATTAGCAGTAAAT-ACATGA  3963
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Qy  5161  AACAGCAGTGGAATAGTGTACTTAGAAAATGTGAAAAATGTAAAATAGATGAGATAA  5220

Db  3964  T--AC-AAGGAACTCAAAAGATAGTTAATTCTTGCCTTAATAAATGTAAA       4020
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Qy  5221  AGAACTAAAGAAAATTAAGAGATCAATTCTTTGCCTTATACCTGCTAATTCTGTAAA  5280

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          |||    |||  | | |||      |        |||  ||||||| ||||| || |||||
Qy  5281  ATTTTTAAAGATATATGCATACCTGGATTTCTTTGAGAATGTAAGAGAAAT  5340

Db  4069  TAAAATCTGAATAAA---TTCTTCCTGTTCACTGGCTTCATTCATTGTCAA        4125
          |||||||||||||||   || |||  || |||| || ||| |  || |||
Qy  5341  TAAAATCTGAATAAAGAAATAAAGAAATTCTTCCTGTTCACTGGCTCTTTTCTCCTCATGCTGAGCA  5400

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Qy  5401  TCTGCTTTTTGGAAGGCCCTGG    5422
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DE Sequence 13, Application US/08299849B.
CC Sequence 13, Application US/08299849B
CC Patent No. 5612201
CC GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5612201man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 13:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2531 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-4 gene
SQ Sequence 2531 BP; 608 A; 593 C; 700 G; 630 T; 0 other;

Query Match   24.78%; Score 1399; DB 7; Length 2531;
Best Local Similarity 84.38%;
Matches 2068; Conservative   0; Mismatches 327; Indels 57; Gaps 27;   Pred. No. 0.00e+00;

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Db      1 GGATCCAGGCCCTGCCTGGGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCC   60
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Qy   3256 GGATCCAGGCCCTGCCCAGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315

Db     61 ACTGCATGAGAGTGGGGACCTGCAGTCCAGCCTACCCCTTGTCACCTGATGGCACTGAGGAC  120
          ||| ||||||||||||||| || |||||||||  |||||||||||||| |||||||||||||
Qy   3316 ACTGCATGAGAGTGGGGATCGCAGAGTCCAGCCACCCACCCCTTGTCACCTGTAGCCGAGAAGC 3375
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Db   121 CGGGGCTGTGCTTACAGTGCTGCGACCTGAACATGGACCCCATGGATTCCTCTCCTAGAGCTCCA 180
Qy   3376 CAGGGCTGTGCTTGCGGTGCTGCACCCTGAGGGGGCCGTGAATTCCTTTCTGGAGCTCCA 3435

Db   181 GGAACAAGGCAGTCAGGCCTTGGTCTGAGACAGTGTCTCAGTTACAGCAGAGGAGGATG 240
Qy   3436 GGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGTCACAGAGCAGGAGGATG 3495

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Qy   3556 CAGGACACATAGGACTCCACAGAGTCTGCCTCCCACTGTCAGTCTCCTGTAGAAT 3615

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Qy   3616 CGACCTCTGCTGCCGGCTGTACCCTGAG-TACCCTCTCACTTCCTCCTTCAGTTTTCA 3674

Db   421 GCAGACAGGCCAACCG-GAG-ACAGGATTCCCTGAGGCCACAGAGGAGCACCAAGGAGA 478
Qy   3675 GGGGACAGGCCAACCCAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 3734

Db   479 AGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTGGTTCTCAGCTGAGGTCTCTC 538
Qy   3735 AGATCTGTAAGTAGGCCCTTTGTTAGAGTCTCCAAGGTTCAGTTCTCAGCTGAGGCCTCTC 3794

Db   539 ACATGCTCCCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCGTTTGCTCCGCCACTCT 598
Qy   3795 ACACTCCCTCTCCTCCCCAGGCCTGTGGGTCTTCAGTTGCCCAGCTCCTGCCCACACTCC 3854

Db   599 TGCCTGCCCCTGACCAGTCATCATGTCTTCTTCTGAGCAGAGAGTCAGCACTGCAAGC 658
Qy   3855 TGCCTGCTGCCCTGACGAGTCATCATGTCTTCTTCTGAGCAGAGAGTCTGCACTGCAAGC 3914

Db   659 CTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCTTGGGGTGCACAGGCTCCTA 718
Qy   3915 CTGAGGAAGGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTCGGTGTGTGCAGGCTGC- - 3972

Qy   3973 ---------CA------C---CTCCTCCTCCTCGTCCTCTGGGCACCCTGG

Db   719 CTACTGAGGAGGAGGAGGTGCTGTCTCCTCCTCCTCCTGGTCCCTGGCACCCTGG 778

Db   779 AGGAAGTGCCTGCTGCTCAGTCAGGTCCTCCCCCAGAGTCCTCAGGGAGCCCTGCCT 838
Qy   4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCCTGCGCT 4070

Db   839 TACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAG 898
Qy   4071 TTCCCACTACCATCAACTTCACTCACGACAGAGGCAACCCAGGTGAGGGTTCCAGCAGCCCGTG 4130

Db   899 AAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGATCCTTGTTCGACGACAGAAGCACTCAGTA 958
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Db   959 ACAAGGTGGATGAGTTGCTCATTTCTGCTCATTTTGGTTTTCTGCTCCAGATCACAGCGGCTGCTTCCTGTGATCT 1018
Qy   4191 AGAAGGTGGCTGCTGATTTGGTTGGTTTTTCTGCTCCTTCAAATATCACAGCGGCCAGGCCAGGAGCCAGGTCA 4250

Db   1019 CAAAGGCCAGAAATGCTGGAGAGAGTCATCAAAAAATTACAGACGGCTGCTTCCTGTGATCT 1078
Qy   4251 CAAAGGCCAGAAATGCTGGAGAGTGTCATCAAAAAATTACAGCAGCACTGTTTTCCTGAGATCT 4310

Db   1079 TCGGCAAAGCCTCCAGTCCTCGAGCGAAAGCCCTGAGTGGACC 1138
Qy   4311 TCGGCAAAGCCTGAGTCCTCGAGTCTTGGCATTGAGCTGACCTGAAGGAAGCAGACC 4370

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Qy   4371 CACCCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG 4430
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Qy  5503                   TCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGAAAGATGAGAGAAAAGTGAGGGGTGAGGGTGTG  5562
Db  2318  GGGCTCCAGTGAGAGTGGTCGGGTGTAAATTCCCGTG-TGGGGCCTTTGGGCTTTGG  2376
Qy  5563  GGGCTCCGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCGCTGGGCATTTGGGCTTTGG  5622
Db  2377  GAAACTGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGTGGGTCC  2428
Qy  5623  GAAACTGCAGTTCCTTCTGGGGGAGCTGATGTTGTAATGATCTTGGTGGATCC  5674


RESULT  9
ID   US-08-299-849B-14 STANDARD; DNA; UNC; 2531 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 14, Application US/08299849B.
CC   Sequence 14, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC     APPLICANT:  De Plaen, Etienne; Boon-Falleur, Thierry;
CC     APPLICANT:  Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC     APPLICANT:  Chomez, Patrick
CC   TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION:  Determining Expression of A Tumor Antigen Precurso
CC   NUMBER OF SEQUENCES:  48
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE:  Felfe & Lynch
CC     STREET:  805 Third Avenue
CC     CITY:  New York City
CC     STATE:  New York
CC     ZIP:  10022
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC     COMPUTER:  IBM
CC     OPERATING SYSTEM:  PC-DOS
CC     SOFTWARE:  Wordperfect
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER:  US/08/299,849B
CC     FILING DATE:  1-SEPTEMBER-1994
CC     CLASSIFICATION:  435
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER:  08/037,230
CC     FILING DATE:  26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER:  PCT/US92/04354
CC     FILING DATE:  22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER:  07/807,043
CC     FILING DATE:  12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER:  07/764,364
CC     FILING DATE:  23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER:  07/728,838
CC     APPLICATION NUMBER:  9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER:  07/705,702
CC     FILING DATE:  23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME:  Hanson, No. 561201man D.
CC     REGISTRATION NUMBER:  30,946
CC     REFERENCE/DOCKET NUMBER:  LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE:  (212) 688-9200
CC     TELEFAX:  (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 14:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH:  2531 base pairs
CC       TYPE:  nucleic acid
CC       STRANDEDNESS:  single
CC       TOPOLOGY:  linear
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Db  1199  GTAATAATCAGATCTTTCCAAGACACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAA  1258
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Db  1259  TGGAGGGCCACAGCCCTTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGTATGGGGGTGT  1318
Qy  4491  TGGAGGGCCGCCATGCCTCTCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGATGTGGGGTGT  4550
Db  1319  ATGATGGAGGGGAGCCACACTGCTCTATGGGGAGCCCAGGAAACTGCTCACCCAAGATTGGG  1378
Qy  4551  ATGATGGAGGGGAGCCACAGTGCCTATGGGGAGCCCAGGAGCTGCTCACCCAAGATTTGG  4610
Db  1379  TGCAGGAAAACTACCTGGAGTACCGGCAGTAATCCGCGCTATGAGT  1438
Qy  4611  TGCAGGAAAAGTACCTGGAGTAC-GGCAGTGCCCGGCACACGCCTATGAGT  4669
Db  1439  TCCTGTGGGGTCCAAGGGCTCTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGG  1498
Qy  4670  TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTGGAGTATGTGA  4729
Db  1499  TCAGGGTCAATGCAAGAGTTCGCATTGCCTACCATCCCTGCGTGAAGCAGCTTTGTTAG  1558
Qy  4730  TCAGGGTCAGTGCAAGAGTTCGCTTTTCTTCCCATCCCGCGTGAAGCAGCTTTGAGAG  4789
Db  1559  AGGAGGAAGAGGGAGGAGTCTGAGCATGAGTTGCAGCCAGGCGTGTGGGGAAGGGGCAGGGCT  1618
Qy  4790  AGGAGGAAGAGGAGTCTGAGCATGAGTTGCAGCCAGTGGCCAAGGCCAGTGGGAGGGGACTGGGGC  4849
Db  1619  GGGCCAGTGCATCTAACAGCCCTGTGCAGCAGCTTCCCTGCCTCGTGTAACATGAGGCC  1678
Qy  4850  CAGTGCAC-CTTCCAGG-GCCGGCCGTCCAGCAGCTTCCCCCGTCTGTGTGACATGAGGCC  4907
Db  1679  CATTCTTCACTCTGTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTTGT  1738
Qy  4908  CATTCTTCACTCTG---AAGAGAGCGGTCAGTGTTCTCAGTAGTAGTTTCTGTTCTAT  4963
Db  1739  TGGATGACTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATGTTCCTTTT-AA  1797
Qy  4964  TGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGTTTGGAATTGTTCAAATGTTTTTTTTAA  5023
Db  1798  TGGATGGTGAATTAACTTCAGCATCCCAAGTTTATGAATCGTAGTTAACGTATATTGCTG  1857
Qy  5024  GGGATGGTGAATGAACTTCAGCATCCCAAGTTTATGAAATGACAGCAGTCACACAGTTCTG  5083
Db  1858  TTAATATAGTTAGGAGTAAGAGTCTTGTTTTTATTCAGATTGGGAAATCCGTTCTATT  1917
Qy  5084  TGTATATAGTTAAGGGTAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATT  5143
Db  1918  TTGTGAATTGGGACATAATAACAGCAGTTGGA-GTA---AGTATT-T-AGAAGTGTGAAT  1971
Qy  5144  TTGTGAATTGGGATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAG  5203
Db  1972  TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATACTTAAATTCCCGCCTTATGCC  2025
Qy  5204  TAAAATAGATGAGATAAAGAACTAAGAATTAAGAGAATTAAGATAGTCAATTCTTGCCTTATACC  5263
Db  2026  TCAGTCTATTCTGTAAAATTAAAATTATATATGCATACCTGGATTTCCTTGGCTTCGT-  2084
Qy  5264  TCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTT  5323
Db  2085  --GAATGTAAGAGAAATTAAAATCTGAATAAATAATTCTTTCTGTTAACTGGCCTCATTTCT  2142
Qy  5324  GAGAATGTAAGAGAAGATAAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTTCT  5383
Db  2143  TCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATACTAGG  2202
Qy  5384  TCTCCATGCACTGAGCATCTGCTCTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAG  5443
Db  2203  GTAAGCCAGACACACCTACCCGATAGGGTGTATTAAGAGTCTAGGAGC-GCCGGTCATATAA  2261
Qy  5444  GTAAGCCAGACTCACTGAGCATCCCACCCATAGGGTCGTA-GAGTCTAGGAGCTGCGAGTCACGTAA  5502
Db  2262  TTAAGGTGACAAGAGTGTCCTCTAA-GATGTAGGGGAAAA-GT-A-ACGAGTGTGGGTATG  2317
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US-08-190-411A-1.rni

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CC    MOLECULE TYPE: genomic DNA
CC    FEATURE:
CC    NAME/KEY: MAGE-41 gene
SQ    Sequence 2531 BP; 607 A; 593 C; 701 G; 630 T; 0 other;

Query Match       24.7%;   Score 1399;  DB 7;  Length 2531;
Best Local Similarity  84.3%;  Pred. No. 0.00e+00;
Matches  2068;  Conservative  0;  Mismatches 327;  Indels  57;  Gaps  27;
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Db      1 GGATCCAGGCCCTGCCTGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCC   60
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Qy   3256 GGATCCAGGCCCTGCCTGCCGGAGAAAATATAAGGGCCCTGAGTGAGAACAGAGGGGTCATCC 3315

Db     61 ACTCCATGAGAGTGGGGACTCACAGAGTCCAGAGTCCACCCTCTTGATGGCACTGAGGGAC  120
          ||| || ||||||||||| |||||||||||||||| || |||| |||||| |  |||||||
Qy   3316 ACTGCATGAGAGTGGCGTGCTGCCGTGCGTGCACCCTCCTGGTAGCACTGAGAAGC 3375

Db    121 CGGGGTGTGTCTTACAGTCTGCACCCTAAGGCCCATGAGTTCCTCTCCTAGGAGTCCA  180
          ||| | |||||||  || | ||||||||||||||||||||||||||||||| ||||||
Qy   3376 CAGGGCTGTGCTGCCAGCAGTGAGGCCTTGGCTGTCACCCTAAGGCCCCACCCTGGGAGCTCCA 3435

Db    181 GGAACAAGGCAGTGAGGCCTTGGTCTGTCTCAGGTTACGAGCAGAGAGGATG  240
          |||| ||||| ||||||||||||||||||||||||||| ||||||||||||
Qy   3436 GGAACAAGGCAGTGAGGCCTTGGTCTGCTGAGACAGTATCCTCAGGTATCCTCAGGAGAGATG 3495

Db    241 CACAGGCTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA  300
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Qy   3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555

Db    301 CAAGCACATAGGACTCCAAAGAGTCTGGCTCACCTCCCTACCACTCTGCAGAAT  360
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Qy   3556 CAGGCACACAGGACTCCACAGAGTCTGGCCTGGCTAC-GCAGGTGCCGCACCCTATGAGT 3615

Db    361 CGACCTTCTGCTGGCCCGCTATACCCTGAGGTGCTTCTCCTTCCTCTTCAGGTTCTGA  420
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Qy   3616 CGACCTTCTGCTGGCCGGCGTGACCCCTGAG-TACCCTCACTTCCTCTTCCAGGTTTTCA 3674

Db    421 GCACAGCAGGCCAACCG-GAG-ACAGATTCCCTGGAGGCCACAGGAGCACCCAAGGAGA  478
          ||  |||||||||||| ||| |  ||||||||||||||||  |||||||||||||||||
Qy   3675 GGGGACACAGGCCAACCCAGGAGGAGTCCCTGGAGGCCACAGCAGGAGCACCCAAGGAGA 3734

Db    479 AGATCTGTAAGTAAGCCTTTGTTAGAGCCTTAAGATTTGGTTCTCAGCTGGTCTCTC  538
          |||||||||| |||||||||| ||| |||||  ||| ||||||||||||| || |||
Qy   3735 AGATCTGTAAGTGAAGTCTGTTGTTTCAGTTCTCAGCTGGCCTCTC 3794

Db    539 ACATGTCCCCTCTCCGTAGGCCTGTGGGTCCCAGTCTTTGCCTGCCACTCT  598
          ||| ||||||||||||||||||||  || ||||||||||||||||||||||
Qy   3795 ACACTCCCCTCTCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCTGCCCACACTCC 3854

Db    599 TGCCTGCTGCCCTGAGCAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGC  658
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy   3855 TGCCTGCCCCTGACGAGAGGTCTCTGAGAGTCTCTGACTGCAAGC 3914

Db    659 CTGAGGAAGGCCAGGTTGAGGCCCAAGAGAGGCCTGTGGGTGCGCAGGCTCCTA  718
          ||||||||||||||  |||| |  ||| ||||||||| || |||||||| ||||
Qy   3915 CTGAGGAAGGCCAGGTTGAGGCCCAACAGGGCCTGTGTGTGTGCAGGCTGC-- 3972

Db    719 CTACTGAGGAGGAGAGGGCCTGCTGCCTGGTCCCTGGCACCCTGG  778
          |||||||||||||||| |||||| ||||||||||||||||||||||
Qy   3973 C--------CA-------C---CTCCCTCCTCCTCCCTGGGCACCCTGG 4010

Db    779 AGGAAGTGCCTGCTGAGTCCAGCAGGCCTGAGGGAGCCCTGCCT  838
          ||||| ||||||| || || ||||||||||||||||||||||||
Qy   4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCCTCCCCCAGGGGAGCCCTCCCGCCT 4070

Db    839 TACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGGTTCAGCAGCCAAG  898
          ||||||||||||||||||||||| || |||||||||||||||||| |||||||||||||
Qy   4071 TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGGGGTTCCAGCAGCCAGTA 4130

Db    899 AAGAGGGGCCAAGCACCTCGCCTGGTTCCGGAGCAGCACTCAGTA  958
          ||||||||||||||||||| ||||||||| ||||||||||||||||
Qy   4131 AAGAGGAGGGCCCAAGCAACCTCTTGATCCTGGAGTCCGAGCAGTAATCACTA 4190

Db    959 ACAAGGTGGATGAGTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGTCA 1018
          | |||||| ||| |||||| ||| |||||  |||||||| || |||||||||||||||
Qy   4191 AGAAGGTGGCTGATTTGGTTGGTTTCGCTCCTCAAATATCGAGCCCAGGAGGCCAGTCA 4250

Db   1019 CAAAGGCAGAAATGCTGGAGAGTCATCAAAAATTACAAGCGCTGCTTCCTGTGATCT 1078
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Qy   4251 CAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCT 4310

Db   1079 TCGGCAAAGCCTCCAGTCCCTGAACGATCTTTGGCATTGACGTGAAGAAGTGACC 1138
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4311 TCGGCAAAGCCTCTGAGTCCTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGAACC 4370

Db   1139 CCACCAGCAACACCTACACCCTTGTCACCTGGCCTTCCTATGATGCCTGCTGG 1198
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Qy   4371 CCACCGGCCACTCCTATGTCCTTGTCACCTGGCCTAGTCTCTCTGCCTATGATGATGCCCTGCTGG 4430

Db   1199 GTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATGCAA 1258
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Qy   4431 GTGATAATCAGATCATGCCCAAGACAGGCCTTCCTGATAATTGTCCTGGTCATGATTGCAA 4490

Db   1259 TGGAGGGGCACAGCCCCCTTGAGGAGGAAAATCTGGAGGAGCAGGCCCCAGGAAAACTGCTCAGGAGGATGGGT 1318
          ||||| || ||| ||||||||| || |||||||||||||||||| ||| | ||||||||||| |||||||||
Qy   4491 TGGAGGGCCGGCCCCATGCTCCTGGAGGAAAATCTGGAGGAGCAGGCCCCAGGAAATCTGGGAGAGCTGTGAGTGTGAGGTGT 4550

Db   1319 ATGATGGGAGGGAGCCACACTGTCTATGGGGAGACCCCAGGAAACTGCTCACCCAAGAATTGGG 1378
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Qy   4551 ATGATGGGAGGGAGCCACAGTGCCTATGGGGAGCCCCAGGAAATCTGGGAGAGCTGCTCACCCAAGAATTGG 4610

Db   1379 TGCAGGAAAACTACCTGGAGTCTGAGACATGAGTTCAGCTGATAATCCTGCGCGCTATGAGT 1438
          ||||||||||||| |||||||||| || || |  |||| | |||||||| | ||| | |||
Qy   4611 TGCAGGAAAGTACCTGGAGTAC--GCAGGTGCCGCACCAGCTGCAGAGTTGCAGCAGCCTATGAGT 4669

Db   1439 TCCTGTGGGGTCCAAGGGTCTGAAACCAGGTGAAAGTCCTGGAGTCCTGGAGTCCTGAGACATGTGG 1498
          ||||| ||||||||||||| | || ||||||||| || || ||||||||||||| |||||||||||
Qy   4670 TCCTGTGGGGTCCAAGGGCCCTGAAACCAGCCAGCTCGCTCCTGCCCGCTCGTGTAACATGTGA 4729

Db   1499 TCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCTCCTCGCTGGAAGCAGCTTTGTTAG 1558
          |||| || |||| | ||||| |||||||| ||||||||||| | |||||||||||||||| |
Qy   4730 TCAAGGTCAGTGCAAGAGTTCGCGTTTCTTCCCAGTCCCGCTGCGTGAAGCAGCTTTGAGAG 4789

Db   1559 AGGAGGAAGGGAGGAGTCTGAGCAGTTCGCAGACATCAGAGTTGCAGCCAAGGGCTGTGGGGAAGGGCCAGGGCCT 1618
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||| |||| || |||||
Qy   4790 AGGAGGAGGGAGGGAGTCTGAGCAGTTCGCAGACATGAGTTCAGCCGGTCAGTGGGAGGGGACTGGGC 4849

Db   1619 GGGCCAGTGCATCTAACAGCCCGTGCAGCAGCTTCCCTTGCCTCCTGGTAACATGGAGGCC 1678
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Qy   4850 CAGTGCAC-CTTCCAGG-GCCGCGGTCCAGGCTCCCGCTGCCTCCCTGCCTGTGACATGAGGGCC 4907

Db   1679 CATTCTTCACTCTGTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGTTTCTATTTTGT 1738
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Qy   4908 CATTCTTCACTCTG-----AAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTGTCTAT 4963

Db   1739 TGGATGACTTGGAGATTTATCTCGTTCCTTTACAATTGTTGAAATGTTCCTTTT-AA 1797
          |||||| ||||||| |||| || |||||||| | |||||| |||| |||||| ||
Qy   4964 TGGGTGACTTGGAGATTTATCTTGTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTTAA 5023

Db   1798 TGGATGGTTGAATTAACTTCAGCATCCAAGTTATGAATCCAGTTAACGTATATTGCTG 1857
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Qy   5024 GGGATGGTTGAATGAACTTCAGCATCCAAGTTATGAATGACAGCAGTTCTG 5083

Db   1858 TTAATAGTTAGGAGTAAGAGTCTGTTTTTATTCAGATTGGGAAATCCGTTCTATT 1917
          ||  ||||| |  |||| || ||||| ||| |||||| ||||||||  |||||||
Qy   5084 TGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCTATT 5143

Db   1918 TTGTGAATTTGGACATAATAACAGCAGTGA--AGTATT-T-AGAAGTGTGAAT 1971
          ||||||||||  ||| || || |||||||| |  |  | | |  |  |||||
Qy   5144 TTGTGAATTGGGATAATAACAGCAGTGGAATAAGTACTTAGAAAATGTGAAAAATGAGCAG 5203

Db   1972 TCACC--G-TGAAATAG-GTG--AGATAAATTAAAAGATACTTAATTCCCGCCTTATGCC 2025
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Qy   5204 TAAAATAGATGAGATAAAGACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACC 5263

Db   2026 TCAGTCTATTCTGTAAAATTTAAAAAATATTAAAAATATATATGCATACCTGGATTCCTTGGCTTCGT- 2084
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CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 561220lman D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 17:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2305 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-51 gene
SQ Sequence 2305 BP; 549 A; 568 C; 611 G; 577 T; 0 other;

Query Match   21.6%; Score 1225; DB 7; Length 2305;
Best Local Similarity 84.1%; Pred. No. 0.00e+00;
Matches 1956; Conservative 0; Mismatches 299; Indels 72; Gaps 32;

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Db     1 GGATCCAGGCCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTC   60
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Qy  3256 GGATCCAGGCCCAGGAGAAAATATRAGGGCCCTGCGTGAGAACAGAGGGGTCATCC     3315

Db    61 ACCCCAAGAGGTGGAGACCTCACAGATTCCAGCTACCCTCCTGTTAGCACTGGGGGGC    120
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Qy  3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCTCCTGGTAGCACTGAGAAGC       3375

Db   121 TGAGGCTGTGCTTGCAGTCTGCACCCTGAGGGGCCATGCATTCCTTCCAGGAGGTCTCCA  180
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Qy  3376 CAGGGCTGTGCTTGCCGGTCTGCACCCTGAGGGGCCGTGAGTTCCTCTCTGGAGCTCCA   3435

Db   181 GGAAACAGACACTGAGGCCTTGGTCTGAGGGCCGTGCCCTGAGGTCACAGAGCAGGAGGAGA 240
         |||| |  ||  ||| ||||||||||  ||  |||| | ||  ||||||||||||||||
Qy  3436 GGAACCAGGCAGGTGAGGCCTTGGTCTGCTGAGACAGTATCCTCAGGTCACAGAGCAGGAGA-- 3493

Db   241 TGCAGACGTCTAGTGCCAGCAGTGAACGTTGCCTTGAATGCACACTAATAGGCCCCATC   300
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Qy  3494 TGCACAGGG-T-GTGCCAGCAGTGAATGTTGCCCTGAATGCACCACCAAGGGCCCACCT   3551

Db   301 GCCCCAGACATATGGACTCCAGACGCACCTGGCCTCACCCTCTCACTGTCTGTCCTGC    360
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Qy  3552 GCCAGCAGGACACATAGGACTCCACAGAGTCTGGCCTCACC-TCCCTACTGTCAGTCCTGT   3610

Db   361 AGAATGCAGCCTCTGCTTGCTTG-TGTACCCTGAGGTGCCCTCACTTTTCTTCCTTCAGGT   419
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Qy  3611 AGAATCGAACCTCCTGCCTCGGGCCTGTACCCTGAG-TACCCTCCTCACTTCCCTTCAGGT   3669

Db   420 TCTCAGGGGACAGCTGACCAGGTCACCAGAGGATCACCAGGAGCCCCAGGAGGCCCT    479
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Qy  3670 TTTCAGGGGACAGGC----CA--A-C-CCAG--AGGAC---AGGATYCCCTGAGGCCCAC   3716

Db   480 AGAGGAGCACCAAAGAGAGAAGAGTCTGTAAGTAAGCTCTTTGTTGAGGCCTTCCAAGGTTCAG  539
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Qy  3717 AGAGGAGCACCAA-GGAGAAGATCTGTAAGTAAGCTGTAAGTAGGCCTTCCAAGGTTCAG     3775

Db   540 TTTTTAGCTGAGCGTCTTCACATGCTCCGTGTTGCGGTGACCAGTCGTCATGTCTCTTGAGCAG 599
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Qy  3776 TTCTCAGCTGAGCCCTCCACACTCCTCCCCAGGTGTCTTCATTGCC               3835

Db   600 CAGCTCCTGCGCCCACACTCCTGCCGTTGCCAGCAGTCGTCTTGAGCAG           659
         |||||||||| ||||||||||||||| |||| |       |  |||||||
Qy  3836 CAGCTCCTGCCCCACACTCCTGCCGTCGCCCTGCGCGAGAGTCATCATGTCTCTTGAGCAG 3895

Db   660 AAGAGTCAGCACTGCAAGCCTGAGGAGGCCTTGACACCCCAAGAAGAG-CCCTGGGCCTG   718
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Qy  3896 AGGAGTCGCACTGCAAGCCTGAGGAGGCCCAACAAGAAGAGCCCTGGGCCTG         3955
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RESULT 10
ID US-08-299-849B-17 STANDARD; DNA; UNC; 2305 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 17, Application US/0829984 9B.
CC Sequence 17, Application US/0829984 9B
CC Patent No. 5612201
CC GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
r
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   APPLICATION NUMBER: 9-JULY-1991

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Qy  5264 TCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATAACCTGGATTCCTTGGCTTCTTT  5323
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Db  2085 --GAATGTAAGACAAAATAAATCTGAATAAATAATTCTTTCGTGTTAACTGGCTCATTTCT  2142

Qy  5324 GAGAATGTAAGACAAAATAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTCT   5383
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Db  2143 TCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGATTAGTAGTGAGAATACTAGG   2202

Qy  5384 TCTCCATGCACTGAGCATCTGCTTTTGGAAGGCCCGGGTAGTAGTGGGATGCTAAG     5443
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Db  2203 GTAAGCCAGCACACACCACCTACCGATAGGGTATTAAGAGATCTAGGAGC-GCGGTCATATAA 2261

Qy  5444 GTAAGCCAGACTCATACCCACCCATAGGGTCGTA-GAGTCTAGGAGCTCAGTCACGTAA   5502
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Db  2262 TTAAGGTGACAAGATGTCCCTCTAA-GATGTAGGGGAAA-GT-A-ACGAGTGTGGGTATG   2317

Qy  5503 TCGAGGTGGCAAGATGTCCTCTAAAAGATGTAGGGAAAAGTGAGAGGGGTGAGGGTGTG   5562
         | ||| || |||||||| ||||||  |||||||||  | || |  ||| |||| || |||
Db  2318 GGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCCTGTG-TGGGGCCTTTTGGGCTTTGG   2376

Qy  5563 GGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTCCCTGAGCCCTGGGCCTTTGG  5622
         |||||| |||||||||||| |  ||||| |  ||||||    ||| ||  |||||||||||
Db  2377 GAAACTCCCATTTTCTTCTGAGGGATCGATCTGATTCTAATGAAGCTTGGTGGTCC      2428

Qy  5623 GAAACTGCAGTTCCTTCGTGGGGAGCTGATTGTAATGATCTTGGGTGGTGGATCC       5674
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Db 719 GTGGGTGTGCACGGCTGCCACTACTGAGGAGCAGGAGGCTGTGTCCTCCTCCTCCTCTG 778
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Qy 3956 GTGTGTGTGCAGGCTGCCAC-----------------CT---CCTCCTCCTCCTCTG 3994

Db 779 GTCCCAGGCACCCTGGGGGGAGGTGCCTGCTGCCCACTGCTGGGTCACCAGGTCCTCTCAAGAGTCCT 838
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Qy 3995 GTCCTGGGCACCCTGGGGGGAGGTGCCCACTGCTGGGTCAACAGATCTCCCCAGAGTCCT 4054

Db 839 CAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACTCTATGGAGGCAATCCATTAAG 898
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Qy 4055 CAGGGAGCCTCCGCCTTTCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAG 4114

Db 899 GGCTTCCAGCAACCAAGAGAGAGGAGGGGCCAAGCACCTCCCCTGACCCAGAGTCTGTGTTC 958
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Qy 4115 GGTTCCAGCCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC 4174

Db 959 CGAGCAGCACTCAGTAGAAGGTGGTCGACTTGATTCATTTTCTGCTCCTCCAAGTATTAA 1018
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Qy 4175 CGAGCAGCAGTAATCACTAGAAGAGTGGTCGTGATTTGGTTTGCTCGTCCTCCAAATATCGA 4234

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Qy 4235 GCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCAC 4294

Db 1079 TGCTTTTCCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCAGCTGGTCTTTGGCATTGAC 1138
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Qy 4295 TGTTTTTCCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCAGCTGGTCTTTGGCATTGAC 4354

Db 1139 GTGAAGGAAGCGGACCCCACCAACACTACACCCTGTCACCTGCCTGGGACTC--C 1196
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Qy 4355 GTGAAGGAAGCAGACCCCACCGCCACTCCTATGTCCTGTCACCTGCCTAGTCTCTCC 4414

Db 1197 TATGATGGCTCGGTGGTT--TAATCAGATCATGCCCAAGACACGGGCCTCCTGATAATCGTC 1254
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Qy 4415 TATGATGGCTCGCTGGTGATAATCAGATCATGCCCAAGACAGCGCTTCCTGATAATTGTC 4474

Db 1255 TTGGGCATGATTGCAATGGAGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTG 1314
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Qy 4475 CTGGTCATGATTGCAATGGAGGCCGGCCATGCTCCTGAGGAGAAATCTGGGAGGAGCTG 4534

Db 1315 GGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGAGCTCCAGGAAGCTG 1374
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Qy 4535 AGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTATGGGAGCTCCAGGAAGCTG 4594

Db 1375 CTCACCCCAAGATTTGGTGCAGGAAAACTACCTGGAGTACCGAGTGCCCAGGATC 1434
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Qy 4595 CTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGAGTGCCGGACAGTGATC 4654

Db 1435 CCATATGCTATGAGTTACTGTGGGGTCCAAGGCACTCGCTG------CT---TGAAAG 1484
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Qy 4655 CCGCACGCTATGAGTTCGCTGCTGGGTCCAAGGCCCTATGTGAAAG 4714

Db 1485 TACTGGACCACGTGCTGCAGGGTCAGGGTCAATGCCAAGAGTTCTCATTCTCCTACCATCCCTGCATG 1544
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Qy 4715 TCCTTGATGTGATCAAGGTCAGTCAGTGCAAGAGTTCGCTTTGTTTCCATCCCCTGCCTG 4774

Db 1545 AAGCAGTTTGAGAGAGGAGGAGAAGAGGAGTCTGAGCATGAGGCTCGCAGCCAAGGCCACTG 1604
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Qy 4775 AAGCAGTTTGAGAGAGGAGGAGAAGAGGAGTCTGAGCATGAGGCTCGAGTTGCAGCCAAGGCCAGTG 4834

Db 1605 CGAGGGGGCTGCGGCCAGTGACTTGGCCAGTGACTTCCCCGTCCCATCCCTGCCTTAA 1664
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Qy 4835 GGAGGGGGACTGGCCAGTGACTTCCCAGGCCGGTTCCCCGTCCCCATCCCCGCCCTGC- 4893

Db 1665 TGTGACATGAGGCCCATTCTTCTCTCTTTGAAGAGGAGCAGTCAACATTCTTAGTAGTGGG 1724
         |||||||||||||||||||| |||| |||| |||||||| |||||| ||| |||||||
Qy 4894 TGTGACATGAGGCCCATTCTTCTTCACTCT--GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGG 4951

Db 1725 TTTCTGTTCTATTGGATGACTTTGGAGATTTGTCTTTGTTTTCCTTTGGAATTGTTCAAAT 1784
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Qy 4952 TTTCTGTTCTATTGGTGACTTCTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAAT 5011

Db 1785 GTTCCTTTTAATGGG-TGGTTGAATGAATGAACTTCAGCATTCAAATTTATGAATGACAGTAGT 1843
         |||| ||| |||||| ||||||| ||||| || |||||||||||||||||||| ||||||||||||
Qy 5012 GTTTTTTTTTAAGGATGGTGTTATATAGTTTATATAGTTTAGGAGTAAGACTCAGCATCCAAGTTATGAATGAATGACAGCAGT 5071

Db 1844 CACACATAGTGCTGTTTATATAGTTTATATAGTTTAGGAGTAAGACTC 1903
         ||||| || |||| ||||||||||||||||||| |||||||||||||
Qy 5072 CACACA--GTTCTGTGTATAGTTTAAGGTGTAAGAGTCTTGTGTTTTATTCAGATTGGG 5129

Db 1904 AAATCCATTCCATTTGTGAATTGGACA-TAGTTACAGCAGTGAA-TAGTATTCATT 1961
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Qy 5130 AAATCCATTCATTTTGTGAGATTGGGATAATAAACAGCAGTGAATAGTACTTAGAAATG 5189

Db 1962 T-AGAAATGTGAA-TGAGC-AGTAAAAACTGATGAGATAAAGAAAATAAAAAGATATTAAT 2018
         | ||||| || |||| | |||||||||| || |||||| || || |||||||||||
Qy 5190 TGAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAGAAAATAAGAGATAGTCAAT 5249

Db 2019 TCTTGCCTATAC-TCAGTCTATTCCGTAAAAATTTTTTTTAAAAATGTGCATACCTGGA 2077
         |||||| |||| |||| |||||||||||| |||||||||| | || |||||||||||||
Qy 5250 TCTTGCCTTATACCCAGTCTATTCCGTAAAAATTTTAA--AGATATATGCATACCTGGA 5307

Db 2078 TTTCCTTGGCTTCTTTGAGAATGTAAGACAAATTAAATCTGAATAAATCATTCTCCCTGT 2137
         ||||||||||||||||||||||||||||| ||| |||||||||||| |||||| ||||||
Qy 5308 TTTCCTTGGCTTCTTTGAGAATGTAAGACTACTGAATAAATCTGAATAAAGAATTCTTCCTGT 5367

Db 2138 TCACTGGCTCATTTATTCTCTATGCACTGAGCACTCACCCTACCACAGGGTAGTAAGTCTAGGA 2197
         |||||||||||||| ||||||||||||||||||||| |||| || |||||||||||||||||
Qy 5368 TCACTGGCTCTTTTCTCTTGAGAATGTAAGACTCGAGCCATCTGCTTTTGGAAGGCCCCTGGGTTAG 5427

Db 2198 TAGTGGAGATGCTAAGGTAAGCACCAGACTCACCCTACCACCCACCCATACCCACCCACCCATCAGGTAGTAAGTCTAGGA 2257
         |||||||||||||||||||||||||| ||| | ||||| || |||||||||||| || | |||||||||||||||||
Qy 5428 TAGTGGAGATGCTAAGGTAAGCACCAGACTCATCATACCCCATACCCCACCCATAGGGGTCGTAGAGTCTAGGA 5487

Db 2258 GCAGCAGTCATATAATTAAGGTGGAGATGCCCCTCTAA-GATGTAG 2303
         |||||||||||| ||||||||||||||||| ||||||| ||||||
Qy 5488 GCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGAGTGTAG 5534

RESULT 11
ID   US-08-299-849B-16 STANDARD; DNA; UNC; 2226 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 16, Application US/08299849B.
CC   Sequence 16, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:

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CC      APPLICATION NUMBER:  07/807,043
CC      FILING DATE:  12-DECEMBER-1991
CC    PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:  07/764,364
CC      FILING DATE:  23-SEPTEMBER-1991
CC    PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:  07/728,838
CC      FILING DATE:  9-JULY-1991
CC    PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:  07/705,702
CC      FILING DATE:  23-May-1991
CC    ATTORNEY/AGENT INFORMATION:
CC      NAME:  Hanson, No. 5612201man D.
CC      REGISTRATION NUMBER:  30,946
CC      REFERENCE/DOCKET NUMBER:  LUD 5355
CC    TELECOMMUNICATION INFORMATION:
CC      TELEPHONE:  (212) 688-9200
CC      TELEFAX:  (212) 838-3884
CC    INFORMATION FOR SEQ ID NO:  16:
CC    SEQUENCE CHARACTERISTICS:
CC      LENGTH:  2226 base pairs
CC      TYPE:  nucleic acid
CC      STRANDEDNESS:  single
CC      TOPOLOGY:  linear
CC    MOLECULE TYPE:  genomic DNA
CC    FEATURE:
CC      NAME/KEY:  MAGE-5 gene
SQ    Sequence 2226 BP: 539 A; 542 C; 582 G; 563 T; 0 other;

Query Match   16.6%;   Score 943;   DB 7;   Length 2226;
Best Local Similarity  84.8%;   Pred. No. 0.00e+00;
Matches  1320;   Conservative   0;   Mismatches  209;   Indels  28;   Gaps  17;

Db    687  CTCCTCTGTCCAGGCACCCTGGGGAGTGCCTGCTCGTGGGTCACCAGGTCCTCTCA  746
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Qy   3987  CTCCTCTGTCTGGGCACCCTGGGCACCCTGAGGAGTGCCCACTGCTCAACAGATCCTCCCC  4046

Db    747  AGAGTCCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGCCATCCTCACTCCTATGGAGGCAAT  806
           ||||||||||||||||| | ||||| | |||||| |||||||  |||||||
Qy   4047  AGAGTCCTCAGGGAGCCTCCGCCTTCCCCACTACCTACCACTCACTGCGACGAGGCAAC  4106

Db    807  CCATTAAGGGCTCAGCAACCAAGAAGGAGGGGCCAAGCACCTCCCCTGACCCCAGAGT  866
           ||||| || ||||| |||| |||||||||||||||||| ||  ||||||||
Qy   4107  CCAGTGAGGGTTCCAGCAGCCGTGAAGAGCGTGAAGAGGGGCCAAGCACCTCTTGTATCCTGGAGT  4166

Db    867  CTGTGTTCCGAGCAGCACACTCAGTAAGGAGGTGGCTGACTTGATTCATTTTCTGCTCCTCA  926
           |  ||||||| |||||||||| || |||||||||||  ||| ||  |||||||||||
Qy   4167  CCTTGTTCCGAGCAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTTGGTTTTCGTCTCCTCA  4226

Db    927  AGTATTAAGTCAAGGAGCTGGTCACAAGGCAGAAATGCTGGAGAGCGTCATCAAAAATT  986
           | ||| | |||| ||||||||||||||||||||||||||| |||||||| ||||||||
Qy   4227  AATATCGAGCCAGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATT  4286

Db    987  ACAAGCCGCTGCTTTCCTGAGATCTTCGGCAAAGGCTCCGAGTCCTTGCAGCTGGTCTTTG  1046
           |||||  ||||| ||||||||||||||||||||| |  |||| || | |||||||||||
Qy   4287  ACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGGCTCCTGAGTCCTTGCAGCTGGTCTTTG  4346

Db   1047  GCATTGACGTGAAGGAAGCGGACCCCACCAGCAACACCCTTGTCACCATGCCCAAGACGGGCTCCTG  1106
           |||||||||||||||||||||||| |||| ||| |  |  |||||||| || |||||
Qy   4347  GCATTGACGTGAAGGAAGCGGACCCCACCAGCAACACCCTTGTCACCTGCAGCTGGTCTTTG  4406

Db   1107  GACTCCTATGATGGCCTGCTGGTTGATAATGAGGGCAAATGCGTCCCTGAGGAGAAAATCTGG  1166
           |||| | |  |  |||||||||||  |  |  ||||||||||||||||||||||||||
Qy   4407  GTCTCCTCCT-ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGCAGGCTTCCTG  4465

Db   1167  ATAATCGTCTTGGGCATGATTGCAATGGACGGGCAAATGCGTCCCTGAGGAGAAAATCTGG  1226
           ||||| |||| ||||||| | || |||| ||||  |||||||||||||||||||||||
Qy   4466  ATAATTGTCTTGGTCATGATTGCCATGATTGCCTGAGGGGCCGCCATGCTCCTGAGGGGAAATCTGG  4525

Db   1227  GAGGAGCTGAGTGCAGTGGAGTGTATGTTGGGAGGAGGGAGCCAGAGTGTCTGTGGGGAGCCC  1286
           ||||||||||||||| ||||||| ||||||||||||||| || || | |||||||||
Qy   4526  GAGGAGCTGACGTGAGTGTGATGGAGGTGTATGATGGGAGGAGGCACAGTGCCTATGGGGAGCCC  4585
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Db   1287  AGGAAGCTGCTCACCCAAGATTGGTGCAGGAGAAAACTACCTGGAGTACCGGCAGGTACCGGCAGGTGCCC  1346
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Qy   4586  AGGAAGCTGCTCACCCAAGATTGGTGCAGGAGAAAAGTACCTGGAGTAC-GGCAGGTGCCG------C  4644

Db   1347  AGCAGTGATCCCATATGCTATGAGTACTGTGGGGTCCAAGGGCACTCCGTG---------C  1399
           ||||||| |  | ||||| | ||| |  ||  |||||||||||||||||||
Qy   4645  GACAGTGATCCCGACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCTGAAACCAGC  4704

Db   1400  T---TGAAAGTACTGGAGCACGTGCTCAGGGTCAGGTCAATGCAAGAGTTCTCATTCCTACCCA  1456
           |   ||||||||||||||||| || | ||||| | |||||| | |||||||||| |||| ||
Qy   4705  TATGTGAAAGTCCTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTCTCTTCCCA  4764

Db   1457  TCCCTGCGTGAAGCAGCTTTGAGAGAGGAAGAGGAGGAGGTCTGAGCATGAGCTGCAGCC  1516
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy   4765  TCCCTGCGTGAAGCAGCTTTGAGAGAGGAAGAGGAGGAGGTCTGAGCATGCAGCATGCAGCC  4824

Db   1517  AGGGCCACTGCGAGGGGGCTGGCCAGTGCCACCTTCCAGGGCTCCGTCCAGTAGTTTCC  1576
           | ||||| ||||||||||  |||||||||||||||||||||||||||  |||  |||
Qy   4825  AAGGCCAGTGGGGAGGGGGGGGGGGGGGGACTGGGCCAGTGCCAGTGCCCGCGTCCCAGCAGCTTCC  4884

Db   1577  CCTGCCTTAATGTGACATGAGGCCCATTCTCTCTCTTGAAGAGCAGCAGTAGTCAACATTCT  1636
           || |||  | ||||| | ||||||||||||| || |||||||||||||||||||
Qy   4885  CCTGCCTCG-TGTGACATGAGGCCCATTCTTCACTCT--GAAGAGAGCGGTCAGTGTTCT  4941

Db   1637  TAGTAGTCGGTTTCTGTTCTATTGATGACTTTGAGATTTGTCTTTGTTCCTTTTGGAA  1696
           |||| ||||||| |  | |||||||||||||||||| ||||||||| |||  ||||||
Qy   4942  CAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTGTCTCTCTTTTGGAA  5001

Db   1697  TTGTTCAAATGTTTCTTTAAGCA-TGGTTGAATGAACTTCAGCATTCAGAATTTATGAA  1755
           |||||||||||| |||| | ||| ||||||||||||||||||||||| |||  ||||||
Qy   5002  TTGTTCAAATGTTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAA  5061

Db   1756  TGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGTAAGAGTCTTGTTTTTAT  1815
           ||||||||||||||||  ||||||||  |||||||||||||||  |||||||||||||||||
Qy   5062  TGACAGCAGTCACACA--GTTCTGTGTATATAGTTTTAAGGGTAAGAGTCTTGTGTTTTAT  5119

Db   1816  TCAGATTGGAAATCCATTCCATTTGTGAATTGGACA-TAGTTACACAGCAGTGAA-TA  1873
           ||||||||||||||||||||||||||| |||| ||  ||| |  ||| |||| ||
Qy   5120  TCAGATTGGGAAATCCATTCATTTTGTGAATTGGGATAATAACAGCAGTGGGAATAAGTA  5179

Db   1874  AGTATTCATTT-AGAAATGTGAA-TGAGC-AGTAAAACTGATGACATAAAGAAATTAAAA  1930
           | || | |||| ||||||||||| |||| ||||||||||||| ||||||||||||||||
Qy   5180  CTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGA  5239

Db   1931  GATATTTAATTCTTGC-TTATAC-TCAGTCTATTCGGTAAAATTTTTTAAAAAATGTG  1988
           ||| |||||||||||| ||| |  |||||||||||| ||||||||||    |  |||||
Qy   5240  GATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAAATTTTA--AAGTATATATG  5297

Db   1989  CATACCTGGATTTCCTTGGCTCATTAATTCTCTATGCACTGAGCATTTGCTCTGTGGAAGGC  2048
           ||||||||||||||||||| |||||||||||| ||||||||||||||| |||| |||||
Qy   5298  CATACCTGGATTTCCTTGGCTCTTTTGAGAATGTAAGTGAAGTGTAAGAGAAATTAAATCTGAATAAATCA  5357

Db   2049  TTCTCCCTGTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTGCTCTGTGTGGAAGGC  2108
           ||||||||||||||||||||| ||| | || | |||||| |||| ||||||||||||||
Qy   5358  TTCTTCCTGTTCACTGGCTCTTTTCCTTTCCATGCACCATGCAGCACTGCTTTTTGGAAGGC  5417

Db   2109  CCTGGGTTAAATGTGGGAGATGCTAAGGTAAGCCACAGTAAGGTGGAGAGATGCCCCTCTAA-GATGTAG  2168
           ||||||| ||| |||| |||||| |||||||||||||||| || ||| ||||||||| |||
Qy   5418  CCTGGGTTAGTAGTGGGAGATGCTAAGGTAAGCCAGACACTCATACCCCACCCATAGGGTCGTA  5477

Db   2169  AGTCTAGGAGCAGCAGTCATAATAATTAAGGTGGAGAGATGCCCTCTAA--GATGTAG  2224
           |||||||||||||| ||||||||| |||||||||||||||||||| | ||
Qy   5478  GAGTCTAGGAGCTGCAGTGCAGTCACGTAATCAGGTGCAAGAGTGTCCTCTAAAGAATGTAG  5534
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RESULT   12
ID    US-08-299-849B-11 STANDARD;  DNA; UNC; 1640 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 11, Application US/08299849B.
CC    Sequence 11, Application US/08299849B
CC    Patent No. 5612201
CC    GENERAL INFORMATION:
```

CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5612201man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 11:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 1640 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: cDNA MAGE-3
SQ   Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match   14.3%;   Score 811;   DB 7;   Length 1640;
Best Local Similarity   81.7%;   Pred. No. 0.00e+00;
Matches 1257;   Conservative 0;   Mismatches 248;   Indels 33;   Gaps 15;

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Db   107 GCCAGTGGGTCTCCATTGCCCAGCTCCTGCCCACACTCCCGCCTCGTGCCCTGACCAGAG   166
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Qy  3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTCGTGCCCTGCCCAGAGAG 3875

Db   167 TCATCATGCCCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAGGCCTTGAGGCCC    226
          |||||||| |||||||||| ||||||| || |||||||| |||| |||||||||||||||||
Qy  3876 TCATCATGTCTTGAGCAGCAGGAGAGTCTGCACTGCAAGCCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935

Db   227 GAGGAGGAGCCCTGGGCCTGGGCCTGTGTGTGTGTGCAGGCT                   286
          | ||||||||||||||||||||||| || ||             |  ||  |     | |     ||
Qy  3936 AACAAGAGGGCCCTGGGCCTGGCCTGTGTGTGTCAGGGCT---GC--C-----A-C-----CT- 3977

Db   287 CCTCCTCCTTCTTACTCTAGTTGAAGTCACCCTGGGGGAGGAGTGCCTGCTGCCGAGTCAC   346
          ||||| ||| || ||  |||| ||| |||||| |||||| ||||||| ||||||||| |||
Qy  3978 CCTCCCCTCT-C--CTCTGGTCCTGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA      4034

Db   347 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCGCCTTCCCACTACCATCAACTACCCTC  406
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||  ||||||
Qy  4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCGCCTTCCCACTACCATCAACTTCACTC  4094

Db   407 TCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAGAGAGGAGGGGCCAAGCACCTTCC    466
          | |||| || ||  |||| || ||||||| |||| | ||||||||||||||||||||| ||
Qy  4095 GACAGAGGCAACCCAGTGAGGGTCCAGCAGCCGTGAAGAGAGGAGGGGCCAAGCACCTCTT   4154

Db   467 CTGACCTGAGTCCGAGTTCCAAGCAGCACTCAGTAGGAGGTGCCGAGTTGGTTCATT     526
          | ||||||||||||  ||||| |||||| |||||| | ||||||||  |||||| ||  |
Qy  4155 GTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTCAAGAGAAGGTGCGTGATTTGGTTGGTT   4214

Db   527 TTCTGCTCCTCAAGTATGCAGCCAGGAGGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG    586
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Qy  4215 TTCTGCTCCTCAAATATCAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG     4274

Db   587 TCGTCGGAAATTGGCAGTATTCTTCCTGTGATCTTCAGCAAAGCTTCCAGTTCCTTGC     646
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Qy  4275 TCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCCTTGAGTCCTTGC   4334

Db   647 AGTTGGTCTTTGGCATCAGCTGATGGAGTGGACCCCATCGGCCCACTGTACATCTTTG     706
          || ||||||||||||| ||| ||| ||| | ||||| |  ||||||||  |  |||  | ||
Qy  4335 AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGAACCCCACCGGCCCACTCCTATGTCCTTG  4394

Db   707 CCACCTGCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGCAGATCATGCCCAAGG   766
          ||||||||| || |||||||| |||| || || ||||||| ||||||  |||||||||||| |
Qy  4395 TCACCTGCTAGGTCTCTCCTATGATGCCCGTGGGTGATAATCAGATCAGATCATGCCCAAGA   4454

Db   767 CAGGCCTCCTGATATCGTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGTCCCCTGAGG    826
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Qy  4455 CAGGCTTCCTGATAATTGTCCTGGTCATCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG 4514

Db   827 AGAAAATCTGGGACGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGGAGACAGTATGT      886
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Qy  4515 AGGAAATCTGGGAGGAGCTGAGTGTGTGATGGAGGTGTATGTGATGATGATGGGGAGGAGCCAGTGCCT 4574

Db   887 TGGGGATCCCAAGAAGCTGCTCACCCAACATTCGTCGCAGGAAAAACTACCTGGAGTACC    946
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Qy  4575 ATGGGGAGCCCAGGAAGCTGCTCACCCAAGAGATTTGGTCGCAGGAAAAAGTACCTGGAGTAC- 4633

Db   947 GGCAGGTCCCGGCAGTCGATCCTGCATGTTATGAATTCCTGTGGGGTCCAAGGGCCCTCG   1006
          |||||||  |||| ||| ||||| ||  |  |||| ||| ||||||||||||||||||||||
Qy  4634 GGCAGGTGCCGGACAGTGATCCCGCACGTATGAGTTCTGTGGGGTCCAAGGGCCCTCG     4693

Db  1007 TTGAAACCAGCTATGTGAAAGTCCTGCCACCATATGTAAAGATCAGTGAGGAGGACCTCACA  1066
          | |||||||||||||||||||||||| | || ||||| | |||| |||  |  ||  |||  |
Qy  4694 CTGAAACCAGCTATGTGAAAGTCCTGAAGTGTCAGTATGTGATCATCAAGGTCAGAGTTCGCT  4753

Db  1067 TTTCCTACCACCCCTGCCGTGAACCTCGTGGTTTGAGAGAGTGGGGAAGAGTGTCTGAGCAC  1126
          ||| | | ||| |||||| ||||  | |   ||| ||| |||||||| |||| | | |||||
Qy  4754 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTCAGGGGGAGAGAGTGGGGAGGAGGAGGAGTCTGAGCAT 4813

Db  1127 GAGTGCAGCAGGCCAGTGGGGAGGGGGTCTGGGCCGCAGTGCACCTTCCGGGCCCATC     1186
          ||||| ||| || |||||||||||||||  ||||||||||  | ||||||||| ||| |
Qy  4814 GAGTTGCAGCCAGGCAAGGCCAGTGGGGAGGGGGGACTGGGCCGCACCTTCCAGGGGCCCGTC   4873

Db  1187 CCTTAGTTCCACTGCCTCCTGTGACGTGAGGCCGTGAGGCCCCATTCTTCACTCTTTGAAGCGAGCAG  1246
          |  |||||||| |||||||||||||| | |||||  |  |||||||||||||||||  |||| | |||
Qy  4874 CAGCAGCTTCCCCTGCCTCCTGTGACATGAGGCCCATTCTTCTCACTCT- -GAAGAGCGGG       4931

Db  1247 TCAGCATTCTTAGTAGTGGGTTCTGTTCTTGTTGTTGGAGATTATTCTTTGTTT        1306
          |||| |||||| ||||| | ||||||||||| |||| ||||||||| |||||| |
Qy  4932 TCAGTGTTCTCAGTAGTAGTTCTGTTCTTCGTTCTTTCATTGGGTGACTTGGAGATTATCTTTGTTC 4991

Db  1307 CCTGTTGGAGTTGTTCAAATGTTCTTTT- -AACCGATGGTTGAATGAGCGTCAGCATCCA   1365
          ||| ||||| |||||||||||||| ||||   || ||||||||||||| | ||||||||||
Qy  4992 TCTTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCA   5051
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SQ  Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match    14.3%;    Score 811;    DB 4;    Length 1640;
Best Local Similarity 81.78%;    Pred. No. 0.00e+00;
Matches 1257;    Conservative   0;    Mismatches 248;    Indels 33;    Gaps 15;

Db  107 GCCAGTGGGCTCCAGCTCCTGCCCACTCCCGCCTGTTGCCCTGACCAGAG 166
            ||| ||||||||  | ||||  |||||||||||||||||||| || ||||
Qy 3816 GCCTGTGGGCTTCATTGCCGCCAATCCAGCTCCTGCCCACTCCCGACGAGAG 3875

Db  167 TCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGAAGGCCTTGAGGCCC 226
            |||||||| |||||||||||||||||| |||||| || |
Qy 3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCGAGCCCTGAGGAGCAGGAGCCCC 3935

Db  227 GAGGAGAGGAGCCCTGGCCCTGGTGGTGCGGCAGGTCCTGCTACTGAGGAGGAGCCTG 286
            | |||||||| ||||| ||||||| |||| || ||   ||  | ||     | |
Qy 3936 AACAAGAGGCCCTGGGCCTGGTGTGGTGTGCCAGGCT--GC--C-----A-C------CT- 3977

Db  287 CCTCCTCCTTCTACTCTAGTTGAAGTCAGGAGTGCCTGCTCCGCCGAGTCAC 346
            |||||||| ||  | |   ||  |  | ||| | ||||| | |  |||||| ||
Qy 3978 CCTCCTCCTCT-C--CTCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAA 4034

Db  347 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCAGCCTACCACTACCCCTC 406
            ||||||||||||||||||||||||||||| | || ||| |||| ||| | |   ||||
Qy 4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCCGCCTTTCCCACTACCATCAACTTCACTC 4094

Db  407 TCTGGAGCCAATCCTATGGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTTCC 466
            |  || |||||| | ||||||||||||||||||||||||||||||||||||||||||  ||
Qy 4095 GACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTT 4154

Db  467 CTGACCTGGAGTCCAGTTCCAAGCAGCACTCAGTAGGAGGAGGTGGCCGAGTTGGTCATT 526
            | |||||||||||| | |||  |||||| |  |   ||||| || || | |||||| |||
Qy 4155 GTATCCTGGAGTCCTTGTTCCGAGCAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTT 4214

Db  527 TTTCGCTCCTCAAGTATGCAGCAGTATTCTTCCTGTGATCTTCAGCAAAGCTTCAGTTCCTTGC 586
            || ||||| ||||  ||| | ||  | |  |  ||||| |||| |||||| |||| |||||||||
Qy 4215 TTCTGCTGCTCCTCAAATATCGAGCCCAGGGAGCCAGTCACAAAGGCAGAATGCTGGAGAGTG 4274

Db  587 TCGTCGGAAATTGGCAGTATTCTTTCCTGTGATCTTCAGCAAAGCTTCAGTTCCTTGC 646
            || ||  aaaatt  a||  |||||||||| | ||| ||||||||  |||||||||||
Qy 4275 TCATCAAAAAATTACAAGCACTGTTTTCCGAGATCTTCGGCAAAGCCCTGAGTCCTTGC 4334

Db  647 AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCCACTTGTACATCTTTG 706
            ||||||||||||||| ||  ||| | ||| | |||||||  |||||||| |||| || |||
Qy 4335 AGCTGGTCTTTGGCATTGACGTGAAGGAAGGCAGACCCCACCACGGCCCACTCCCTATGTCCTTG 4394

Db  707 CCACCTGCCTGGCCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGG 766
            ||||||||||  ||||||||| ||||||||||||||||||| |||||||||||||||||
Qy 4395 TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGA 4454

Db  767 CAGGCCTCCTGATAATCGTCCTGGCCATAGTCGTGTGCCCGGAGG 826
            ||||| ||||||||||| ||||||  ||| |  | |   |||||
Qy 4455 CAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCCATGCTCCTGAGG 4514

Db  827 AGAAAATCGGAGGAGCGAGCTGAGTGGTGTTAGGAGTGTTGGGGGGAGACAGTATGT 886
            || ||||| |||||||| ||||||| | ||  | || ||| | ||||| ||||||  |
Qy 4515 AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGGAGAAAACTACCTGGCCT 4574

Db  887 TGGGGGATCCCAAGAAGCTGCTCACCCAAGATGCTGAGTGAGTACC 946
            ||||| |  ||||||||||||||||||||||| | | | | |||||
Qy 4575 ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTAC- 4633

Db  947 GGCAGGTCCCGCAGTGATCCTGCATGTTATGAATTCCTGTGGGTCCCAAGGGCCCTCG 1006
            |||||||| || | ||||||| ||  | |  | |||||||||||||||||||||||||
Qy 4634 GGCAGGTGCCGGACAGTGATCCCGCACGCTAGGAGTCCTGTGGGTCCCAAGGGCCCTCG 4693

Db 1007 TTGAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGAGGACCTCACA 1066
            |||||||||||||||||||||||| |   || |||||||||||||||||| |  |  ||
Qy 4694 CTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAGAGAGTCGCT 4753

Db 1067 TTTCTACCCACCCCTGCGTGAAGCAGCTTGGAGAGGGGAAGAGGGAGTCTGACAC 1126
            |||  | ||||||| ||||||||||| ||| ||||| ||||||||||||||||| |
Qy 4754 TTTTCTTCCATCCCGCGTGAAGCAGTTTGAGAGGAGGAAGAGGGAGTCTGAGCAT 4813
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Db 1366 GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGGAGTAAGAGTCT 1425
            ||||||||||||||||  ||||||||    |||||| |||||||||||  || |||||||||
Qy 5052 AGTTTATGAATGACAGCAGTCACACA--GTTCTGTGTATATAGTTTAAGGGTAAGAGTCT 5109

Db 1426 TGTTTTTTTACTCAAATTGGAAATCCATTCCATTTGTGATTGTGACATAATAATAGCA 1485
            |||  |||| ||||||||||||||||||||||||  |||| ||||||   |||||||||
Qy 5110 TGTGTTTTATTCAGATTGGGAAATCCATTCCATTCTATTTTGTGAATTGGGA--TAATAACAGCA 5167

Db 1486 GTGGTAAAAGTATTGCTTAAAATGTGAGCGAATTAGCAGTAACATACTACATGAGATAACT 1545
            |||| | ||||| ||  |||||||||| |  | ||| ||||| |||||||| |||||||||
Qy 5168 GTGGAATAAGTACTTAGA-AATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACT 5226

Db 1546 CAAGAATCAAAAGATAGTTGATTCTTGCCTTGACCTGACCTGTAAAATT---- 1602
            ||||||| || | ||||| |||||||||||| | | || | || ||||||
Qy 5227 AAGAAATTAAGAGATAGTCAATTCTTGCCTTTATACCTCAGTGCTATTTCTGTAAAATTTTT 5286

Db 1603 AAACAAATATGCAAACCAGGATTTCCTTGACTTCTTTG 1640
            ||| |||||||||  || ||||||||||| |||||||||
Qy 5287 AAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG 5324
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RESULT  13
ID   US-07-807-043B-11 STANDARD; DNA; UNC; 1640 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 11, Application US/07807043B.
CC   Sequence 11, Application US/07807043B
CC   Patent No. 5342774
CC   GENERAL INFORMATION:
CC      APPLICANT: Boon, Thierry, Van den Eynde, Beno t
CC      TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
CC      TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CC      NUMBER OF SEQUENCES: 16
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Felfe & Lynch
CC         STREET: 805 Third Avenue
CC         CITY: New York City
CC         STATE: New York
CC         ZIP: 10022
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC         COMPUTER: IBM
CC         OPERATING SYSTEM: PC-DOS
CC         SOFTWARE: Wordperfect
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/07/807,043B
CC         FILING DATE: 19911212
CC         CLASSIFICATION: 424
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/764,364
CC         FILING DATE: 23-SEPTEMBER-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/728,838
CC         FILING DATE: 9-JULY-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/705,702
CC         FILING DATE: 23-May-1991
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Hanson, No. 5342774man D.
CC         REGISTRATION NUMBER: 30,946
CC         REFERENCE/DOCKET NUMBER: LUD 253.3
CC      TELECOMMUNICATION INFORMATION:
CC         TELEPHONE: (212) 688-9200
CC         TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 11:
CC      SEQUENCE CHARACTERISTICS:
CC         LENGTH: 1640 base pairs
CC         TYPE: NUCLEIC ACID
CC         STRANDEDNESS: singular
CC         TOPOLOGY: linear
CC      MOLECULE TYPE: cDNA to mRNA
CC      FEATURE:
CC         NAME/KEY: cDNA MAGE-3
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Db  1127 GAGTTGCAGCCAGCCAGTGGGAGGGGGTCTGGGCCAGTGCCACCTTCCGGGGCCCGCATC 1186
          ||||||||||||||||||||||||||| |||||||   |||||||||| |||||||| ||
Qy  4814 GAGTTGCAGCCAGCCAGTGGGAGGGGGACTGGGCCACCTTCCAGGGCCGCGTC        4873

Db  1187 CCTTAGTTCCACTGACCTCCGTGACGTGAGGCCATTCTTTGAAGCGAGCAG         1246
          ||| |||| |||||  |||||| ||||||||||  |||||||| ||| ||||
Qy  4874 CAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT--GAAGAGAGCGG  4931

Db  1247 TCAGCATTCTTAGTAGTGGGTTTCTGTCTGTTGGATGACTTTGAGATTATTCTTTGTTT   1306
          |||| | |||||||||||| |||||||  ||| |||| ||| |||||| | ||||||||
Qy  4932 TCAGTGTCTCAGTAGTAGTTCTGTTCGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTC  4991

Db  1307 CCTGTTGGGAGTTGTTCAAATGTTCCTTTT-AACGGATGGTTGAATGAGCGTCAGCCATCCA  1365
          ||| ||||| ||||||||||||| ||||||||  ||||||||||||||||  ||| |||||||
Qy  4992 TCTTTTGGAATTGTTCAAATGTGTTTTTTTTTAAGGGAATTGGTTGAATGAGAACTTCAGCATCCA  5051

Db  1366 GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT   1425
          ||||||||||||||| |||||||||  ||| |||| |||||||||||  |||||||||||
Qy  5052 AGTTTATGAATGACAGCAGTCACACA--GTTCTGTGTATATAGTTTAAGGGTAAGAGTCT   5109

Db  1426 TGTTTTTTACTCAAATTGGGAAATCCATTCCATTCTATTTTGTGAATTGGGA--TAATAACAGCA  1485
          ||| ||||| ||||||||||||||||||||||||||||||||||||||||||  |||||||||||
Qy  5110 TGTGTTTTATTCAGATTGGGAAATCCATTCCATTCTATTTTGTGAATTGGGA--TAATAACAGCA  5167

Db  1486 GTGGTAAAAGTATTCGCTTAAAATTGTGAGCGAATTAGCAATAACATACATGAGATAACT   1545
          |||| | |||| || ||| ||||||| ||||||| ||||| |||| |||| |||||||| |
Qy  5168 GTGGAATAAGTACTTAGA-AATGTGAAAAATGAGCAGTAAAATAGATGAGATAAGAGACT   5226

Db  1546 CAAGAAGAAATCAAAAGATAGTAGTTGATTCTTGCCTTGTACCTCAAATCTATTCTGTAAAAATT---  1602
          ||| |||  |  || | ||||| |||||||||||||| |||||||| ||||||||||||||||
Qy  5227 AAAGAAATTAAGAGAGTAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAAATTTTTT      5286

Db  1603 AAACAAATATGCAAACCAGGATTTCCTTGACTTCTTTG  1640
          ||| ||||||||||  ||| |||||||||| ||||||||
Qy  5287 AAAGATATATGCAATACCTGGATTTCCTTGGCTTCTTTG  5324
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RESULT 14
ID   US-07-807-043B-13 STANDARD; DNA; UNC; 1067 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 13, Application US/07807043B.
CC   Sequence 13, Application US/07807043B
CC   Patent No. 5342774
CC   GENERAL INFORMATION:
CC   APPLICANT: Boon, Thierry, Van den Eynde, Beno t
CC   TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
CC   TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CC   NUMBER OF SEQUENCES: 16
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/807,043B
CC   FILING DATE: 19911212
CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702

CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5342774man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 253.3
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 13:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 1067 base pairs
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: singular
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: cDNA MAGE-4
SQ   Sequence 1067 BP; 258 A; 222 C; 301 G; 286 T; 0 other;

Query Match   12.0%; Score 682; DB 4; Length 1067;
Best Local Similarity 84.6%; Pred. No. 0.00e+00;
Matches 901; Conservative   0; Mismatches 153; Indels 11; Gaps   7;

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Db     1 GGGCCAAGCACCTGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTG      60
          |||||||||||||   |||||| |||||||||||||||||| || ||||||| ||||||||
Qy  4139 GGGCCAAGCACCTCTTGTTCCTGAGTCCTTGTTCCGAGCAGTAATCACTCAAGAGGTG    4198

Db    61 GATGAGTTGGCTCATTTCTGTCTCCCCAAGTATCGAGCCAAGGACCAAGGAGCTGGTCACAAAGCA  120
          | ||| |||||| ||||||||||  ||  | |||||||| ||| |||||||||||||||||||||||
Qy  4199 GCTGATTTGGTTGGTTTCTGTCTCCTCCTCAAATATCGAGCCAAGGACCAAGGAGCTGGTCACAAAGCA  4258

Db   121 GAAATGCTGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTTTCCTGAGATCTTCGGCAAA  180
          ||||||||| || |||| |||||||||||| | | ||||||||||||  |||||||||||||||||
Qy  4259 GAAATGCTGGAGAGTGTCATCAAAAATTACAGACACTGTTTTCCTGAGATCTTCGGCAAA  4318

Db   181 GCCTCCGAGTCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGC  240
          ||||| ||||||||  |  | ||||||||||||||||||||||||| |||| ||| |||
Qy  4319 GCCTCTGAGTCCTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGC  4378

Db   241 AACACCTACACCTGCCTGACGCAGAGTCCTTGTTCCGAGAATGATGGCCTGTAATAAT   300
          |    ||| | |||||||| | |||||   |||  | |||  ||||||||| |||||||
Qy  4379 CACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGTCGGTGATAAT   4438

Db   301 CAGATCTTTCCCAAGACACAGGCCTTCAGATAATCGTCCTGGCCACAATTGCAATGGAGGGC  360
          ||||| |  |||||||| ||||||| | | |||||||||||| ||| |||||||||||||||
Qy  4439 CAGATCATGCCCAAGACAGGCTTCCTGTATAATTGTCCTGGTCATGATTGCAATGGAGGGC  4498

Db   361 GACAGCGCCCTTGAGGAGGAAATCTGGGAGGAGCTGGTGTGTGATGGGTGTATGATGGG  420
          | | | || || ||||||||||||||||||||||||  ||||||   || |||||||||
Qy  4499 GGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGAGTGTGATGATGGG  4558

Db   421 AGGGAGCACACTGTCTATGGGAGCCCAGGAAACTGCTCACCCAGCTAAATCCTGGCGCGCAGTAATC  480
          ||||||| ||| || |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4559 AGGGAGCCACAGTGCCTATGGGAGCCCCAGGAAACTGCTCACCCAGCTAAATCCTGGCGCGCAGTAATC  4618

Db   481 AACTACCTGAGTGAGTACCGGCAGTAGCCCGGCAGTACCCGGCAGTAATCCTGGCCGCGCCATGAGTTCCTGTGG  540
          | |||||| |||||||| ||||||| ||| |||||| | ||| || ||  ||  |||||||||||||||||||
Qy  4619 AGTACCTGGAGTAC--GGCAGTGCCGGACAGTGATCCCGGACAGTAGTGGTGAAAGTCCTGGCATGAGTTCCTGTGG  4677

Db   541 GGTCCAAGGGCTTCGGCTGAAACCACCTATGTGAAAGTCCTGGAGCATGTCTGAGCATGTCAGGGTC  600
          ||||||||||| | | ||||||||| ||||||||||||||| || |||| | | || |||||||||
Qy  4678 GGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTGAAGTCCTTGAGTATGTGATTCAAGGTC  4737

Db   601 AATGCAAGAGTTCGCATTCGCCATCCCTACCCATCCCTCGTGAAGCAGCTTTGTTAGAGAGGAGGAA  660
          | ||||||||||| || |   |||| | ||||  | ||| || ||||||||||| |||||||||||
Qy  4738 AGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAA  4797

Db   661 GAGGGAGTCTGAGCATGAGTTGCAGCATGAGTTGCAGCCAAGGCAGTGTGGGGAGGGCTGGGCCAGT  720
          ||||||||||||||||||||||||| ||||||||||||||||||    | |||  |||||||||||
Qy  4798 GAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAAGGCAGTGGGAGGGGACTGGGCCCAGTGCAC  4857

Db   721 GCATCTAACAGCCCTGTCAGCAGCTTCCCTTGCCTCGTGTAACATGAGGCCCATTCTTC  780
          |||| |  | ||||| ||  |||||||||| ||||||||||| |||||||||||||||||
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CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMUNICATION INFORMATION:
CC      TELEPHONE: (212) 688-9200
CC      TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 15:
CC   SEQUENCE CHARACTERISTICS:
CC      LENGTH: 1068 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: cDNA MAGE-4
SQ   Sequence 1068 BP; 258 A; 222 C; 302 G; 286 T; 0 other;

Query Match          12.0%;     Score 683;  DB 7;  Length 1068;
Best Local Similarity 84.6%;    Pred. No. 0.00e+00;
Matches  902;  Conservative  0;  Mismatches 153;  Indels 11;  Gaps  7;

Db      1 GGGGCCAAGCACCTCGCCTGACGCAGCTCCTTGTTCCGAGAAGCACTCAGTAACAAGGT 60
          ||||||||||||||||||   |  ||||||||||||||  ||||||   ||||  ||||
Qy   4138 GGGGCCAAGCACCTCCTTGTGTATCCTGGAGTCCTTGTTCCGAGCAGCAGTAATCACTAAGGAAGGT 4197

Db     61 GGATGAGTTGGCTCATTTCTGCTCCGCAAGTATCGAGCCAAGGAGTCGTCACAAGGC 120
          ||  || |||| |||||||||||||    ||||||||||||||||    ||||| |||
Qy   4198 GGCTGATTTGGTTGGTTTCTGCTCCTCCTCAAATATCGAGCCAAGGAGCCAGTCACAAAGGC 4257

Db    121 AGAAATGCTGGAGAGAGTCATCAAAAATTACAGCGCTGCTTTCCTGTGATCTTCGGCAA 180
          |||||||||||||||| |||||||||||||||||| ||| ||||| ||||||||||||
Qy   4258 AGAAATGCTGGAGAGTGTCATCAAAAATTACAGCACTGTTTTCCTGAGATCTTCGGCAA 4317

Db    181 AGCCTCCGAGTCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCGCCAG 240
          |||||| |||||||  | | ||||||||||||||| |||  ||| ||| |     | |
Qy   4318 AGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGGTCTTTGGGAGGTGTATGATGG 4377

Db    241 CAACACCTACACCCTTGTCACCTGCCTGGGCCTTCTCCTATGATGGCCTGCTGGGTAATAA 300
          |   | ||| |||||  |||||||||| | ||| ||||||||||||||| |||||| ||||
Qy   4378 CCACTCCTATGTCCTTGCCACCTGCCTCCCTAGGTCCTCCTATGATGGCCTGGCTGGGTGATAA 4437

Db    301 TCAGATCTTCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGG 360
          |||||| || |||||||||||||| ||| || |||| ||||| ||||||| |||||||
Qy   4438 TCAGATCATGCCCAAGACAGGCTTCTCCGGTCATAATTGTCCTGGTCATAATTGCAATGGAGGG 4497

Db    361 CGACAGCCGCCTGTGAGGAGGAAATCTGGAGGAGCTGGGGTGTGATGGGGTGTATGATGG 420
          | | |  || |||| ||||||||||||||||||||    |||||||| || ||||||||
Qy   4498 CGGCCATGTCCTCCTGAGGAGGAAATCTGGAGGAGCTGAGTGTGATGGGTGTGAGGTGTATGATGG 4557

Db    421 GAGGGAGCACACTGTCTATGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGA 480
          ||||| |||||||||| | |  |||| ||||||||||| |||||||||| ||| |||||
Qy   4558 GAGGGAGCACAGTGTCCATGGGAGCCCAGGAAACTGCTCACCCAAGATTTGGTGCAGGA 4617

Db    481 AAACTACCTGGAGTACCGGCAGTACCCGGCTAATCCTCGCGCGCTATGAGTTCCTGTG 540
          |||  | | |||||||| ||||| |  ||| ||| ||| | ||||||||||||||||||
Qy   4618 AAAGTACCTGGAGTAC-GCAGGTGCCGGACAGTGACAGTAGTTCCTGTG 4676

Db    541 GGGTCCAAGGGCTCGGCTGAAAACCAGCTAGTGTGGAGCATGTGGTCAGGGT 600
          ||||||||||  |||| |||||  |||| |||||  |||||||| ||| | |
Qy   4677 GGGTCCAAGGGCCTCGCTGAAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGT 4736

Db    601 CAATGCAAGAGTTCGCATTGCCTACCATCCGCTGAAGCAGCTTTGTTGTAGAGGAGGA 660
          |||| |||||||| | |  |||||||| |||  |||||||||| || |||||||||||
Qy   4737 CAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCGCTCGCGAAGCAGCTTTGTGAGAGGAGGA 4796

Db    661 AGAGGGAGTCTGAGCATGAGTTGCAGCAGCTTCCAGCCCAAGGCCAGGGGTCTGGGCCAG 720
          ||||||||  ||||  |||||||||||||||  | |   |      ||||||||||||||
Qy   4797 AGAGGGAGTCTGAGCATGAGTTGCAGCAGCTGGGCACCAGTGCA 4856

Db    721 TGCATCTAACAGCCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAACATGAGGCCCATTCTT 780
          ||| ||| |  ||||||||||||  || |  |||   |||   ||||||||||||||
Qy   4857 C-CTTCCAGG-GCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCTT 4914

Db    781 CACTCTGTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGTTTCTATTTGTTGGATGA 840
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Qy   4858 -CTTCCAGG-GCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCTTC 4915
Db    781 ACTCTGTTGAAGAAAATAGTCAGTGTTCTAGTAGTAGTGGTTTCTATTTGTTGGATGAC 840
          ||||| |  |||    |  ||||| |||||| || || |||||| |||||  | ||||
Qy   4916 ACTCTG---AAGAGAGCGGTCAGTGTTCTCCAGTAGTAGGTTTCTGTTCTATTGGGTGAC 4971
Db    841 TTGGAGATTATCTCTGTTCCTTTACAATGTTGAAATGTTCCTTT--AATGGATGGT 899
          |||||||| ||| ||||| | ||| ||  |||| |||||   ||  |||| |||||
Qy   4972 TTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTAAGGGATGGT 5031
Db    900 TGAATTAACTTCAGCATCCAAGTTATGAATCGTAGTAACGTATATTGCTGTAATATA 959
          |||| ||||||||||||||||||| ||||| | | || | |    |  ||||||||||
Qy   5032 TGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTTCGTCACACAGTTCGTGTATATA 5091
Db    960 GTTTAGGAGTAAGAGTCTTGTTTTATTCAGATTGGGAAAATCCGTTCATTTTGTGAAT 1019
          ||||| ||||||||||||||| |||||||||||||||||| |||| |||||||||||||
Qy   5092 GTTTAAGGGTAAGAGTCTTGTGTTTATTCAGATTGGGAAATCCATTCATTTTGTGAAT 5151
Db   1020 TTGGACATATAACAGCAGTGGAGTAAGTAGTATTTAGAAGTGTGAA 1064
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RESULT 15
ID   US-08-299-849B-15 STANDARD; DNA; UNC; 1068 BP.
AC   xxxxxxx
DT   01-JAN-1900
DE   Sequence 15, Application US/08299849B.
CC   Sequence 15, Application US/08299849B.
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC      APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC      APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC      APPLICANT: Chomez, Patrick
CC      TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC      TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   r
CC      NUMBER OF SEQUENCES: 48
CC      CORRESPONDENCE ADDRESS:
CC         ADDRESSEE: Felfe & Lynch
CC         STREET: 805 Third Avenue
CC         CITY: New York City
CC         STATE: New York
CC         ZIP: 10022
CC      COMPUTER READABLE FORM:
CC         MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC         COMPUTER: IBM
CC         OPERATING SYSTEM: PC-DOS
CC         SOFTWARE: Wordperfect
CC      CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER: US/08/299,849B
CC         FILING DATE: 1-SEPTEMBER-1994
CC         CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 08/037,230
CC         FILING DATE: 26-MARCH-1993
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: PCT/US92/04354
CC         FILING DATE: 22-MAY-1992
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/807,043
CC         FILING DATE: 12-DECEMBER-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/764,364
CC         FILING DATE: 23-SEPTEMBER-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/728,838
CC         FILING DATE: 9-JULY-1991
CC      PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER: 07/705,702
CC         FILING DATE: 23-May-1991
CC      ATTORNEY/AGENT INFORMATION:
CC         NAME: Hanson, No. 5612201man D.
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Qy  4915 CACTCTG----AAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA 4970

Db   841 CTTGGAGATTTATCTCTGTTCCTTTACAATTGTTGAAATGTTCCTTT-AATGGATGG 899
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Search completed: Tue Apr 7 20:56:43 1998
Job time : 316 secs.

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| \  / || |__) | (___  | |__) || |    | \  / |
| |\/| ||  ___/ \___ \ |  _  / | |    | |\/| |
| |  | || |     ____) || | \ \ | |____| |  | |
|_|  |_||_|    |_____/ |_|  \_\ \_____|_|  |_|   (TM)
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    Release 2.1D John F. Collins, Biocomputing Research Unit.
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             Distribution rights by IntelliGenetics, Inc.

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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 22:19:51 1998;   MasPar time 49.50 Seconds
                                   843.008 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-1
Description: (3931-4761) from 5541104.seq
Perfect Score: 831
N.A. Sequence: 3931 GGCCCAACAAGAGAGCCCTGG..........CAAGAGTTCGCTTTTCTTC 4761
Comp: CCGGGTTGTTCTCCGGACC..........GTTCTCAAGCGAAAAGAAG

Scoring table: TABLE default
                Gap 6

Nmatch   STD : Dbase 0: Query 0

Searched: 96465 seqs, 25105746 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-issued
                1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90
                10:PCT91 11:PCT92 12:PCT93 13:PCT94 14:PCT95 15:PCT96

Statistics: Mean 8.492; Variance 4.464; scale 1.902

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES

                %
Result   Query
No.   Score Match Length DB ID   Description   Pred. No.
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 1   831   100.0   2419   7 US-08-299- Sequence 7, Applicatio 0.00e+00
 2   831   100.0   2419   4 US-07-807- Sequence 7, Applicatio 0.00e+00
 3   831   100.0   5674   6 US-08-190- Sequence 8, Applicatio 0.00e+00
 4   831   100.0   5674   7 US-08-299- Sequence 1, Applicatio 0.00e+00
 5   831   100.0   5674   7 US-08-299- Sequence 8, Applicatio 0.00e+00
 6   584   70.3   2531   7 US-08-299- Sequence 14, Applicati 0.00e+00
 7   582   70.0   2531   7 US-08-299- Sequence 13, Applicati 0.00e+00
 8   513   61.7   2305   7 US-08-299- Sequence 17, Applicati 0.00e+00
 9   502   60.4   1640   7 US-07-807- Sequence 11, Applicati 0.00e+00
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11   500   60.2   2226   7 US-08-299- Sequence 11, Applicati 0.00e+00
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17   391   47.1   1947   7 US-08-299- Sequence 19, Applicati 3.12e-287
18   385   46.3   1412   7 US-08-299- Sequence 21, Applicati 2.24e-282
19   342   41.2   1107   7 US-08-299- Sequence 23, Applicati 1.24e-247
20   184   22.1   184   6 US-08-403- Sequence 1, Applicatio 3.56e-121
21   149   17.9   225   7 US-07-807- Sequence 15, Applicati 1.21e-93
22   149   17.9   225   4 US-08-299- Sequence 18, Applicati 1.21e-93
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31   58   7.0   7218   7 US-08-232- Sequence 14, Applicati 1.23e-24   c
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36   27   3.2   27 12 PCT-US93-0 Sequence 1, Applicatio 5.62e-04
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38   27   3.2   27   5 US-08-073- Sequence 1, Applicati   5.62e-04
39   25   3.0   27   5 US-07-938- Sequence 10, Applicati 8.11e-03
40   24   2.9   75 14 PCT-US95-1 Sequence 99, Applicati 2.98e-02   c
41   24   2.9   82 14 PCT-US95-1 Sequence 97, Applicati 2.98e-02   c
42   23   2.8   74 14 PCT-US95-1 Sequence 94, Applicati 1.07e-01
43   23   2.8   74 14 PCT-US95-1 Sequence 100, Applicat 1.07e-01   c
44   23   2.8   74 14 PCT-US95-1 Sequence 94, Applicati 1.07e-01   c
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                              ALIGNMENTS

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AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 7, Application US/08299849B.
CC   Sequence 7, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
r
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:

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Qy   4651  GATCCCGCACGCTATGAGTTCCTGTGGGTCCGTGGGGTCCCAAGGGGCCCTGCTGAAACCAGCTATGTG  4710

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RESULT   2
ID   US-07-807-043B-7 STANDARD; DNA; UNC; 2419 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 7, Application US/07807043B.
CC   Sequence 7, Application US/07807043B
CC   Patent No.5342774
CC   GENERAL INFORMATION:
CC   APPLICANT: Boon, Thierry, Van den Eynde, Beno t
CC   TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
CC   TITLE OF INVENTION: Rejection Antigens and Uses Thereof
CC   NUMBER OF SEQUENCES: 16
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: WordPerfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/07/807,043B
CC   FILING DATE: 1911212
CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5342774man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 253.3
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 7:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2419 base pairs
CC   TYPE: NUCLEIC ACID
CC   STRANDEDNESS: singular
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
SQ   Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 other;

Query Match   100.0%; Score 831; DB 4; Length 2419;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 831; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   736 TCTGTGTCCTGGGCACCCTGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG   795
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Qy   4051 TCCTCAGGGAGCCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

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CC          APPLICATION NUMBER: US/07/807,043B
CC          FILING DATE: 1991212
CC          CLASSIFICATION: 424
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: 07/764,364
CC          FILING DATE: 23-SEPTEMBER-1991
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: 07/728,838
CC          FILING DATE: 9-JULY-1991
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: 07/705,702
CC          FILING DATE: 23-May-1991
CC          ATTORNEY/AGENT INFORMATION:
CC          NAME: Hanson, No. 5342774man D.
CC          REGISTRATION NUMBER: 30,946
CC          REFERENCE/DOCKET NUMBER: LUD 253.3
CC          TELECOMMUNICATION INFORMATION:
CC          TELEPHONE: (212) 688-9200
CC          TELEFAX:   (212) 838-3884
CC     INFORMATION FOR SEQ ID NO: 8:
CC          SEQUENCE CHARACTERISTICS:
CC          LENGTH: 5674 base pairs
CC          TYPE: NUCLEIC ACID
CC          STRANDEDNESS: singular
CC          TOPOLOGY: linear
CC          MOLECULE TYPE: genomic DNA
CC          FEATURE:
CC          NAME/KEY: MAGE-1 gene
SQ     Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

Query Match          100.0%;   Score 831;  DB 4;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches   831;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy  4051 TCCTCAGGGGAGCTTCCGGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

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Db   916 GTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATA 975
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Qy  4171 GTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATA 4230

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Qy  4351 TGACGTGAAGGAAGCAGAGCCCACCGGCCCACTCCTATGTCCTGTCCTGCCTAGGTCT 4410

Db  1156 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 1215
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Qy  4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470

Db  1216 TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 1275
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Qy  4471 TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530

Db  1276 GCTGAGTGTGATGGAGTGTGTATGATGGGAGGGAGGGAGCACAGTCCTATGGGGAGGCCACGGAA 1335
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Qy  4531 GCTGAGTGTGATGGAGTGTGTATGATGGGAGGGAGGGAGCACAGTCCTATGGGGAGGCCACGGAA 4590

Db  1336 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGAAAGTACCTGGAGTGCCGGCACAGT 1395
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Qy  4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGAAAGTACCTGGAGTGCCGGCACAGT 4650

Db  1396 GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTGCGCTGAAACCAGCTATGTG 1455
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Qy  4651 GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTGCGCTGAAACCAGCTATGTG 4710

Db  1456 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCCCTTTTTCTTC 1506
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Qy  4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCCCTTTTTCTTC 4761
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Db  4531  GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCCACAGTGCCTATGGGAGCCCAGGAA  4590
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Qy  4531  GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCCACAGTGCCTATGGGAGCCCAGGAA  4590

Db  4591  GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT  4650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4591  GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT  4650

Db  4651  GATCCCGCACCGCTATGAGTTCCTGTGGGTCCAAGGGCCCTGCTGAAACCAGCTATGTG  4710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4651  GATCCCGCACCGCTATGAGTTCCTGTGGGTCCAAGGGCCCTGCTGAAACCAGCTATGTG  4710

Db  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC  4761
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC  4761
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RESULT  4
ID   US-08-190-411A-1 STANDARD; DNA; UNC; 5674 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 1, Application US/08190411A.
CC   Sequence 1, Application US/08190411A
CC   Patent No. 5541104
CC   GENERAL INFORMATION:
CC   APPLICANT:  Chen, Yao-Tseng; Stockert, Elisabeth;
CC   APPLICANT:  Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
CC   APPLICANT:  van der Bruggen, Pierre; Boon-Falleur, Thierry;
CC   APPLICANT:  Old, Lloyd J.
CC   TITLE OF INVENTION:  MONOCLONAL ANTIBODIES WHICH BIND TO
CC   TITLE OF INVENTION:  TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBIN
CC   ANT MAGE-1,
CC   TITLE OF INVENTION:  AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
CC   NUMBER OF SEQUENCES:  4
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE:  Felfe & Lynch
CC   STREET:  805 Third Avenue
CC   CITY:  New York City
CC   STATE:  New York
CC   ZIP:  10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER:  IBM
CC   OPERATING SYSTEM:  PC-DOS
CC   SOFTWARE:  Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER:  US/08/190,411A
CC   FILING DATE:  01-FEBRUARY-1994
CC   CLASSIFICATION:  436
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  037,230
CC   FILING DATE:  26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  PCT/US92/04354
CC   FILING DATE:  22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  07/807,043
CC   FILING DATE:  12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  07/764,364
CC   FILING DATE:  23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  07/728,838
CC   FILING DATE:  9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:  07/705,702
CC   FILING DATE:  23-MAY-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME:  Hanson, No. 5541104man D.
CC   REGISTRATION NUMBER:  30,946
CC   REFERENCE/DOCKET NUMBER:  LUD 5354
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE:  (212) 688-9200
CC   TELEFAX:  (212) 838-3884
CC   INFORMATION FOR SEQ ID NO:  1:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH:  5674 base pairs
CC   TYPE:  nucleic acid
CC   STRANDEDNESS:  single
CC   TOPOLOGY:  linear
CC   MOLECULE TYPE:  genomic DNA
CC   FEATURE:
CC   NAME/KEY:  MAGE-1 gene
SQ   Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;
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Query Match     100.0%;  Score 831;  DB 6;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  831;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db  3931  GGCCCAACAACAGAGGCCCTGGTCGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCC  3990
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Qy  3931  GGCCCAACAACAGAGGCCCTGGTCGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCC  3990

Db  3991  TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG  4050
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Qy  3991  TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG  4050

Db  4051  TCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  4110
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Qy  4051  TCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  4110

Db  4111  TGAGGGTTCCAGCAGCCGTGAAGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCTT  4170
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Qy  4111  TGAGGGTTCCAGCAGCCGTGAAGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCTT  4170

Db  4171  GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGTTTCGTCTCCTCAAATA  4230
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Qy  4171  GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGTTTCGTCTCCTCAAATA  4230

Db  4231  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  4290
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Qy  4231  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  4290

Db  4291  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT  4350
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Qy  4291  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT  4350

Db  4351  TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCCTGCTCCTAGGTCT  4410
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Qy  4351  TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCCTGCTCCTAGGTCT  4410

Db  4411  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT  4470
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Qy  4411  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT  4470

Db  4471  TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA  4530
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Qy  4471  TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA  4530

Db  4531  GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCCACAGTGCCTATGGGAGCCCAGGAA  4590
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Qy  4531  GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCCACAGTGCCTATGGGAGCCCAGGAA  4590

Db  4591  GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT  4650
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Qy  4591  GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT  4650

Db  4651  GATCCCGCACCGCTATGAGTTCCTGTGGGTCCAAGGGCCCTGCTGAAACCAGCTATGTG  4710
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Qy  4651  GATCCCGCACCGCTATGAGTTCCTGTGGGTCCAAGGGCCCTGCTGAAACCAGCTATGTG  4710

Db  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC  4761
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Qy  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC  4761
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Qy   3931 GGCCAACAAGAGAGGCCCTGGGCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC 3990
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Db   3991 TCTGGTCCTGGGCACCTGGAGGAGGTGCCACTGCTGGTCAACAGATCCTCCCCAGAG 4050
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Db   4051 TCCTCAGGGAGCCTTCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110
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Qy   4051 TCCTCAGGGAGCCTTCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

Db   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170
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Qy   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170

Db   4171 GTTCCGAGCAGTAATCACTAAGAAGGTGCTGATTGGTTGGTTTTCTGCTCCTCAAATA 4230
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Qy   4171 GTTCCGAGCAGTAATCACTAAGAAGGTGCTGATTGGTTGGTTTTCTGCTCCTCAAATA 4230

Db   4231 TCGAGCCAGGGAGCCAGTCACAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290
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Qy   4231 TCGAGCCAGGGAGCCAGTCACAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290

Db   4291 GCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGCTCCTTGCAGCTGGTCTTTGGCAT 4350
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Qy   4291 GCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGCTCCTTGCAGCTGGTCTTTGGCAT 4350

Db   4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT 4410
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Qy   4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT 4410

Db   4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470
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Qy   4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470

Db   4471 TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530
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Db   4531 GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCGCACAGTGCCTATGGGGAGCCCAGGAA 4590
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Qy   4531 GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCGCACAGTGCCTATGGGGAGCCCAGGAA 4590

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Qy   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT 4650

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Qy   4651 GATCCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTGCGCTGAAACCAGCTATGTG 4710

Db   4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 4761
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RESULT   6
ID   US-08-299-849B-14 STANDARD; DNA; UNC; 2531 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 14, Application US/08299849B.
CC   Sequence 14, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
r
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue

RESULT   5
ID   US-08-299-849B-8 STANDARD; DNA; UNC; 5674 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 8, Application US/08299849B.
CC   Sequence 8, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
r
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5612201man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LJD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 8:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 5674 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-1 gene
CC   Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 other;

SQ

Query Match   100.0%;   Score 831;   DB 7;   Length 5674;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 831;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db   3931 GGCCAACAAGAGAGGCCCTGGGCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC 3990
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CC    CITY: New York City
CC    STATE: New York
CC    ZIP: 10022
CC  COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC    COMPUTER: IBM
CC    OPERATING SYSTEM: PC-DOS
CC    SOFTWARE: Wordperfect
CC  CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: US/08/299,849B
CC    FILING DATE: 1-SEPTEMBER-1994
CC    CLASSIFICATION: 435
CC  PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: 08/037,230
CC    FILING DATE: 26-MARCH-1993
CC  PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: PCT/US92/04354
CC    FILING DATE: 22-MAY-1992
CC  PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: 07/807,043
CC    FILING DATE: 12-DECEMBER-1991
CC  PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: 07/764,364
CC    FILING DATE: 23-SEPTEMBER-1991
CC  PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: 07/728,838
CC    FILING DATE: 9-JULY-1991
CC  PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: 07/705,702
CC    FILING DATE: 23-May-1991
CC  ATTORNEY/AGENT INFORMATION:
CC    NAME: Hanson, No. 5612201man D.
CC    REGISTRATION NUMBER: 30,946
CC    REFERENCE/DOCKET NUMBER: LUD 5355
CC  TELECOMMUNICATION INFORMATION:
CC    TELEPHONE: (212) 688-9200
CC    TELEFAX: (212) 838-3884
CC  INFORMATION FOR SEQ ID NO: 14:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 2531 base pairs
CC    TYPE: nucleic acid
CC    STRANDEDNESS: single
CC    TOPOLOGY: linear
CC    MOLECULE TYPE: genomic DNA
CC    FEATURE:
CC    NAME/KEY: MAGE-41 gene
SQ  Sequence 2531 BP; 607 A; 593 C; 701 G; 630 T; 0 other;

Query Match            70.3%;    Score 584;  DB 7;  Length 2531;
Best Local Similarity  87.2%;    Pred. No. 0.00e+00;
Matches  690; Conservative  0; Mismatches 100; Indels  1; Gaps  1;

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Qy   3966 AGGCTGCCACCTCCTCCTCCTCCTCCTCCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCCACTG 4025

Db    794 CTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCAGGGAGCCTTACCCACTACCATCA 853
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Qy   4026 CTGGGTCAACAGATCCTCCCCAGAGTCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCA 4085

Db    854 GCTTCACTTGCTGGAGGCAACCCAATGAGAGGTTCCAGCAGCCAAGAGAGAGGGGGCCAA 913
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Qy   4086 ACTTCACTCGACAGAGCAACCCAGTGAGGGTTCCAGCAGCCGTGAGAGAGGGGGCCAA 4145

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Qy   4146 GCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTGAAGAAGGTTGGCTGATT 4205

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Qy   4206 TGGTTGGTTTTTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGC 4265

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Qy   4266 TGGAGAGTGTCATCAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTG 4325

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Qy   4386 ATGTCCTTGCACCTGCCTCCTAGGTCTCTCCTATGATGCCTGCTGGGTGATAATCAGATCA 4445

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Qy   4446 TGCCCAAGACAGGCGTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATG 4505

Db   1274 CCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGGGTGTATGGGGTGTGATGGGGAGGGAGC 1333
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Qy   4506 CTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGGTGTATGATGGGGAGGGAGC 4565

Db   1334 ACACTGTCTATGGGAGCCCAGGAGAACTGCTCACCCCAAGATTGGGTGCAGGAAAACTACC 1393
          || ||| ||||||  ||||||||||  ||||||||||||||||||||||||||||| ||||
Qy   4566 ACAGTGCCTATGGGGAGCCCAGGAGCTGCTCACCCCAAGATTGGGTGCAGGAAAGTACC 4625

Db   1394 TGGAGTACCGGCAGTACCGGCCAGTAATCCTGCGCGTATGAGTTCCTGTGGGTCCAA 1453
          |||||||| ||||| | ||| ||||| |||||  | |||||||||||||||||||||
Qy   4626 TGGAGTAC-GGCAGGTGCCGGACAGTGATCCGCACCGCTATGAGTTCCTGTGGGTCCAA 4684

Db   1454 GGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAA 1513
          ||||  ||||||||||||||||||||||||||| |||| ||||| |||| || |||||||
Qy   4685 GGGCCCTGCCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGTCAAGTCAGTGCAA 4744

Db   1514 GAGTTCGCATT 1524
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Qy   4745 GAGTTCGCTTT 4755

RESULT 7
ID   US-08-299-849B-13 STANDARD; DNA; UNC; 2531 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 13, Application US/08299849B.
CC   Sequence 13, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC    APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC    APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC    APPLICANT: Chomez, Patrick
CC    TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC    TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
r
CC    NUMBER OF SEQUENCES: 48
CC    CORRESPONDENCE ADDRESS:
CC    ADDRESSEE: Felfe & Lynch
CC    STREET: 805 Third Avenue
CC    CITY: New York City
CC    STATE: New York
CC    ZIP: 10022
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC    COMPUTER: IBM
CC    OPERATING SYSTEM: PC-DOS
CC    SOFTWARE: Wordperfect
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: US/08/299,849B
CC    FILING DATE: 1-SEPTEMBER-1994
CC    CLASSIFICATION: 435
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: 08/037,230
CC    FILING DATE: 26-MARCH-1993
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: PCT/US92/04354
CC    FILING DATE: 22-MAY-1992
CC    PRIOR APPLICATION DATA:
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CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   APPLICATION NUMBER: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5612201man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LJD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 13:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2531 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-4 gene
SQ Sequence 2531 BP: 608 A; 593 C; 700 G; 630 T; 0 other;

Query Match   70.0%; Score 582; DB 7; Length 2531;
Best Local Similarity 87.1%; Pred. No. 0.00e+00;
Matches 689; Conservative   0; Mismatches 101; Indels   1; Gaps   1;

Db   734 AGGCTGCTGCTCCTCCTCCTCCTGTCCCTGGAGCACCCTGGAGGAAGTGCCTGCTG 793
          ||||||| |||||||||||||||||||||||||||||||| ||||| ||
Qy   3966 AGGCTGCCACCTCCTCCTCTCTCTCTGTCTCTGGGCACCCTGGAGGAGTGCCCACTG 4025

Db   794 CTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGAGCCTCAGGAGTCCTACCCACTACCATCA 853
          ||||| ||| || |||||||||| |||||||||||||||||| |||||| |||||||||||
Qy   4026 CTGGGTCAACAGATCTCCCCAGAGTCCTCAGGAGCCTCCGCCTTCCCACTACCACTACCATCA 4085

Db   854 GCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCAGCAGCCAAGGAGAAGAGGGGCCAA 913
          |||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||
Qy   4086 ACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAA 4145

Db   914 GCACCTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGT 973
          ||||||| |- || ||||| |||||||||||| |- ||| ||| || |||||| |||||
Qy   4146 GCACCTCCTGTATCCTGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATT 4205

Db   974 TGGCTCAATTTCTGCTCCGCCAAGTATCAGCCAAGGAGCTGGTCACAAAGGCAGAAAATGC 1033
          ||| |- |||||||| ||| ||||||||||| |||||| |||| ||||||||||||||||
Qy   4206 TGGTTGGTTTTCTCTGTCTCCTCAAATATCAGCAGCAGGCAGTCACAAAGGCAGAAAATGC 4265

Db   1034 TGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGAAGCCTCCGGGCAAAGCCTCCG 1093
          ||||||||| ||||||||||||||| ||| || ||| |||||||||||| | ||||||||
Qy   4266 TGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTG 4325

Db   1094 AGTCCTGAAGATGATCTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCAACACCT 1153
          ||||||| ||||| || |||||| || |||||| ||||||| |||||||| ||
Qy   4326 AGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACACCCCACTCCT 4385

Db   1154 ACACCCTTGTCACCTGCCTGGGCCTTCCTATGATGGCCTGCTGCTGGGTAATAATCAGATCT 1213
          | ||||||||||||||||||| ||||||||||| || |||||||||| ||||||||||||
Qy   4386 ATGTCCTTGTCACCTGCCTAGTGTCTCCTATGATGATGGCTGGGTGATAATCAGATCA 4445

Db   1214 TTCCCAAGACAGGCCTTCTGATAATCGTCCTGGGCCACAATTGCAAGTGAAGGGGCGACAGCG 1273
          | |||||||||| | ||||||||||| || |||||||||||||||||||||||||||||||
Qy   4446 TGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGCAATGGCCGCCATG 4505

Db   1274 CCTCTGAGGAGAAATCTGGAGGAGCTGGGTGTGGGTGATGGGGTGTATGATGGGAGGGAGC 1333
          | ||||||||||||||||||||||||||||| |||||||||||||| |||||||||||||
Qy   4506 CTCCTGAGGAGAAATCTGGAGGAGCTGGGTGTGAGTGTGATGGGGTGTATGATGGGAGGGAGC 4565

Db   1334 ACACTGTCTATGGGGAGGCCAGAGAAACTGCTCACCCAAGATTGGGTGCAGGAAAACTACC 1393
          ||| || |||||||||||||||||||||| ||||||||||||| ||||||||||| ||||
Qy   4556 ACAGTGCCTATGGGGAGGCCAGGAGAGCTGCTCACCAAGATTCGTGCGAGGAAAAGTACC 4625

Db   1394 TGGAGTACCGGCAGTACCCGGCAGTAATCCTCGCGCGCTATGAGTTCCTGTGGGGTCCAA 1453
          ||||||| |||||||| |||||||||||| ||| |||||||||||||||||||| ||||
Qy   4626 TGGAGTAC-GGCAGGTGCCGGACAGTGACCGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAA 4684

Db   1454 GGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAA 1513
          |||| || ||||||||||||||||||||||||||||| || |||||||||||||||||
Qy   4685 GGGCCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAA 4744

Db   1514 GAGTTCGCATT 1524
          |||||||| ||
Qy   4745 GAGTTCGCTTT 4755

RESULT   8
ID US-08-299-849B-17 STANDARD; DNA; UNC; 2305 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 17, Application US/08299849B.
CC Sequence 17, Application US/08299849B
CC Patent No. 5612201
CC GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   r
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   APPLICATION NUMBER: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5612201man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LJD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 17:

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CC    SEQUENCE CHARACTERISTICS:
CC      LENGTH: 2305 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: genomic DNA
CC      FEATURE:
CC        NAME/KEY: MAGE-51 gene
SQ    Sequence 2305 BP: 549 A; 568 C; 611 G; 577 T; 0 other;

Query Match            61.7%;  Score 513; DB 7;  Length 2305;
Best Local Similarity  86.4%;  Pred. No. 0.00e+00;
Matches  633;  Conservative  0;  Mismatches  96;  Indels  4;  Gaps  2;

Db    748 GCAGGAGGGCTGTCCTCCTCCTCCTCCTCCAGGCACCCTGGGGAGGTGCCTGC 807
          |||| || |||||||||||||||||||||| |||||||| ||||||||||||
Qy   3964 GCAGGCTGCCACCTCCTCCTCCTCCTCCTGGTCCTGGGCACCCTGGGGAGGTGCCCAC 4023

Db    808 TGCTGGGTCACCAGGTCCTCAAGAGTCCTCAGGGAGCCTCCGCCATCCCACTGCCAT 867
          |||||||| ||| |||||||||| ||||||||||||||| | ||||| ||||
Qy   4024 TGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCAT 4083

Db    868 CGATTTCACTCATGGAGGCAATCATTAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCC 927
          ||||||||||||||||| ||||| ||| |||||| ||||| || ||||| ||||
Qy   4084 CAACTTCACTCGACAGAGGCAACCCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGCC 4143

Db    928 AAGCCACCTCCCCTGACCCAGAGTCTGTTCCGACGCACTCAGTAAGAAGGTGGCTGA 987
          ||||||||| || || || |||||||||||| |||||||||| | ||||||||||
Qy   4144 AAGCACCTCTTGTATCCTGAGTCCTTGTTCCGACAGCAGTAATCACTCAAGAGGTGGCTGA 4203

Db    988 CTTGATTCATTTCTGCTCCTCAAGTATTAAGTCAAGGAGCCGGTCACAAAGGCAGAAAT 1047
          || ||| || || |||||||||||| ||| || ||||||||||||||||||||
Qy   4204 TTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAAT 4263

Db   1048 GCTGGAGAGGTCATCAAAAATTACAGAGGCGCTGCTTTCCTGAGATCTTCGGCAAAGCCTC 1107
          || ||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||
Qy   4264 GCTGGAGAGTGTCATCAAAAATTACAGACACTGTTTTCCTGAGATCTTCGGCAAAGCCTC 4323

Db   1108 CGAGTCCTTGCAGCTGGTGTCTTGGCATTGACGTGAAGGAAAGCGGACCCCACCAACAC 1167
          ||||||||||||||||||||||| |||||| |||||||| | |
Qy   4324 TGAGTCCTTGCAGCTGGTGTCTTGGCATTGACGTGAAGGAAGCAGAACCCCACCGGCCACTC 4383

Db   1168 CTACACCCTTGTCACCTGCCTGGACTC--CTATGATGGCCTGGTGTT--TAATCAGAT 1223
          || ||||||||||||||||||||| ||||| | ||||||||| ||| |||||||||
Qy   4384 CTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGGGTGATAAATCAGAT 4443

Db   1224 CATGGCCCAAGACGGCGCCTCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAATG 1283
          ||||||||||||||||||||||||||||||| ||| ||||||| |||||||||
Qy   4444 CATGCCCAAGACAGGCCCTCCTGATAATTGTCCTGGTCATAATTGCAATGGAGGGCGGCCA 4503

Db   1284 CGTCCCTGAGGAGAAAAATCTGGGAGAGCTGGGTGTGATGAAGGTGTATGTGGGAGGGA 1343
          | |||||||||||||||||||||||||||||| |||||| |||||||||||||||||||
Qy   4504 TGCTCCTGAGGAGAAATCTGGGGAGGCTGGGTGTGATGGTGTATGTGGGAGGGA 4563

Db   1344 GCACAGTGTCTGTGGGGAGCCCAGGAGCCCAGGAAACTA 1403
          |||||||||||| |||||||||||||||||||| ||
Qy   4564 GCACAGTGTCGCCTATGGGGAGCCCAGGAGCCCAGGAAAGTA 4623

Db   1404 CCTGGAGTACCGCAGGTGCCCAGCCAGTGATCCCATATGCTATGAGTTACTGTGGGTCCA 1463
          |||||||||||||||||||||||||| | ||||||||||| |
Qy   4624 CCTGGAGTACGGCAGGTGCCAGCGCCACGGCGATCCCACGCTATGAGTTCTCCTGTGGGGTCCA 4683

Db   1464 AGGGCACTCGCTG 1476
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Qy   4684 AGGGCCCTCGCTG 4696
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RESULT    9
ID    US-07-807-043B-11 STANDARD; DNA; UNC; 1640 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 11, Application US/07807043B.
CC    Séquence 11, Application US/07807043B
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Patent No. 5342774
GENERAL INFORMATION:
    APPLICANT: Boon, Thierry, Van den Eynde, Beno t
    TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
    TITLE OF INVENTION: Rejection Antigens and Uses Thereof
    NUMBER OF SEQUENCES: 16
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Felfe & Lynch
        STREET: 805 Third Avenue
        CITY: New York City
        STATE: New York
        ZIP: 10022
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
        COMPUTER: IBM
        OPERATING SYSTEM: PC-DOS
        SOFTWARE: Wordperfect
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/07/807,043B
        FILING DATE: 1991212
        CLASSIFICATION: 424
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/764,364
        FILING DATE: 23-SEPTEMBER-1991
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/728,838
        FILING DATE: 9-JULY-1991
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/705,702
        FILING DATE: 23-May-1991
    ATTORNEY/AGENT INFORMATION:
        NAME: Hanson, No. 5342774man D.
        REGISTRATION NUMBER: 30,946
        REFERENCE/DOCKET NUMBER: LUD 253.3
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 688-9200
        TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1640 base pairs
        TYPE: NUCLEIC ACID
        STRANDEDNESS: singular
        TOPOLOGY: linear
        MOLECULE TYPE: cDNA to mRNA
    FEATURE:
        NAME/KEY: cDNA MAGE-3
SQ  Sequence 1640 BP: 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match            60.4%;  Score 502; DB 4;  Length 1640;
Best Local Similarity  81.8%;  Pred. No. 0.00e+00;
Matches  652;  Conservative  0;  Mismatches  144;  Indels  1;  Gaps  1;

Db    276 GCAGGAGGGCTGCCTCCTCCTCCTTCTCCTACTCTAGTTGAAGTCACCCTGGGGAGGTGCCTGC 335
          |||||| ||  ||||||||||||||||||| |||  ||||||||||||||
Qy   3964 GCAGGCTGCCACCTCCTCCTCCTCTCTGGTCCTGGGCACCCTGGGGAGGTGCCCAC 4023

Db    336 TGCCGGAGTCACCAGATCCTCCCAGAGTCCTCAGGGAGCCTCCAGCGTCTCCCACTACCAT 395
          |||| |||||||||| |||||||||||||||||||||||||||  |  ||||||||||||
Qy   4024 TGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCAT 4083

Db    396 GAACTACCCTCTGACGAGCCAATCCTCATGAGACTCCATGATTGCAATCGCCAGTGAGGGGGC 455
          |||||| |||  |||   ||||| | |  |||||||||||||  || |||
Qy   4084 CAACTTCACTCGACAGAGGCAACCCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGCC 4143

Db    456 AAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTAGGCAGCACTCAGTAGGCCGA 515
          ||||||||  |||| |  ||||||||| ||  ||||||||||||||||||||||
Qy   4144 AAGCACCTCTTGTATCCTGAGTCCTTGTTCCGACGCAGTAATCACTCAAGAGGTGGCTGA 4203

Db    576 GCTGGGGAGTGTCGTCGGAAATTGGCAGTATTCTTTCCTCGTGTGATCTTCAGCAAAGCTTC 635
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Qy |||||| ||||||| || ||||| |||| | | | ||||||| |||||| ||
     4264 GCTGGAGAGTGTCATCAAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTC 4323

Db   636 CAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGAGTGAAGTGGACCCCATCGGCCACTT 695
          ||||||||||||||||| || |||| |||| |||||||||||| |||||||
Qy   4324 TGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGACGTGGAGGCAGCAGCCCCACCGGCCACTC 4383

Db   696 GTACATCTTTGCCACCTGCCTCTCCTACGATGCCTGCCTGGGTGACAATCAGAT 755
          ||| |||| |||| |||| |||| ||| ||||| ||||| |||||||||
Qy   4384 CTATGTCCTTGTCACCTGCCTAGTCTCTCCTATGATGGCCTGCGTGGGTGATAATCAGAT 4443

Db   756 CATGCCCAAGGCAGGCCCCTGATAATCGTCCTGCCCATAATCGTCCTGCCCATAATCGTC 815
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Qy   4444 CATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCA 4503

Db   816 TGCCCCTGAGGAGAAATCGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGA 875
          ||| ||||||||| |||| || || |||| |||||||| || ||||||
Qy   4504 TGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGGAGGGA 4563

Db   876 AGACAGTATGTTGGGGATCCCAAGAGCTGCTCACCCAACATTCGTGCAGAAAACTA 935
          | || |||||||||| |||| |||||||| |||||
Qy   4564 GCACAGTGCCTATGGGGAGCCCCAGGAAGCTGCTCACCCAAGAATTGGTGCAGGAAAAGTA 4623

Db   936 CCTGGAGTACCGGCGAGGTCCCCGGGGCCGAGTGATCCTGCAATGTTATGTAATTCCTGTGGGGTCC 995
          |||||||| || || | ||||| || |||| | ||||||| |||
Qy   4624 CCTGGAGTAC-GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCC 4682

Db   996 AAGGGCCCTGTTGAAACCAGCTATGTGAAAGTCCTGCACCATATGTAAAGATCAGTGG 1055
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Qy   4683 AAGGGCCCTGCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGC 4742

Db   1056 AGGACCTCACATTTCCT 1072
          || | |||| ||||
Qy   4743 AAGAGTTGCTTTTTCT 4759

RESULT 10
ID   US-08-299-849B-11 STANDARD; DNA; UNC; 1640 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 11, Application US/08299849B.
CC   Sequence 11, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:

CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   APPLICATION NUMBER: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 561220Iman D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LJD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 11:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 1640 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA to mRNA
CC   FEATURE:
CC   NAME/KEY: CDNA MAGE-3
SQ   Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match   60.4%; Score 502; DB 7; Length 1640;
Best Local Similarity   81.8%; Pred. No. 0.00e+00;
Matches   652; Conservative 0; Mismatches 144; Indels 1; Gaps 1;

Db   276 GCAGGAGGCTGCCTCCTCCTCCTCTCCTACTCTAGTGAAGTCACCCTGGGGGAGGTGCCTGC 335
          ||||| || |||||||||||| ||| |||| | | |||||||| ||||||||| ||
Qy   3964 GCAGGCTGCCACCTCCTCCTCCTCCTCGTCGTCCTGGCACCCTGGGAGGAGGTGCCCAC 4023

Db   336 TGCCGAGTCACCAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTTCCCACTACCAT 395
          |||| | || |||||| |||| ||||| | |||||||| || | |||||||||||||
Qy   4024 TGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTCCGCCTTTCCCACTACCAT 4083

Db   396 GAACTACCCTCCTGGACAGAAGCTGCTCACCCAATCCATGGTTGAGGACTCCAGCAACAACAAGAGAGAGGGGC 455
          |||| |||| | || || ||||| ||| || | ||| |||| ||| ||| | |||||||| ||||
Qy   4084 CAACTTCACTGACAGAGGCAACCCAGTGAGGTTCCAGCAGCCACTCAGTAGGAAGGTGGCCGA 4143

Db   456 AAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGA 515
          |||||||| | |||||||||| ||| || | |||||||| ||| | ||
Qy   4144 AAGCACCTCTTGTATCCTGAGTCCTTGTTCCCAGCAGTAATCACTAAGAAGGTGGCTGA 4203

Db   516 GTTGGTTCATTTTCTGCTCCTCCAAGTATCGAGCCCAGGAGATCGAGCCCAGGAGATCG 575
          | ||||||| ||||||||||||| ||| |||||| ||||||| |||||| ||||||||||
Qy   4204 TTTGGTTGGTTTGTCCTCCTCCAAAATATCGAGCCCAGGAGATCCAAAAGGCAGAAAT 4263

Db   576 GCTGGGGAGTGTCGTCGAGTGGAAATTGGCCAGTAGTTTCTTTTCCTGTGTGATCTTCCACGAT 635
          |||| ||||| || |||| || ||||| | | |||| | | ||||| |||
Qy   4264 GCTGGAGAGTGTCATCAAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTC 4323

Db   636 CAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGAGTGAAGTGGACCCCATCGGCCACTT 695
          |||| ||||||||||||||||| ||| | | ||||||| || |||||| |||
Qy   4324 TGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGACGTGGAGGCAGCAGCCCCACCGGCCACTC 4383

Db   696 GTACATCTTTGCCACCTGCCTCTCCTACGATGCCTGCCTGGGTGACAATCAGAT 755
          || |||| |||| |||| |||| ||| ||||| ||||| |||||||||
Qy   4384 CTATGTCCTTGTCACCTGCCTAGTCTCTCCTATGATGGCCTGCGTGGGTGATAATCAGAT 4443

Db   756 CATGCCCAAGGCAGGCCCCTGATAATCGTCCTGCCCATAATCGTCCTGCCCATAATCGTC 815
          ||||||||||| ||| ||||||||| ||||| || | ||| || |||||
Qy   4444 CATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCA 4503

Db   816 TGCCCCTGAGGAGAAATCGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGA 875
          ||| ||||||||| ||| ||| |||| |||| |||||||| || ||||||
Qy   4504 TGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGATGGAGGTGTATGGAGGGA 4563

Db   876 AGACAGTATGTTGGGGGATCCAAGAAGCTGCTCACCCAACATTTCGTGCAGGAAAACTA 935
          ||||| | ||||| |||| |||||||||||||| |||| ||||||||||| ||
Qy 4564 GCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTA 4623

Db   936 CCTGGAGTACCGGCAGGTCCCGGCCAGTGATCCTGCCATGTTATGAATTCCGTGGGGTCC 995
          |||||||||| ||||||| ||||||| || | || | |||| ||||||||||||||
Qy 4624 CCTGGAGTAC-GGCAGGTGCCGGACAGTGATCCCGCCATGCTATGAATCCCGTGGGGTCC 4682

Db   996 AAGGGCCCCGTTGAAACCAGCTATGTGAAAGTCCTGCCACCATATGGTAAAGATCAGTGG 1055
          |||||||||| ||||||||||||||||||| | ||| | || | | |||| |||
Qy 4683 AAGGGCCCCGTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGC 4742

Db 1056 AGGACCTCACATTTCCT 1072
          | || || || ||
Qy 4759 AAGAGTTCGCTTTTTCT 4759

RESULT 11
ID   US-08-299-849B-16 STANDARD; DNA; UNC; 2226 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 16, Application US/08299849B.
CC   Sequence 16, Application US/08299849B
CC   Patent No. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 561220lman D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 16:

CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 2226 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
CC   TOPOLOGY: linear
CC   MOLECULE TYPE: genomic DNA
CC   FEATURE:
CC   NAME/KEY: MAGE-5 gene
SQ   Sequence 2226 BP; 539 A; 542 C; 582 G; 563 T; 0 other;

Query Match   60.2%; Score 500; DB 7; Length 2226;
Best Local Similarity   85.8%; Pred. No. 0.00e+00;
Matches   611; Conservative   0; Mismatches 99; Indels   2; Gaps   2;

Db   687 CTCCTCTGGTCCCAGGCACCCTGGGGAGGTGCTGCTGGTCACCAGGTCCTCTCTCA 746
          |||||||||||||||||||||||||||||||||| |||||||||||||||| ||||
Qy 3987 CTCCTCTGGTCCTGGGGACCCTGAGGAGGTGCCCACTGCTGCGGTCAACAGATCCTCCCC 4046

Db   747 AGAGTCCTCAGGAGGCCTCGCCATCCCGCCATCGATTCGATTCTATGGAGGCAAT 806
          |||||||||||||||||||||||| |||||| | |||||| | |||||||||||
Qy 4047 AGAGTCCTCAGGAGGCCTCGCCCTTCCCACTACCATCAACTTCACTCACAGAGGCAAC 4106

Db   807 CCATTAAGGGCTCCAGAACCAAGAACCAAGGAGGGAGGGCCAAGCACCTCCCTGACCCAGAGT 866
          ||| ||| | |||||| ||||| | || |||| ||| ||||||||| ||||||| |||
Qy 4107 CCAGTGAGGTTCCAGCAGCCGTGAAGAGAGAGGGGCCAAGCACCCTTGTATCCTGGAGT 4166

Db   867 CTGTTCCGAGCAGCAGCACTCAGTAAGAAGGTGCTGACTTGATTCATTTTCTGCCTCCTCA 926
          | |||||||||||||| | || |||||| |||||| ||| || |||| ||||||| |||
Qy 4167 CCTTGTTCCGAGCAGTAATCACTAAGAAGGTGCTGATTTGGTTTGGTTTTCTGCTCCTCA 4226

Db   927 AGTATTAAGTCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGCGTCATCAAAAATT 986
          | || || ||||| ||| |||||| ||||||||||||||||| |||||||||||||
Qy 4227 AATATCGAGCCAGGGAGCCCAGTCACACAAAGCAGAAATGCTGGAGAGTGTCATCAAAAATT 4286

Db   987 ACAAGCCGCTGCTTTCCTGAGATCTTCGGCCAAAGCTCCGAGTTCCTTGCAGCTGGTCTTTG 1046
          |||||| | ||| ||||||||||||||||| ||||| ||||| || |||||||||||||
Qy 4287 ACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCTCCTGAGTCCTTGCAGCTGGTCTTTG 4346

Db 1047 GCAATTGACGTGAAGGAAGCGGACCCCACCCAGCAACCACTCACACCCTTGTCACCTGCCTGG 1106
          |||||||||||||||||||| |||||||||| | ||||| | |||| ||||||||||| |
Qy 4347 GCAATTGACGTGAAGGAAGCAGACCCCACCCACGCCCACTCCTATGTCCTTGTCACCTGCCTAG 4406

Db 1107 GACTCCTATGATGCCTGCTGTGGTTGATATAATCAGATCATGCCCAAGACAGCGGCCTCCTG 1166
          | || ||||||| |||| | |||||||||||||||||||||||||||||| ||| ||||
Qy 4407 GTCTCTCCT-ATGATGGGCTGCTGGGTGATAATCAGATCATGCCCAAGACAGCAGGCTTCCTG 4465

Db 1167 ATAATCGTCTTGGGCATGATTGCAATGGAGGGGAAATGCGTCCTGAGAGGAAAATCTGG 1226
          ||||| ||| | | |||||||||||||||| | | ||| |||||||||||||||||
Qy 4466 ATAATTGTCTGGTCATGATTGCAATGGAGGCGGCCATGCTCCTGAGGAGGAAAATCTGG 4525

Db 1227 GAGGAGCTGAGTGATGAAGGTGTATGTTGGGAGGAGCTGTCTGTGGGAGCCC 1286
          ||||||||||||| ||||||||||| | |||||||| | || | ||||||
Qy 4526 GAGGAGCTGAGTGTGATGAGGTGTATGATGGGAGGAGCCACAGTGTATGGGGAGCCC 4585

Db 1287 AGGAAGCTGCTCACCCAAGATTTGTGCAGGAAAACTACCTGGAGTACCGCGCAGGTGCCC 1346
          ||||||||||||||||||||||| | ||||||| |||||||||||| |||||||||| |
Qy 4586 AGGAAGCTGCTCACCCAAGATTTGGTCAGGAAAAGTACCTGGAGTAC-GGCAGGTGCCG 4644

Db 1347 AGCAGTGATCCCATATGCTATGAGTAGTTACTGTGGGGTCCAAGGGCCACTCCGCTG 1398
          |||||||||||| | || ||||||| || || |||| || |||||| | ||||||
Qy 4645 GACAGTGATCCCGCACGCTATGAGTTCCTGTGGGTCCCAAGGGCCCTCCGCTG 4696

RESULT 12
ID   US-08-299-849B-9 STANDARD; DNA; UNC; 4157 BP.
AC   xxxxxx
DT   01-JAN-1900
DE   Sequence 9, Application US/08299849B.
CC   Sequence 9, Application US/08299849B
CC   Patent NO. 5612201
CC   GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;

```
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC     ADDRESSEE: Felfe & Lynch
CC     STREET: 805 Third Avenue
CC     CITY: New York City
CC     STATE: New York
CC     ZIP: 10022
CC   COMPUTER READABLE FORM:
CC     MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC     COMPUTER: IBM
CC     OPERATING SYSTEM: PC-DOS
CC     SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC     APPLICATION NUMBER: US/08/299,849B
CC     FILING DATE: 1-SEPTEMBER-1994
CC     CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 08/037,230
CC     FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: PCT/US92/04354
CC     FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 07/807,043
CC     FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 07/764,364
CC     FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 07/728,838
CC     FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC     APPLICATION NUMBER: 07/705,702
CC     FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Hanson, No. 5612201man D.
CC     REGISTRATION NUMBER: 30,946
CC     REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: (212) 688-9200
CC     TELEFAX: (212) 838-3884
CC   INFORMATION FOR SEQ ID NO: 9:
CC     SEQUENCE CHARACTERISTICS:
CC       LENGTH: 4157 base pairs
CC       TYPE: nucleic acid
CC       STRANDEDNESS: single
CC       TOPOLOGY: linear
CC     MOLECULE TYPE: genomic DNA
CC     FEATURE:
CC       NAME/KEY: MAGE-2 gene
SQ   Sequence 4157 BP; 953 A; 1134 C; 1185 G; 885 T; 0 other;

Query Match   58.7%;  Score 488;  DB 7;  Length 4157;
Best Local Similarity  81.2%;  Pred. No. 0.00e+00;
Matches  641;  Conservative  0;  Mismatches 147;  Indels  1;  Gaps  1;

Db  2710 CGGCTTCTTCCTCTTCCTACTCTAGTGGAAGTTACCCTGGGGAGAGTGCCTGCTGCCGACT 2769
         ||| || ||||| ||| |||| ||| |||||||||||||| |||||  |||||
Qy  3972 CCACCTCCTCCTCCTCCTCCTGTCTCCTGGCACCCTGGCACGAGTGCCCTGCTGGGT 4031
Db  2770 CACCGGAGTCCTCCCCACAGTCCTCAGGGAGCCTCCAGCTTCTGACTACCATCAACTACA 2829
         || | ||||||| |||| ||||||||||||||| ||| | |||||||||||||||| ||
Qy  4032 CAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCCAGCTTCCCACTACCATCAACTTCA 4091
Db  2830 CTCTTTGGAGACAATCCGATGAGGGCTCCAGCAACCAAGAACAAGAGAGGGCCAAGAATGT 2889
         ||| ||| ||| |||||||| ||||| |||||||||| || |||||||||||||| |
Qy  4092 CTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCGCGTGAAGAGGAGGAGGGCCAGCACCT 4151
Db  2890 TTCCCGACCTGGAGTCCGAGTTCCAAGCAGCAGCAATCAGTAGGAAGATGGTTGAGTGGTTC 2949
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Qy  4152 CTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAGAGGTGGCTGATTTGGTTG 4211
         |||||||||||  |||||  |||||  ||| |  ||||||  |||  |||  |||  ||||||
Db  2950 ATTTTCTGCTCCTCAAGTATCGACCCAGGAGGCCGGTCACAAAGGCAGAAATGCTGGAGA 3009
Qy  4212 GTTTTCTGCTCCTCAAATATCGAGCCAGGAGGCCAGTCACAAAGGCAGAAATGCTGGAGA 4271
Db  3010 GTGTCCTCAGAAATTGCCAGGACTTCTTTCCCGTGATCTTCAGCAAAGCCTCCAGTACT 3069
Qy  4272 GTGTCATCAAAATTACAGCACTGTTTTCCTGAGATCTTCGGCAAGAGCCTCTGAGTCCT 4331
Db  3070 TGCAGCTGGTCTTTGGCATCGAGTGGTGGAAGTGGTCCCCATCAGCCACTTGTACATCC 3129
Qy  4332 TGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACAGACCCACCGGCCACTCCTATGTCC 4391
Db  3130 TTGTCACCTGCCTGCCCTCCTCACGATGGCCCTGCTGGGCGACAATCAGGTCATGCCCA 3189
Qy  4392 TTGTCACCTGCCTAGGTCTCTCCTATGATGGCCCTGGGTGATAATCAGATCATGCCCA 4451
Db  3190 AGACAGGCCTCCTGTGATAATCGTCCTGGCCATAATCGCAATAGAGGGGCGACTGTGCCCCTG 3249
Qy  4452 AGACAGGCTTCCTGTGATAATTGTCTGGTCATGATTGCAATGCAGGCGGCCATGCTCCTG 4511
Db  3250 AGGAGAAAATCTGGGAGAGCGTGAGTATGTTGGAGGTGTTTGAGGGAGGAGGAGGACAGTG 3309
Qy  4512 AGGAGGAAATCTGGGAGGAGCTGAGTGTTGATGGAGGTGTATGATGGGAGGAGCCACAGTG 4571
Db  3310 TCTTCGCACATCCCAGGAGAGTGCTCATCAGAGATCTGTGCAGGAAAACTACCTGGAGT 3369
Qy  4572 CCTATGGGGAGCCCAGGAAGCTGCTCACCCAGATTTGTGCAGGAAAAGTACCTGGAGT 4631
Db  3370 ACCGGCAGGTGCCGGCAGTGATCCTGCATGCTACGAGTTCCTGTGGGTCCAAGGGCCC 3429
Qy  4632 AC-GGCAGGTGCCGGCACAGTGATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCC 4690
Db  3430 TCATTGAAACCAGTCAGTGATGTGAAAGTCCTGCCACCATACACTAAAGATCGGTGGAGAACCTC 3489
Qy  4691 TCGGTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTC 4750
Db  3490 ACATTTCCT 3498
         ||| || ||
Qy  4751 GCTTTTTCT 4759
```

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Db  3370 ACCGGCAGTGCCCGCAGTGATCCTGCATGCTACGAGTTCCTGTGGGTCCAAGGGCCC 3429
         ||  ||||||||| | ||||||||| ||| |||| ||||||||||||||||||||||
Qy  4632 AC-GGCAGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCC 4690

Db  3430 TCATTGAAACCAGCTATGTGAAAGTCCTGCACCATACACTAAAGATCGGTGGAGACCTC 3489
         |||||||||||||||||||||| |||||||| |||||||||| || | |||||||||
Qy  4691 TCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTC 4750

Db  3490 ACATTTCCT 3498
         |  ||| ||
Qy  4751 GCTTTTTCT 4759
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RESULT 14
ID US-08-299-849B-20 STANDARD; DNA; UNC; 1810 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 20, Application US/08299849B.
CC Sequence 20, Application US/08299849B
CC Patent No. 5612201
CC GENERAL INFORMATION:
CC   APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
CC   APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
CC   APPLICANT: Chomez, Patrick
CC   TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
CC   TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precurso
CC r
CC   NUMBER OF SEQUENCES: 48
CC   CORRESPONDENCE ADDRESS:
CC   ADDRESSEE: Felfe & Lynch
CC   STREET: 805 Third Avenue
CC   CITY: New York City
CC   STATE: New York
CC   ZIP: 10022
CC   COMPUTER READABLE FORM:
CC   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
CC   COMPUTER: IBM
CC   OPERATING SYSTEM: PC-DOS
CC   SOFTWARE: Wordperfect
CC   CURRENT APPLICATION DATA:
CC   APPLICATION NUMBER: US/08/299,849B
CC   FILING DATE: 1-SEPTEMBER-1994
CC   CLASSIFICATION: 435
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 08/037,230
CC   FILING DATE: 26-MARCH-1993
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: PCT/US92/04354
CC   FILING DATE: 22-MAY-1992
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/807,043
CC   FILING DATE: 12-DECEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/764,364
CC   FILING DATE: 23-SEPTEMBER-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/728,838
CC   FILING DATE: 9-JULY-1991
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER: 07/705,702
CC   FILING DATE: 23-May-1991
CC   ATTORNEY/AGENT INFORMATION:
CC   NAME: Hanson, No. 5612201man D.
CC   REGISTRATION NUMBER: 30,946
CC   REFERENCE/DOCKET NUMBER: LUD 5355
CC   TELECOMMUNICATION INFORMATION:
CC   TELEPHONE: (212) 688-9200
CC   TELEFAX: (212) 838-3884
CC INFORMATION FOR SEQ ID NO: 20:
CC   SEQUENCE CHARACTERISTICS:
CC   LENGTH: 1810 base pairs
CC   TYPE: nucleic acid
CC   STRANDEDNESS: single
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        FILING DATE: 23-SEPTEMBER-1991
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/728,838
        FILING DATE: 9-JULY-1991
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 07/705,702
        FILING DATE: 23-May-1991
      ATTORNEY/AGENT INFORMATION:
        NAME: Hanson, No. 534277 4man D.
        REGISTRATION NUMBER: 30,946
        REFERENCE/DOCKET NUMBER: LUD 253.3
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 688-9200
        TELEFAX: (212) 838-3884
    INFORMATION FOR SEQ ID NO: 9:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 4157 base pairs
        TYPE: NUCLEIC ACID
        STRANDEDNESS: singular
        TOPOLOGY: linear
      MOLECULE TYPE: genomic DNA
      FEATURE:
        NAME/KEY: MAGE-2 gene
SQ  Sequence 4157 BP; 953 A; 1134 C; 1185 G; 885 T; 0 other;
```

Query Match   58.7%;   Score 488; DB 4; Length 4157;
Best Local Similarity   81.2%;   Pred. No. 0.00e+00;
Matches   641;   Conservative   0;   Mismatches 147;   Indels   1;   Gaps   1;

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Db  2710 CCGCTTCACTGCTGTCTCTCTTCCTCTTCACTGTCAGTGGAAGTTACCCTGGGGGAAGGTGCCTGCCTGCCGACT 2769
         || | ||||| ||  |  |||| ||| ||| |||||||| |||||||  ||||||| | ||
Qy  3972 CCACCTCCTCCTCCTCCCTCCTCTGGTCCTGGCACCCTGGAGGAGGTGCCCACTGCTGGGT 4031

Db  2770 CACCGAGTCCTCCCACAGTCCTCAGGGAGCCTCAGTTCTGACTACCATCAACTACA 2829
         || | ||||||||  |||||||||||||||||  ||| |||||||||||||||| ||
Qy  4032 CAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCACTACCATCAACTTCA 4091

Db  2830 CTCTTTGGAGACAATCCGATGAGGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGAATGT 2889
         ||  |   ||  |  |||||| ||||| ||||||||||||||||||||||||  |||||||
Qy  4092 CTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCCGTGAAGAGGAGGGGCCAAGCCACCT 4151

Db  2890 TTCCCGACCTGGAGTCCGAGTTCCAAGCAGCAATCAGTAGGAGATGGTTGAGTTGGTTC 2949
         |||||||||||||||  ||||| |||||||| || | ||| ||||| |||||||||||||
Qy  4152 CTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAGAGGTGGCTGATTTGGTTG 4211

Db  2950 ATTTTCTGCTCCTCAAGTATCGAGCCAGGGCGGTCACAAAGCAGAAATGCTGGAGA 3009
         |||||| |  ||||| | |||  |||||||||||||||||||||||||||||||||
Qy  4272 GTGTCATCAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCT 4331

Db  3010 GTGTCCTCAGAAATTGCCAGGACTTCTTTCCCGTGATCTTCAGCAAAGCCTCCGAGTACT 3069
         |||| |||| ||  |||  || |  | |||  |||||||||||||||| |||| ||||||
Qy  4272 GTGTCATCAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCT 4331

Db  3070 TGCAGTGATCTTGGCATCGAGGTGGTGGAAGTGGTCCCCATCAGCCACTGTACATCC 3129
         ||||| |||  ||||||  ||||| |||| ||||  || | ||||||| |  |||||
Qy  4332 TGCAGCTGGTCTTTGGCATTGACGTGAAGGAGCAGAGCCCACCTCCTATGTCC 4391

Db  3130 TTGTCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGCGGCGACAATCAGGTCATGCCCA 3189
         | ||||||||  || |  || | || |||||||||||||||||| | |||||| |||||||
Qy  4392 TTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCA 4451

Db  3190 AGACAGGCCTCCTGATAATCGTCCTGCCCATAATAGAGGGGCGACTGTGCCCCTG 3249
         || ||||| || || |||||||||||| ||| | || || ||||||||||||||
Qy  4452 AGACAGGCTTCCTGATAATTGTCCTGGTCAATGATTGCAATGGAGGGGCCGGCCATGCTCCTG 4511

Db  3250 AGGAGAAAATCTGGAGGAGCTGAGTATGTTGAGGGAGGAGGACAGTG 3309
         ||| ||||||||||  |||| |||||  |  ||||||||||||| |||
Qy  4512 AGGAGAAAATCTGGAGGAGCTCAGTGTGTCATGGTGTATGGGAGGAGCCACAGTG 4571

Db  3310 TCTTCGCCACATCCCAGGAAGCTGCTCATGCAAGAATCTGTGCAGCAGAAAACTACCTGGAGT 3369
         |  | |||  |||||||||||||| | ||| ||||| |||||||||| ||||  ||||||||
Qy  4572 CCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGTGCAGGAAAAGTTGGTGCAGGAAAAGTACCTGGAGT 4631
```

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CC      TOPOLOGY: linear
CC      MOLECULE TYPE: genomic DNA
CC      FEATURE:
CC        NAME/KEY: MAGE-8 gene
SQ   Sequence 1810 BP; 402 A; 463 C; 508 G; 437 T; 0 other;

Query Match      55.8%;  Score 464;  DB 7;  Length 1810;
Best Local Similarity 82.2%;  Pred. No. 0.00e+00;
Matches  663;  Conservative  0;  Mismatches 133;  Indels 11;  Gaps  6;

Db    556  GCAGAAGGTGCATCCTCCTCCTCACTCTGATCATGGGAACCCTGAGGAGGTGACTGA 615
           |||||  || ||||| ||||||||||||||||  |||| ||||||  ||||||| |
Qy   3964  GCAGGCGCCACCTCCTCCTCCTCTCTCGGTCCTCTGGGCACCCTGGGGAGTGCCCAC 4023

Db    616  TTCTGGGTCACCAAGTCCTCCCCCAGAGTCCTGAGGGTGCCTCCTTCCCTGACTGTCAC 675
           | |||||||||||||| |||||||||||||||||||||| | |||  || ||  |
Qy   4024  TGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCCCGCCCTTCCCACTACCAT 4083

Db    676  CGACAGCACTCTGTGGAGCAATCCGATGAGGGTTCAGCAGCAATGAAGAGGAGGGGC 735
           | || ||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy   4084  CAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCC 4143

Db    736  AAGCACCTCCCCCGACCCCAGCTCACCTGAGTCCCTGTTCCGGGAAGCACTTGATGAGAA 795
           ||||||||   |     |  | || |  |  |||||| | |||||   | | |||
Qy   4144  AAGCACCTCT--GT---A--TC--CTGGAGTCCTTGGTTCCGAGCAGTAATCACTAAGAA 4194

Db    796  AGTGGCTGAGTTAGTTCGTTCCTGCTCCCCCAAATATCAAATTAAGGAGCCGGTCACAAA 855
           ||||||||||| || || |||||||||||   ||||| || ||  | |||||||||||||
Qy   4195  GGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCCAGGGAGCCAGTCACAAA 4254

Db    856  GGCAGAAATGCTTGAGAGTGTCATCAAAAATTACAGAGAACCACTTTCCTGATATCTTCAG 915
           ||||||| |||||||||||||||||||||||| ||  |||||| || |||||||||||
Qy   4255  GGCAGAAATGCTGGAGAGTGTCATCAAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGG 4314

Db    916  CAAAGCCCTGAGTGCATGCAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCCTGC 975
           |||  |||| ||  | ||||||||||| |||||  |||||||| ||||| ||  |||||
Qy   4315  CAAAGCCCTGGTGTCCTTGCAGCTGGTCTTGGCATTGACGTGAAGGAAGCAGAGCCCCAC 4374

Db    976  CGGGCCACTCCTACATCCTTGTCACCTGCCTGGCCTCTCCTATGATGAGGCCTGGGTGA 1035
           |||||||||||||||  |||||||||||||||||||||||||||||||| |||||||||
Qy   4375  CGGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGA 4434

Db   1036  TGATCAGATACGGCCCAAGCACCGGCCTCCTGATATCGTCCTGATGATCTTAATGGA 1095
           | ||||| ||||||||||||||   ||||||||| ||  |||||  ||||| ||||
Qy   4435  TAATCAGATCATGCCCAAGAACAGCAGGCTTCCGTGATAATTGTCCTGGTCATGATTGCAATGGA 4494

Db   1096  GGCAGCCGCGCCGCCCCCGGGAGGAGCCAATCTGGGAAGCATTGGGGGCTGTATG 1155
           |||| || || |||||||||||||||||| | ||||| | || ||||||| ||||
Qy   4495  GGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGGTGATGGAGG-TGTATG 4553

Db   1156  ATGGGAGGGAGCACAGTGTCTATTGGAAGCTCAGGAAGCTGCTCACCCAAGAGTGGGTGC 1215
           |||||||||||||||||||| ||  || || |||||  |||||||||||  |||||||||
Qy   4554  ATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAGCTGCTCACCCAAGATTTGGTGC 4613

Db   1216  AGGAGAACTACCTGGAGTACCGGCCCAGGCCGCCCGGCGCCTGTGCCTACGAGTTCC 1275
           ||||||| || |||||||||| |  | | |||||| | | ||||| |||||||||||
Qy   4614  AGGAAAAGTACCTGGAGTACGGC-AGGTGCCGGACAGTGAGCGTTTCTCGTGATCTTCGGCAA 4672

Db   1276  TGTGGGGTCCAAGGGCCCTTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCA 1335
           ||||||||||||||||||||||||||||||||||| ||||| || |||| |  ||||| |
Qy   4673  TGTGGGGTCCAAGGGCCCTCGCTGAAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCA 4732

Db   1336  GGGTCAATGCAAGAGTTCGCATTTCCT 1362
           ||||| |||||||||||||| ||| ||
Qy   4733  AGGTCAGTGCAAGAGTTCGCTTTTTTCT 4759

RESULT   15
ID    US-08-299-849B-15 STANDARD; DNA; UNC; 1068 BP.
AC    xxxxxx
DT    01-JAN-1900
DE    Sequence 15, Application US/08299849B.
CC    Sequence 15, Application US/08299849B.
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Qy   4258 AGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAA 4317
          ||||||||||||||||  ||||||||||||||||||||||| ||| ||||||| |||||||||||||

Db    181 AGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAG 240
          |||||| |||||| -||-||-||| |||||||||||||||||| ||||||| |||-|||-
Qy   4318 AGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGG 4377

Db    241 CAACACCTACACCCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAA 300
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Qy   4378 CCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAA 4437

Db    301 TCAGATCTTTCCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGG 360
          ||||||| |||||||||||| - |||||| ||||||||| -|| |||||||||||||||
Qy   4438 TCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTGCATGATTGCAATGGAGGG 4497

Db    361 CGACAGCGCCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGTGTATGATGG 420
          ||- || ||||||||||||||||||||||||||||||||| |||||||||||||||||
Qy   4498 CGGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGG 4557

Db    421 GAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAACTGCTCACCCAAGATTGGGTGCAGGA 480
          |||||||||| || ||||||||||||| |||||||||| |||||||| |||||||||
Qy   4558 GAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGA 4617

Db    481 AAACTACCTGGAGTCCCGGCCAGGTACCCGGCAGTAATCCTGCGGCGTATGAGTTCCTGTG 540
          ||| |||||||||||||| ||-||| ||| -||||||||||||-||||||||||||||
Qy   4618 AAAGTACCTGGAGTAC-GGCAGGTGCCGGACAGTGAATCCCGCACGCTATGAGTTCCTGTG 4676

Db    541 GGGTCCAAGGGCTCTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGCTCAGGGT 600
          |||||||||||| ||- ||||||| ||||||||||||||||| ||| ||||| ||| |||
Qy   4677 GGGTCCAAGGGCCCCTCGCTGAAACCAGCTATCTGAGTATGTGAGTATGTGATCAAGGT 4736

Db    601 CAATGCAAGAGTTCGCATT 619
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Qy   4737 CAGTGCAAGAGTTCGCTTT 4755
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Search completed: Tue Apr 7 22:20:44 1998
Job time : 53 secs.

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 **************************************
 *   M P S R C H                (TM)  *
 **************************************

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 **************************************

MPsrch_nn    n.a.  -  n.a. database search, using Smith-Waterman algorithm

Run on:         Tue Apr  7 21:57:15 1998;  MasPar time 152.21 Seconds
                                           1266.269 Million cell updates/sec

Tabular output not generated.

Title:          >US-08-190-411A-1
Description:    (57-219) from 5541104.seq
Perfect Score:  163
N.A. Sequence:  57 ACCCATCCAAACATCTTCAC.........TCGGTCTGAGGGGCGGCTTG 219
    Comp:          TGGGTAGTTGTAGAAGTG.........AGCCAGACTCCCGCCCGAAC

Scoring table:  TABLE default
                Gap 6

Nmatch  STD :   Dbase 0:  Query 0

Searched:       354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       embl53
                1:em_in  2:em_or  3:em_om  4:em_ov  5:em_pl  6:em_htg
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                13:em_pat

Database:       genbank105
                14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
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                26:gb_htg

Statistics:     Mean 8.931;  Variance 4.495;  scale 1.987

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	163	100.0	5674	25	I24013	Sequence 1 from patent	1.03e-107
2	163	100.0	5674	25	I36923	Sequence 8 from patent	1.03e-107
3	71	43.6	4157	25	I36924	Sequence 9 from patent	2.47e-34
4	70	42.9	662	25	I36925	Sequence 10 from paten	1.43e-33
5	32	19.6	215	25	I28278	Sequence 2 from patent	2.13e-06
6	28	17.2	215	25	I28278	Sequence 5 from patent	6.77e-04
7	24	14.7	565	25	E04076	gDNA encoding envelope	1.55e-01
8	22	13.5	105	25	I14734	Sequence 13 from paten	2.01e+00
9	22	13.5	448	25	I59655	Sequence 7 from patent	2.01e+00
10	21	12.9	531	14	AF013283	Mus musculus T-box fam	6.93e+00
c 11	21	12.9	565	25	E04076	gDNA encoding envelope	6.93e+00
12	21	12.9	902	16	AF020225	Sauromalus obesus stra	6.93e+00
13	21	12.9	1442	25	I08570	Sequence 13 from Paten	6.93e+00
14	21	12.9	1442	15	DOGSP18A	Dog pulmonary surfacta	6.93e+00

	15	21	12.9	1442	25	I08031	Sequence 4 from patent	6.93e+00
	16	21	12.9	1453	25	I00318	Sequence 3 from Patent	6.93e+00
c	17	21	12.9	2364	19	STMSSPP	Streptomyces griseus s	6.93e+00
c	18	21	12.9	3233	19	TTARGOPER	T.thermophilus arg ORF	6.93e+00
	19	21	12.9	7218	25	I66494	Sequence 14 from paten	6.93e+00
	20	21	12.9	11434	19	AE001097	Archaeoglobus fulgidus	6.93e+00
	21	21	12.9	13725	19	AE000832	Methanobacterium therm	6.93e+00
	22	21	12.9	78064	26	HSAC000376	*** SEQUENCING IN PROG	6.93e+00
	23	21	12.9	119069	26	HS138B7	Human DNA sequence ***	6.93e+00
c	24	21	12.9	179017	26	HS102D24	Human DNA sequence ***	6.93e+00
	25	21	12.9	238000	26	HSAC000134	Homo sapiens clone 137	6.93e+00
c	26	20	12.3	69	21	I41362	Sequence 142 from pate	2.30e+01
	27	20	12.3	1491	14	MMU69135	Mus musculus UCP2 mRNA	2.30e+01
	28	20	12.3	2393	15	OAINIGFII	Ovis aries insulin gen	2.30e+01
c	29	20	12.3	3946	16	GGDMIACK	G.gallus Mia-CK gene.	2.30e+01
c	30	20	12.3	7218	25	I66494	Sequence 14 from paten	2.30e+01
c	31	20	12.3	15975	14	D10911	Mus musculus DNA for M	2.30e+01
	32	20	12.3	110000	26	AC003656	*** SEQUENCING IN PROG	2.30e+01
	33	19	11.7	3157	25	I68739	Sequence 3 from patent	7.35e+01
c	34	19	11.7	3225	14	RNMAFAEX1	R.norvegicus MAFA gene	7.35e+01
c	35	19	11.7	3658	14	AF035045	Mus musculus MaxiK pot	7.35e+01
	36	19	11.7	5275	16	GGAX1EX	G.gallus axonin-1 gene	7.35e+01
	37	19	11.7	32458	17	CER10E11	Caenorhabditis elegans	7.35e+01
	38	19	11.7	36470	19	U00014	Mycobacterium leprae c	7.35e+01
c	39	19	11.7	47165	26	HSLUCA7	Human DNA sequence ***	7.35e+01
	40	19	11.7	103290	26	HS234H5	Human DNA sequence ***	7.35e+01
c	41	19	11.7	115060	26	HS73E16	Human DNA sequence ***	7.35e+01
c	42	19	11.7	129913	26	HS989H11	Human DNA sequence ***	7.35e+01
	43	19	11.7	140596	26	HS745E8	Human DNA sequence ***	7.35e+01
c	44	19	11.7	149436	26	HS222E13	Human DNA sequence ***	7.35e+01
c	45	19	11.7	223457	26	AC003658	Homo sapiens; HTGS pha	7.35e+01

ALIGNMENTS

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RESULT        1
LOCUS         I24013
DEFINITION    Sequence 1 from patent US 5541104.
ACCESSION     I24013
NID           g1603883
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 5674)
  AUTHORS     Chen,Y., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J., van der
              Bruggen,P., Boon-Falleur,T. and Old,L.J.
  TITLE       Monoclonal antibodies which bind to tumor rejection antigen
              precursor mage-1
  JOURNAL     Patent: US 5541104-A 1 30-JUL-1996;
FEATURES             Location/Qualifiers
     source          1..5674
                     /organism="unknown"
BASE COUNT     1276 a   1644 c   1569 g   1185 t
ORIGIN

Query Match    100.0%;  Score 163;  DB 25;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 1.03e-107;
  Matches 163;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db      57 ACCCATCCAAACATCTTCACGCTCACCCCCAGCCAGCCAGGCAGAATCCGGTTCCACC 116
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Qy      57 ACCCATCCAAACATCTTCACGCTCACCCCCAGCCAGCCAGGCAGAATCCGGTTCCACC 116

Db     117 CCTGCTCTCAACCCAGGGAAGCCCAGATGTGACGGCCACTGACTTGAGCATTA 176
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Qy     117 CCTGCTCTCAACCCAGGGAAGCCCAGATGTGACGGCCACTGACTTGAGCATTA 176

Db     177 GTGGTTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTG 219
           |||||||||||||||||||||||||||||||||||||||||||
Qy     177 GTGGTTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTG 219
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RESULT     2
LOCUS        I36923        5674 bp    DNA              PAT        21-APR-1997
DEFINITION   Sequence 8 from patent US 5612201.
ACCESSION    I36923
NID          g2084883
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 5674)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 8 18-MAR-1997;
FEATURES             Location/Qualifiers
  source             1..5674
                     /organism="unknown"
BASE COUNT    1276 a    1644 c    1569 g    1185 t
ORIGIN

Query Match          100.0%;   Score 163;  DB 25;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 1.03e-107;
Matches   163;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     57 ACCCATCCAAACATCTTCACGCTCACCCCAGCCCAGCCCAAGCCCAGGCAGAATCCGGTTCCACC 116
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Qy     57 ACCCATCCAAACATCTTCACGCTCACCCCAGCCCAGCCCAAGCCCAGGCAGAATCCGGTTCCACC 116

Db    117 CCTGCTCTCAACCCAGGGAAGCCCAGTGCCCAGTGACGCCACTGACCTTGAGCATTA 176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    117 CCTGCTCTCAACCCAGGGAAGCCCAGTGCCCAGTGACGCCACTGACCTTGAGCATTA 176

Db    177 GTGGTTAGAGAGAAGCCAGGTTTTCGGTCTGAGGGGCGGCTTG 219
          |||||||||||||||||||||||||||||||||||||||||||
Qy    177 GTGGTTAGAGAGAAGCCAGGTTTTCGGTCTGAGGGGCGGCTTG 219


RESULT     3
LOCUS        I36924        4157 bp    DNA              PAT        21-APR-1997
DEFINITION   Sequence 9 from patent US 5612201.
ACCESSION    I36924
NID          g2084884
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 4157)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 9 18-MAR-1997;
FEATURES             Location/Qualifiers
  source             1..4157
                     /organism="unknown"
BASE COUNT     953 a    1134 c    1185 g     885 t
ORIGIN

Query Match          43.6%;    Score 71;  DB 25;  Length 4157;
Best Local Similarity 77.1%;   Pred. No. 2.47e-34;
Matches   108;  Conservative   0;  Mismatches  31;  Indels   1;  Gaps   1;

Db      3 CATCCAGAATCCCCATCCGGGCGGCAGAATCCCGGTTCCACCCTTGCCGTGAACCCAGGGAAGTC 62
          || |||  |||| | ||||||||||| ||||||||||| ||| |||||||||||||||||
Qy     80 CACCCCCAGCCCAGCCCAAGCCCAGGCAGAATCCGGTTCCACCCCTCTCCACCCCAGGGAAGCC 139

Db     63 ACGG-GCCCGGATGTGACGCCACTGACTTGACATTGAGGTCAGAGGACCAGCGAGATTC 121
          || |||||||||||||||||||||||||||| |||| |  ||  || |||||| ||
Qy    140 CAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTT 199

Db    122 TCGCCCTGAGCAACGGCCTG 141
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Qy    200 TCGGTCTGAGGGGCGGCTTG 219


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DEFINITION   Sequence 10 from patent US 5612201.
ACCESSION    I36925
NID          g2084885
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 662)
  AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE      Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL    Patent: US 5612201-A 10 18-MAR-1997;
FEATURES             Location/Qualifiers
  source             1..662
                     /organism="unknown"
BASE COUNT     155 a     244 c     176 g      87 t
ORIGIN

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Best Local Similarity 80.0%;   Pred. No. 1.43e-33;
Matches   100;  Conservative   0;  Mismatches  24;  Indels   1;  Gaps   1;

Db     15 CCAGGAAGAATCCAGTTCACCCCCTGCTGTGAACCCAGGAAGTCACGGGGCCG-GATGT 73
          |||||  ||||||||| |||||||||||||||||  ||||||||| || ||||  ||||
Qy     95 CCAGGCAGAATCCGGTTCCACCCCTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGT 154

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          |||||||||||| |||| | |||  || ||||| |||  ||||||| ||||||| ||
Qy    155 GACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCG 214

Db    134 GCCTG 138
          || ||
Qy    215 GCTTG 219


RESULT     5
LOCUS        I28278         215 bp    DNA              PAT        30-OCT-1996
DEFINITION   Sequence 5 from patent US 5569830.
ACCESSION    I28278
NID          g1819054
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 215)
  AUTHORS    Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
  TITLE      Plant inhibitors of fungal polygalacturonases and their use to
             control fungal disease
  JOURNAL    Patent: US 5569830-A 5 29-OCT-1996;
FEATURES             Location/Qualifiers
  source             1..215
                     /organism="unknown"
BASE COUNT      15 a       8 c      25 g      26 t     141 others
ORIGIN

Query Match          19.6%;    Score 32;  DB 25;  Length 215;
Best Local Similarity 17.6%;   Pred. No. 2.13e-06;
Matches   15;  Conservative  37;  Mismatches  33;  Indels   0;  Gaps   0;

Db     96 DSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSDK 155
          :::  :  |  :  :  : | | :::      : :| :: :|::|:::
Cp    163 AGTGGGGTCACATCTGGCACCTGGGCTTCCCTGGGTTGAGAGCAGAGGGTGGAACCGGAT 104

Db    156 NTKKHAKNSADGKVGSKNNGDRNNR 180
          :::::|||||||| :::  :: ||
Cp    103 TCTGCCTGGCTTGGGCTGGGGGTGA 79
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RESULT   6
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ACCESSION   I28278
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KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 215)
AUTHORS   Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
TITLE   Plant inhibitors of fungal polygalacturonases and their use to
              control fungal disease
JOURNAL   Patent: US 5569830-A 5 29-OCT-1996;
FEATURES   Location/Qualifiers
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BASE COUNT   15 a   8 c   25 g   26 t   141 others
ORIGIN

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Best Local Similarity 13.7%; Pred. No. 6.77e-04;
Matches   13; Conservative   46; Mismatches 35; Indels   1; Gaps   1;

Db   79 HYTHTNVSGADSKTVIDSYNASGTSSSNGGTDGNRSGA-DSYGSSKTAMTSRNRTGKTA 137
               :::|: |:|::|: |::|:| :::|:: | ::||:   :::|:| |:
Qy   121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGGCCACTGACTTGAGCATTAGTGG 180

Db   138 NNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSK 172
               |::::: : ::||:: : ||::|::||:|:|
Qy   181 TTAGAGAAGGCAGGGTTTTCGGTCTGAGGGGCGG 215

RESULT   7
LOCUS   E04076   565 bp   RNA   PAT   26-NOV-1996
DEFINITION   gDNA encoding envelope region of type C hepatitis virus.
ACCESSION   E04076
NID   g2172286
KEYWORDS   JP 1993349885-A/1.
SOURCE   Hepatitis C virus.
ORGANISM   Hepatitis C virus
              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
              Hepatitis C-like viruses.
REFERENCE   1 (bases 1 to 565)
AUTHORS   Tsutae,M., Kazuaki,C., Hiromitsu,K. and Yataro,I.
TITLE   NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
              AND METHOD FOR DETECTING THE SAME
JOURNAL   Patent: JP 1992349885-A 1 04-DEC-1992;
              TEIJIN LTD
              ICHIKAWA YATARO
COMMENT   OS   Hepatitis C virus
              PN   JP 1992349885-A/1
              PD   04-DEC-1992
              PF   29-MAY-1991 JP 1991152169
              PI   MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, PI
              PC   C12N15/10,C12Q1/68,C12Q1/70//C12N15/11;
              CC   strandedness: Single;
              CC   topology: Linear;
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              /db_xref="taxon:11103"
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ORIGIN

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Best Local Similarity 30.9%; Pred. No. 1.55e-01;
Matches   21; Conservative   25; Mismatches 22; Indels   0; Gaps   0;

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               |:|| ||:||::|| |:::::|:| : :|||:: :|:|:: |:|::|| : |::|:
Qy   67 ACATCTTCACGCTCACCCCCAGCCCCAGGCCAGAATCCGGTTCCACCCCTGCTCTCA 126

Db   482 AYSCYGGS 489
               |:::| ||:
Qy   127 ACCCAGGG 134

RESULT   8
LOCUS   I14734   105 bp   DNA   PAT   20-SEP-1995
DEFINITION   Sequence 13 from patent US 5451670.
ACCESSION   I14734
NID   g997217
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 105)
AUTHORS   Miller,M.M.
TITLE   Restriction fragment length polymorphism test for haplotyping
              domesticated fowl
JOURNAL   Patent: US 5451670-A 13 19-SEP-1995;
FEATURES   Location/Qualifiers
source   1..105
              /organism="unknown"
BASE COUNT   15 a   0 c   8 g   1 t   81 others
ORIGIN

Query Match   13.5%;   Score 22; DB 25; Length 105;
Best Local Similarity 11.6%; Pred. No. 2.01e+00;
Matches   8; Conservative   24; Mismatches 37; Indels   0; Gaps   0;

Db   28 KNSGKNKSANAVNNGNNAKNSNNMGTRDKNNRRNAAKNNNSGVADNKNNASNNYD 87
               : ::: ::| | || : :: ::|:| |:|| : ::|: :|: : ||:::
Qy   127 TTGAGAGCAGGGTGGAACCGGATTCTGCCTGGCTTGGGCTGGGGTGAGCGTGAAGATG 68

Db   88 NGSGVADNK 96
               |:|::.:
Qy   67 TTTGGATGG 59

RESULT   9
LOCUS   I59655   448 bp   DNA   PAT   15-AUG-1997
DEFINITION   Sequence 7 from patent US 5654173.
ACCESSION   I59655
NID   g2478287
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 448)
AUTHORS   Jacobs,K., McCoy,J.M., LaVallie,E.R., Racie,L.A., Merberg,D.,
              Treacy,M. and Spaulding,V.
TITLE   Secreted proteins and polynucleotides encoding them
JOURNAL   Patent: US 5654173-A 7 05-AUG-1997;
FEATURES   Location/Qualifiers
source   1..448
              /organism="unknown"
BASE COUNT   121 a   103 c   120 g   78 t   26 others
ORIGIN

Query Match   13.5%;   Score 22; DB 25; Length 448;
Best Local Similarity 27.8%; Pred. No. 2.01e+00;
Matches   10; Conservative   19; Mismatches   7; Indels   0; Gaps   0;

Db   76 RGAKYATRRYGVGRKKTYYRYYSKGKWKSMGGSTT 111
               :||| ::::::|| |:::::::| ::::||||:|
Qy   183 AGAGGAAGCGAGGTTTTCGGTCTGAGGGGCGCTT 218

RESULT   10
LOCUS   AF013283   531 bp   mRNA   ROD   10-JAN-1998
DEFINITION   Mus musculus T-box family member (MmTbx7) mRNA, partial cds.
ACCESSION   AF013283
NID   g2735916

```
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 531)
  AUTHORS   Wattler,S., Russ.A., Evans.M. and Nehls,M.
  TITLE     A combined analysis of genomic and primary protein structure
            defines the phylogenetic relationship of new members of the T-box
            family
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 531)
  AUTHORS   Wattler,S., Russ.A., Evans.M. and Nehls,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-1997) New Technologies, Lexicon Genetics
            Incorporated, 4000 Research Forest Drive, The Woodlands, TX 77381,
            USA
FEATURES    Location/Qualifiers
     source 1..531
            /organism="Mus musculus"
            /db_xref="taxon:10090"
     gene   <1..>531
            /gene="MmTbx7"
     CDS    <1..>531
            /gene="MmTbx7"
            /note="T-box family member; T-box domain"
            /codon_start=1
            /db_xref="PID:g2735917"
            /translation="LWEEFNQLGTEMIVTKAGRMFPTFQVKIILGMDTLADYALLMDFI
            PLDDKRYRYAFHSSAWLVAGKADPATPGRVHFHPDSPAKGAQWMRQIVSFDKLKLTNN
            LMDDNGHIIFNSMHRYQPRFHVVFVDPRKDSARYAQENFKSFVFTETQFTAVTAYQNH
            RITQLKIASNPFAKGFR"
BASE COUNT    129 a    154 c    135 g    113 t
ORIGIN

Query Match     12.9%;    Score 21;   DB 14;  Length 531;
Best Local Similarity   69.8%;   Pred. No. 6.93e+00;
Matches   37;  Conservative   0;  Mismatches   16;  Indels   0;  Gaps   0;

Db   206 CCACGCCTGCAGGGTGCACTTCCACCCTGACTCCGCAGCCAAGGGTGCCCAG 258
         ||| ||| |||| |  |  ||||||||    ||| | ||| || |||||
Qy    90 CCAAGCCAGGCAGAATCCGGTTCCACCCCTGCTCAACCCAGGGAAGCCCAG 142

RESULT 11
LOCUS       E04076        565 bp   RNA           PAT       26-NOV-1996
DEFINITION  gDNA encoding envelope region of type C hepatitis virus.
ACCESSION   E04076
NID         g2172286
KEYWORDS    JP 1992349885-A/1.
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepatitis C-like viruses.
REFERENCE   1 (bases 1 to 565)
  AUTHORS   Tsutae,M., Kazuaki,C., Hiromitsu.K. and Yataro.I.
  TITLE     NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
            AND METHOD FOR DETECTING THE SAME
  JOURNAL   Patent: JP 1992349885-A 1 04-DEC-1992;
            TEIJIN LTD
COMMENT     OS   Hepatitis C virus
            PN   JP 1992349885-A/1
            PD   04-DEC-1992
            PF   29-MAY-1991 JP 1991152169
            PI   MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, PI
            ICHIKAWA YATARO
            PC   C12N15/10,C12Q1/68,C12Q1/70//C12N15/11;
            CC   strandedness: Single;
            CC   topology: Linear;
FEATURES    Location/Qualifiers
     source 1..565
            /organism="Hepatitis C virus"
            /db_xref="taxon:11103"
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BASE COUNT     60 a     93 c    107 g     85 t    220 others
ORIGIN

Query Match     12.9%;    Score 21;   DB 25;  Length 565;
Best Local Similarity   25.4%;   Pred. No. 6.93e+00;
Matches   16;  Conservative   27;  Mismatches   19;  Indels   1;  Gaps   1;

Db   251 ARRYRRYNNYTCBMGNTGYTGGGYRGGCTBACYCCCACGSTYGCVRCYAGRRAYVBYA 310
         |:: ::::  :: :||||:   : :||||  :  :||::::  :: :||:::|   ||
Cp   168 AAGTCAGTGGCGTCACAT-CTGGGACACCTGGGCTTCCCTGGGTTGAGAGCAGGGGGGAA 110

Db   311 VYV 313
         :::
Cp   109 CCG 107

RESULT 12
LOCUS       AF020225      902 bp   DNA           VRT       30-SEP-1997
DEFINITION  Sauromalus obesus strain obesus cytochrome b (cytb) gene,
            mitochondrial gene encoding mitochondrial protein, partial cds.
ACCESSION   AF020225
NID         g2444306
KEYWORDS    .
SOURCE      Sauromalus obesus.
  ORGANISM  Mitochondrion Sauromalus obesus
            Eukaryotae; Metazoa; Chordata; Vertebrata; Lepidosauria; Squamata;
            Iguania; Iguanidae; Sauromalus.
REFERENCE   1 (bases 1 to 902)
  AUTHORS   Petren,K. and Case,T.J.
  TITLE     A Phylogenetic analysis of body size evolution and biogeography in
            chuckwallas (Sauromalus) and other iguanines
  JOURNAL   Evolution 51, 206-219 (1997)
REFERENCE   2 (bases 1 to 902)
  AUTHORS   Petren,K. and Case,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-AUG-1997) EEB, Princeton University, Guyot Hall,
            Washington Rd., Princeton, NJ 08544-1003, USA
FEATURES    Location/Qualifiers
     source 1..902
            /organism="Sauromalus obesus"
            /mitochondrion
            /strain="obesus"
            /db_xref="taxon:51219"
            /note="specimen from Panamint Springs, CA (pop. #15)"
     gene   <1..>902
            /gene="cytb"
     CDS    <1..>902
            /gene="cytb"
            /codon_start=2
            /product="cytochrome b"
            /db_xref="PID:g2444307"
            /transl_table=2
            /translation="LIDLPAPSNISAWNNFGSLLGLCLIIQILGLFLAMHYTADISS
            AFSSIAHICRDVQYGWLIRNLHANGASMFFICLYLHIGRGLYYGSYLFKETWNIGVVL
            LLVMATAFVGYVLPWGQMSFWGATVITNLLSAIPYVGATLVKWIWGGFSVDNATLTR
            FFTFHFLLPFMIGLTMMHLLFLHETGSNNPTGLNSNPDKIPFHPYFSYKDLLGATLM
            IILLTLALFSPNLLGDPENFTPAIPLVTPPHIKPEWYFLFAYAILRSIPNKLGGVLA
            LLFSILIMIIPLLHLSKQRSNTF"
BASE COUNT     244 a    320 c    120 g    218 t
ORIGIN

Query Match     12.9%;    Score 21;   DB 16;  Length 902;
Best Local Similarity   81.8%;   Pred. No. 6.93e+00;
Matches   27;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Db   588 CCAACCCAGACAAAATCCCGTTCCATCCCTACT 620
         |||| |||| || ||||||| || |||||||||
Qy    90 CCAAGCCAGGCAGAATCCGGTTCCACCCCTGCT 122

RESULT 13
LOCUS       I08570       1442 bp                 PAT       14-NOV-1994
DEFINITION  Sequence 13 from Patent WO 8706588.
```

```
RESULT 15
LOCUS       I08031
DEFINITION  Sequence 4 from Patent EP 0251449.                    PAT    14-NOV-1994
ACCESSION   I08031
NID         g589252
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1442)
AUTHORS     Schilling,J.W., White,R.T., Cordell,B. and Benson,B.J.
TITLE       Recombinant alveolar surfactant protein
JOURNAL     Patent: EP 0251449-A2 4 07-JAN-1988;
FEATURES    Location/Qualifiers
   source   1..1442
            /organism="unknown"
BASE COUNT  307 a   452 c   388 g   295 t
ORIGIN

Query Match             12.9%;  Score 21;  DB 25;  Length 1442;
Best Local Similarity   67.8%;  Pred. No. 6.93e+00;
Matches    40;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Db  1215 CTCACACCCAACTGAGACCAGGCCAGCTCCCGTAACCCCCAGCGCTGGTCCAGGGAA 1273
         |||||| |||| | |||||||| ||| ||||| | |||| |  |||||||||
Qy    78 CTCACCCCCAGCCCAAGCCAGGCAGAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAA 136

Search completed: Tue Apr  7 21:59:54 1998
Job time : 159 secs.
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ACCESSION   I08570
NID         g588720
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1442)
AUTHORS     Schilling,J.W., White,R.T., Cordell,B. and Benson,B.J.
JOURNAL     Patent: WO 8706588-A 13 05-NOV-1987;
FEATURES    Location/Qualifiers
   source   1..1442
            /organism="unknown"
BASE COUNT  307 a   452 c   388 g   295 t
ORIGIN

Query Match             12.9%;  Score 21;  DB 25;  Length 1442;
Best Local Similarity   67.8%;  Pred. No. 6.93e+00;
Matches    40;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Db  1215 CTCACACCCAACTGAGACCAGGCCAGCTCCCGTAACCCCCAGCGCTGGTCCAGGGAA 1273
         |||||| |||| | |||||||| ||| ||||| | |||| |  |||||||||
Qy    78 CTCACCCCCAGCCCAAGCCAGGCAGAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAA 136

RESULT 14
LOCUS       DOGSP18A  1442 bp  mRNA         MAM      15-DEC-1988
DEFINITION  Dog pulmonary surfactant protein 18 (SP 18) mRNA, partial cds.
ACCESSION   M15170
NID         g164077
KEYWORDS    pulmonary surfactant-associated protein.
SOURCE      Dog lung, cDNA to mRNA, clones pDSP-1-[1,3,4].
            Canis sp.
ORGANISM    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1 (bases 1 to 1442)
AUTHORS     Hawgood,S., Benson,B.J., Schilling,J., Damm,D.L., Clements,J.A. and
            White,R.T.
TITLE       Nucleotide and amino acid sequences of pulmonary surfactant protein
            SP 18 and evidence for cooperation between SP 18 and SP 28-36 in
            surfactant lipid absorption
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 84, 66-70 (1987)
MEDLINE     87092398
FEATURES    Location/Qualifiers
   source   1..1442
            /organism="Canis sp."
            /db_xref="taxon:9616"
   sig_peptide  <1..540
            /note="surfactant protein 18 signal peptide"
   CDS      <1..1092
            /note="surfactant protein 18 precursor"
            /codon_start=1
            /db_xref="PID:g164078"
            /translation="LLWLLLLPTLCGLGAADWSAPSLACARGPAFWCQSLEQALQCRA
            LGHCLQEVWGNARADDLCQECQDIVRILTKMTKEAIFQDMVRKFLEHECDVLPLKILT
            PQCHMLGTYFPVVVDYFQSOINPKIICKHLGLCKPGLPEPEQESELSDPLLDKLILP
            ELPGALQVTGPHTQDLSEQOLPIPLPYCWLCRTLIKRIQAMIPKGVLAVTVGQVCHVV
            PLVVGICQCIGERYTVLLDALLGRMLPQLVCGLVLRCSHEDSAGPALASLPSEWSP
            QESKCQLCMFVTTOAGNHSEQATPQAIRQACLSSWLDRQKCEQFVEQHMPRLQTLASG
            GRDAHTTCQALGACRTTFSPLQCIHIPHF"
   mat_peptide  541..1092
            /note="surfactant protein 18"
BASE COUNT  307 a   452 c   388 g   295 t
ORIGIN

Query Match             12.9%;  Score 21;  DB 15;  Length 1442;
Best Local Similarity   67.8%;  Pred. No. 6.93e+00;
Matches    40;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Db  1215 CTCACACCCAACTGAGACCAGGCCAGCTCCCGTAACCCCCAGCGCTGGTCCAGGGAA 1273
         |||||| |||| | |||||||| ||| ||||| | |||| |  |||||||||
Qy    78 CTCACCCCCAGCCCAAGCCAGGCAGAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAA 136
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MPsrch_nn  n.a. - n.a. database search, using Smith-Waterman algorithm

Run on:        Tue Apr  7 22:05:00 1998:   MasPar time 673.40 Seconds
                                           1459.176 Million cell updates/sec

Tabular output not generated.

Title:        >US-08-190-411A-1
Description:  (3931-4761) from 5541104.seq
Perfect Score: 831  3931 GGCCCAACAAGAGGCCCTGG..........CAAGAGTTCGCTTTTCTTC 4761
N.A. Sequence:      CCGGGTTGTTCTCCCGGACC..........GTTCTCAAGCGAAAAGAAG
     Comp:

Scoring table: TABLE default
               Gap 6

Nmatch    STD :

Searched:      354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:      embl53
               1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pl 6:em_htg
               7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
               13:em_pat
Database:      genbank105
               14:gb_ro 15:gb_om 16:gb_ov 17:gb_ov 18:gb_pl 19:gb_ba
               20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
               26:gb_htg

Statistics:    Mean 10.687; Variance 5.190;  scale 2.059

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                          SUMMARIES
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Result No.	Score	% Query Match	Query Length	DB	ID	Description	Pred. No.
1	831	100.0	2419	25	I36922	Sequence 7 from patent	0.00e+00
2	831	100.0	5674	25	I36923	Sequence 8 from patent	0.00e+00
3	831	100.0	5674	25	I24013	Sequence 1 from patent	0.00e+00
4	584	70.3	2531	25	I36929	Sequence 14 from paten	0.00e+00
5	582	70.0	2531	25	I36928	Sequence 13 from paten	0.00e+00
6	513	61.7	2305	25	I36932	Sequence 17 from paten	0.00e+00
7	502	60.4	1640	25	I36926	Sequence 11 from paten	0.00e+00
8	500	60.2	2226	25	I36931	Sequence 16 from paten	0.00e+00
9	488	58.7	4157	25	I36924	Sequence 9 from patent	0.00e+00
10	464	55.8	1810	25	I36935	Sequence 20 from paten	0.00e+00
11	452	54.4	1068	25	I36930	Sequence 15 from paten	0.00e+00
12	391	47.1	1947	25	I36934	Sequence 19 from paten	0.00e+00
13	385	46.3	1412	25	I36936	Sequence 21 from paten	5.56e-298
14	342	41.2	1107	25	I36938	Sequence 23 from paten	1.32e-260

15	184	22.1	1866	25	I32295	Sequence 1 from patent	5.95e-125
16	149	17.9	225	25	I36933	Sequence 18 from paten	1.43e-95
17	141	17.0	943	25	I36927	Sequence 12 from paten	6.43e-89
18	137	16.5	1609	14	MMU19033	Mus musculus Smage-3 p	1.33e-85
19	136	16.4	2150	25	I36939	Sequence 24 from paten	8.94e-85
20	136	16.4	3809	14	MMU19031	Mus musculus Smage-1 p	8.94e-85
21	135	16.2	2099	25	I36940	Sequence 25 from paten	6.00e-84
22	135	16.2	7428	14	MMU19032	Mus musculus Smage-2 p	6.00e-84
23	123	14.8	288886	26	AC002406	Mus musculus; HTGS pha	4.61e-74
24	102	12.3	920	25	I36937	Sequence 22 from paten	5.55e-57
25	87	10.5	687	25	I32298	Sequence 4 from patent	5.20e-45
26	62	7.5	461	25	I32296	Sequence 2 from patent	1.01e-25
27	59	7.1	1585	14	MUSNECDIN	M.musculus necdin mRNA	1.74e-23
28	59	7.1	3899	14	MUSNCP	Mouse gene for necdin,	1.74e-23
29	58	7.0	7218	25	I66494	Sequence 14 from paten	9.56e-23
30	53	6.4	476	25	I32297	Sequence 3 from patent	4.35e-19
31	39	4.7	2471	14	MMAJ2366	Mus musculus mRNA for	2.50e-09
32	39	4.7	7218	25	I66494	Sequence 14 from paten	2.50e-09
33	36	4.3	215	25	I28278	Sequence 5 from patent	2.30e-07
34	36	4.3	77778	26	HS1409	Human DNA sequence ***	2.30e-07
35	29	3.5	215	25	I28278	Sequence 5 from patent	4.91e-03
36	27	3.2	27	25	I15293	Sequence 1 from patent	6.98e-02
37	25	3.0	3172	22	KIFENAN	Bacteriophage KIF endo	8.92e-01
38	25	3.0	144921	26	HS29C18	Human DNA sequence ***	8.92e-01
39	24	2.9	1489	14	RNENKE	R.norvegicus gene for	3.05e+00
40	24	2.9	1663	15	MVU92534	Mustela vison microsat	3.05e+00
41	24	2.9	164296	25	HSAC000380	*** SEQUENCING IN PROG	3.05e+00
42	23	2.8	354	17	OFU89259	Oxytricha fallax 57kD	1.01e+01
43	23	2.8	2721	14	RATGLURA	Rat glutamate receptor	1.01e+01
44	23	2.8	33270	17	CELR02Fl1	Caenorhabditis elegans	1.01e+01
45	23	2.8	170309	26	AC003061	*** SEQUENCING IN PROG	1.01e+01

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                            ALIGNMENTS

RESULT        1
LOCUS         I36922         2419 bp    DNA              PAT        21-APR-1997
DEFINITION    Sequence 7 from patent US 5612201.
ACCESSION     I36922
NID           g2084882
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 2419)
  AUTHORS     De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
              Chomez,P.
  TITLE       Isolated nucleic acid molecules useful in determining expression of
              a tumor rejection antigen precursor
  JOURNAL     Patent: US 5612201-A 7 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1..2419
                     /organism="unknown"
BASE COUNT      562 a    581 c    677 g    599 t
ORIGIN

Query Match     100.0%;  Score 831; DB 25; Length 2419;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches  831;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db       676 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCTCC 735
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Qy      3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCTCC 3990

Db       736 TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 795
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      3991 TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050

Db       796 TCCTCAGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 855
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      4051 TCCTCAGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

Db       856 TGAGGGTTCCAGCAGCCGTGAAGAGAGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 915
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Left column (sequence alignment):

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Qy   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTGTATCCTGGAGTCCTT 4170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 GTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTTGGTTTCTGCTCCTCAAATA 975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4171 GTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTTGGTTTCTGCTCCTCAAATA 4230
Db    976 TCGAGCCAGGGAGCCAGTCACAAAGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 1035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4231 TCGAGCCAGGGAGCCAGTCACAAAGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290
Db   1036 GCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 1095
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4291 GCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350
Db   1096 TGACGTGAAGCAGCAGACCCCACCGGCTTCACTCCTATGTCCTTGTCACCTGCCTAGTCT 1155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4351 TGACGTGAAGCAGCAGACCCCACCGGCTTCACTCCTATGTCCTTGTCACCTGCCTAGTCT 4410
Db   1156 CTCCTATGATGGCTGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 1215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4411 CTCCTATGATGGCTGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470
Db   1216 TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 1275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4471 TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530
Db   1276 GCTGAGTGTGATGGAGGTGTATGATGGGACAGTGCCTATGGGGAGCCCAGGAA 1335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4531 GCTGAGTGTGATGGAGGTGTATGATGGGACAGTGCCTATGGGGAGCCCAGGAA 4590
Db   1336 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT 1395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT 4650
Db   1396 GATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 1455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4651 GATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710
Db   1456 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC 1506
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Qy   4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC 4761
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RESULT   2
LOCUS      I36923         5674 bp   DNA                      PAT     21-APR-1997
DEFINITION Sequence 8 from patent US 5612201.
ACCESSION  I36923
NID        g2084883
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 5674)
AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
           Chomez,P.
TITLE      Isolated nucleic acid molecules useful in determining expression of
           a tumor rejection antigen precursor
JOURNAL    Patent: US 5612201-A 8 18-MAR-1997;
FEATURES   Location/Qualifiers
    source       1..5674
                 /organism="unknown"
BASE COUNT    1276 a    1644 c    1569 g    1185 t
ORIGIN
Query Match     100.0%;  Score 831;  DB 25;  Length 5674;
Best Local Similarity 100.0%;
Matches  831;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db   3931 GGCCCAACAAGAGAGGCCCTGGCCTGGTGTGTGCAGGCTGGCACCTTCCTCCTCCTCC 3990
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3931 GGCCCAACAAGAGAGGCCCTGGCCTGGTGTGTGCAGGCTGGCACCTTCCTCCTCCTCC 3990
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Right column (sequence alignment):

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Db   3991 TCTGGTCCTGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCAGAG 4050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3991 TCTGGTCCTGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCAGAG 4050
Db   4051 TCCTCAGGGAGCCTTCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110
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Qy   4051 TCCTCAGGGAGCCTTCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110
Db   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTGTATCCTGGAGTCCTT 4170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTGTATCCTGGAGTCCTT 4170
Db   4171 GTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATA 4230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4171 GTTCCGAGCAGTAATCACTAAGAAGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATA 4230
Db   4231 TCGAGCCAGGGAGCCAGTCACAAAGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4231 TCGAGCCAGGGAGCCAGTCACAAAGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290
Db   4291 GCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4291 GCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350
Db   4351 TGACGTGAAGGAAGCAGAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGTCT 4410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4351 TGACGTGAAGGAAGCAGAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGTCT 4410
Db   4411 CTCCTATGATGGCTGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT 4470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4411 CTCCTATGATGGCTGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT 4470
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Qy   4471 TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCGGGAGGA 4530
Db   4531 GCTGAGTGTGATGGAGGTGTATGATGGGACAGTGCCTATGGGGAGCCCAGGAA 4590
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Qy   4531 GCTGAGTGTGATGGAGGTGTATGATGGGACAGTGCCTATGGGGAGCCCAGGAA 4590
Db   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT 4650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT 4650
Db   4651 GATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4651 GATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710
Db   4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC 4761
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Qy   4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC 4761
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RESULT   3
LOCUS      I24013         5674 bp   DNA                      PAT     14-AUG-1996
DEFINITION Sequence 1 from patent US 5541104.
ACCESSION  I24013
NID        g1603883
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1  (bases 1 to 5674)
AUTHORS    Chen,Y., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J., van der
           Bruggen,P., Boon-Falleur,T. and Old,L.J.
TITLE      Monoclonal antibodies which bind to tumor rejection antigen
           precursor mage-1
JOURNAL    Patent: US 5541104-A 1 30-JUL-1996;
FEATURES   Location/Qualifiers
    source       1..5674
                 /organism="unknown"
BASE COUNT    1276 a    1644 c    1569 g    1185 t
ORIGIN
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Left column (RESULT 4)

Query Match   100.0%;   Score 831;   DB 25;   Length 5674;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches 831;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db 3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC 3990
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC 3990

Db 3991 TCTGGTCCTGGGCACCTGGAGGAGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3991 TCTGGTCCTGGGCACCTGGAGGAGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050

Db 4051 TCCTCAGGGAGGCCTCCGCCTTTCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4051 TCCTCAGGGAGGCCTCCGCCTTTCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

Db 4111 TGAGGGTTCCAGCAGCCGTGAAGAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170
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Qy 4111 TGAGGGTTCCAGCAGCCGTGAAGAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170

Db 4171 GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGTCCTCAAATA 4230
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Qy 4171 GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGTCCTCAAATA 4230

Db 4231 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGTCACGAGAGTGTCATCAAAAATTACAA 4290
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4231 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGTCACGAGAGTGTCATCAAAAATTACAA 4290

Db 4291 GCACTGTTTCCTGAGATCTTCGGCAAAGCCTCGAGTCCTTGCAGCTGGTCTTTGGCAT 4350
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Qy 4291 GCACTGTTTCCTGAGATCTTCGGCAAAGCCTCGAGTCCTTGCAGCTGGTCTTTGGCAT 4350

Db 4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT 4410
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Qy 4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT 4410

Db 4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT 4470
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Qy 4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT 4470

Db 4471 TGTCCTGGTCATGATTGATTGCAATGGAGGGCGGCCATGCGTCCTCCTGAGGAGGAAATCTGGGAGGA 4530
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Qy 4471 TGTCCTGGTCATGATTGATTGCAATGGAGGGCGGCCATGCGTCCTCCTGAGGAGGAAATCTGGGAGGA 4530

Db 4531 GCTGAGTGTGATGGAGGTGTATGATGGAGGAGGCACAGTGCCTATGGGAGCCCAGGAA 4590
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Qy 4531 GCTGAGTGTGATGGAGGTGTATGATGGAGGAGGCACAGTGCCTATGGGAGCCCAGGAA 4590

Db 4591 GCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACGGCCAGGTGCCGGACAGT 4650
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Qy 4591 GCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACGGCCAGGTGCCGGACAGT 4650

Db 4651 GATCCCCGACGCGTCACCGTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710
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Qy 4651 GATCCCCGACGCGTCACCGTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710

Db 4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 4761
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Qy 4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 4761
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RESULT 4
LOCUS   I36929   2531 bp   DNA   PAT   21-APR-1997
DEFINITION Sequence 14 from patent US 5612201.
ACCESSION   I36929
NID   g2084889
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2531)
AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J., De Smet,C. and

Right column (RESULT 5)

Query Match   70.3%;   Score 584;   DB 25;   Length 2531;
Best Local Similarity 87.2%;   Pred. No. 0.00e+00;
Matches 690;   Conservative 0;   Mismatches 0;   Indels 100;   Gaps 1;

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Db  734 AGGCTGCTGTCTCCTCCTCCTCCTCCTCCTGGTCCTGGCACCCTGGAGGAGTGCTGCTGCTG 793
        ||||||         |||||||||||||||||||||||||||||||||  ||||||||
Qy 3966 AGGCTGCCACCTCCTCCTCCTCTCCTCTCCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTG 4025

Db  794 CTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGGCCCTCGCCTTACCCACTACCATCA 853
        ||| ||  ||| ||||||||||||||||||||||  |||| |||||||||||||||||
Qy 4026 CTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGGCCTCCGCCTTTCCCACTACCATCA 4085

Db  854 GCTTCACTTGCTGGAGCAACCCAATCAGAGGGTTCAGCAGCCAAGAAGAGGAGGGGCCAA 913
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Qy 4086 ACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAA 4145

Db  914 GCACCTCCGCCTGACGCGAGCAGTCCTTGTCCGACAGAGTCCTTGTCTGGAGAAGTGGATGAGT 973
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Qy 4146 GCACCTCTTGTATCCTGGAGTCCTTGTTCCGACAGTAATCACTAAGAAGGTGGCTGATT 4205

Db  974 TGGCTCATTTTCTGTCCGCAGTCATCGAGCCAAGGACCAAGGACTGGTCACAAAGGCAGAAATGC 1033
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Qy 4206 TGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGC 4265

Db 1034 TGGAGAGAGTCATCAAAAATTACAAGCCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCG 1093
        ||||  ||| |||||  |||||||||||||| |  |  ||||||||||||||||||||||
Qy 4266 TGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTG 4325

Db 1094 AGTGCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGACCCCACCAGCAACACCT 1153
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Qy 4326 AGTGCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGGCCACTCCT 4385

Db 1154 ACACCCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCT 1213
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Qy 4386 ATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCA 4445

Db 1214 TTCCCAAGACAGGCCTTCTGATAATGTCCTGGTCACAATTGCAATTGCAATTGGAGGCGCACAGCG 1273
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Qy 4446 TGCCCAAGACAGGCTTCCTGATAATTGTCATGATTGCAATTGCAATGGAGGGCGGCCATG 4505

Db 1274 CCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGATGGGGAGTGTATGATGGAGGGGAGC 1333
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Qy 4506 CTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGAGGAGGAGC 4565

Db 1334 ACACTGTCTATGGGAGGCCCAGGAAACTGCTCACCCAAGATTGGTGTCGCAGGAAAACTACC 1393
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Qy 4566 ACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACC 4625

Db 1394 TGGAGTACGGCCAGTACCGGCTACCCGGCGTAATCCTGCGCGCCTCTGTGGGGTCCAA 1453
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Qy 4626 TGGAGTAC-GGCCAGGTGCCGGACAGTGATCCCGGCCACGGTGATCCCGGTGTGGGGTCCAA 4684

Db 1454 GGGCTTCGGCTGAAACCAGCTATGTGAAAGTCCTGGTGAAAGTCCTGAGGCATGTGCATGAATGCAA 1513
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Qy 4685 GGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAA 4744

Db 1514 GAGTTCGCATT 1524
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Qy 4745 GAGTTCGCTTT 4755
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RESULT 5
LOCUS   I36928   2531 bp   DNA   PAT   21-APR-1997

DEFINITION Sequence 13 from patent US 5612201.
ACCESSION   I36928
NID   g2084888
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2531)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
            Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 13 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..2531
                     /organism="unknown"
BASE COUNT   608 a   593 c   700 g   630 t
ORIGIN

Query Match   70.0%; Score 582; DB 25; Length 2531;
Best Local Similarity 87.1%; Pred. No. 0.00e+00;
Matches 689; Conservative   0; Mismatches 101; Indels   1; Gaps   1;

Db   734 AGGCTGCCGTGTCCTCCTCCTCCTCCTCGTCCCTGGTCCCTGGAGGAAGTGCCTGCTG 793
           ||||||| ||||||||||||||||||||||||||||||||||| ||||| || ||
Qy   3966 AGGCTGCCACCTCCTCCTCCTCCTCGTCCCTGGGCACCCTGGAGGAGGTGCCCACTG 4025

Db   794 CTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGGCCTCTGCCTTACCCACTACCATCA 853
           ||| |||| || |||||||||||||||||||||||| ||||| |||||||||||||||
Qy   4026 CTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGGCCTCCGCCTTTCCCACTACCATCA 4085

Db   854 GCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGGCCAA 913
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Qy   4086 ACTTCACTGCACGAGAGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGGCCAA 4145

Db   914 GCACCTCGCCTGACGGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGT 973
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Qy   4146 GCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTACAAGAAGGTGGCTGATT 4205

Db   974 TGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGTCACAAAGGCAGAAATGC 1033
           ||| |||||||||||||||| |||| |||||||||||| ||||||||||||||||||
Qy   4206 TGGGTCATTTTCTGCTCCTCAAATATCGAGCCAGGGAGCTGTCACAAAGGCAGAAATGC 4265

Db   1034 TGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTCCTGTGATCTTCGGCAAAGCCTCCG 1093
           ||||||||||| ||||||||||||||||||||||||||| || |||||||||||||
Qy   4266 TGGAGAGTGTCATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAAAGCCTCTG 4325

Db   1094 AGTCCCTGAAGATGATCTTGGCATTGAAGGAAGTGACGTGGAGGAGTGACCCCGCAGCAACACT 1153
           |||||||||||||||||||||||||| || |||||||||||||||||||||||||||
Qy   4326 AGTCCTTGCAGCTGGTCTTTGGCATTGAAGGAAGCAGAGACCCCACCGGCCACTCCT 4385

Db   1154 ACACCCTGTGCACCTGCTGGGCCTTTCCTATGATGGCCTGGGTAATATAATCAGATCT 1213
           | ||||||||||||||||||| |||| ||||||||||||||||| ||||||||||
Qy   4386 ATGTCCTTGTCATGCCTGCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCA 4445

Db   1214 TTCCCAAGACAGGCAAATCGGGAGGAGCTGGGGTGTGATGGGGTGCACAATTGCAATGGAGGGCGCACGCG 1273
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Db   1274 CCTCTGCAGGAGGAAATCGGGGAGGAGCTGGGGTGTATGGGGTATGATGGGGAGC 1333
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Qy   4506 CTCCTGAGGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGGGGAGC 4565

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Qy   4566 ACAGTGCCTATGGGAGCCCAGGAAACTGCTCACCCAAGAATTGGTGCAGGAAAAGTACC 4625

Db   1394 TGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGGCCTAATCCTGGGCTATGAGTTCCTGTGGGTCCAA 1453
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Qy   4626 TGGAGTAC-GGCAGGTGCCGGACAGTGATCCCGCACGTAGTGCCTATGAGTTCCTGTGTGGGTCCAA 4684

Db   1454 GGGGCTGCCTGGAAACCAGCTATGTGAAAGTCTGAAGCTGCTCACCCAAGAGTCCAGTGCAA 1513
           |||| ||||||||||||||||||||||||| |||||||||||||||||| ||||
Qy   —

RESULT   6
LOCUS   I36932   2305 bp   DNA   PAT   21-APR-1997
DEFINITION Sequence 17 from patent US 5612201.
ACCESSION I36932
NID   g2084892
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE 1 (bases 1 to 2305)
  AUTHORS De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
           Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
           a tumor rejection antigen precursor
  JOURNAL Patent: US 5612201-A 17 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..2305
                    /organism="unknown"
BASE COUNT   549 a   568 c   611 g   577 t
ORIGIN

Query Match   61.7%; Score 513; DB 25; Length 2305;
Best Local Similarity 86.4%; Pred. No. 0.00e+00;
Matches 633; Conservative   0; Mismatches 96; Indels   4; Gaps   2;

Db   748 GCAGGAGGCGTGTCCTCCTCCTCCTCGTCCCTGGTCCCAGGCACCCTGGGGGAGGTGCCTGC 807
           ||||| || |||||||||||||||||||||||||||||||| ||||||||| || ||
Qy   3964 GCAGGCTGCCACCTCCTCCTCCTCCTCGTCCCTGGTCCCTGGGCACCCTGGAGGAGTGCCCAC 4023

Db   808 TGCTGGGTCACCAGGTCCTCAAGAGTCCTCAAGAGTCCTCAGGGAGCCTCCGCCATCCCACTGCCAT 867
           ||||||||||||| ||||| | ||||||| | |||||||||| ||| ||||| ||||
Qy   4024 TGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCAT 4083

Db   868 CGATTCACTCTATGGAGGCAATCCATTAGGGCTCCAGCAACCAAGAAGAGGAGGGGCC 927
           | |||||||| ||||| || |||| | |||||||||||||||||||||||||||
Qy   4084 CAACTTCACTGCACGAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGGCC 4143

Db   928 AAGCACCTCCCCTGACCCAGAGTCTGTGTTCCGACGACGTCAGTCAGTAAGAAGGTGTGGCTGA 987
           ||||||| ||||| | |||||||||||||||| |||||| ||||| |||||||||
Qy   4144 AAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTACAAGAAGGTGGCTGA 4203

Db   988 CTTGATTCATTTTCTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCACAAAGGCAGAAAT 1047
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Qy   4204 TTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCTGGTCACAAAGGCAGAAAT 4263

Db   1048 GCTGGAGAGCGTCATCAAAAATTACAAGCGGCTGCTTCCTGAGATCTTCGGCAAAGCCTC 1107
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Qy   4264 GCTGGAGAGTGTCATCAAAAATTACAACACTGTTTCCTGAGATCTTCGGCAAAGCCTC 4323

Db   1108 CGAGTCCCTGGTCTTTGGCATTGACGTGGACTC--CTATGATGGGCCTGGTGGTT--TAATCAGAT 1167
           ||| | |||||||||||||| | ||| ||||| ||| | |||||||||| |||||||
Qy   4324 TGAGTCCTTGCAGCTGGTCTTTGGCATTGAAGGAAGCAGAGACCCCACCGGCCACTC 4383

Db   1168 CTACACCCTTGTCACCTGCCTGGGACTC--CTATGATGGCCTGGTGTT--TAATCAGAT 1223
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Qy   4384 CTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGTGATAATCAGAT 4443

Db   1224 CATGCCCAAGACGGGGCCTTCCTGGAGGAGCTGGGTGCATGATGGCAGGGCAAATG 1283
           ||||||||||||||||| ||| |||||||||| ||||||| || ||||||||
Qy   4444 CATGCCCAAGACAGGCTTCCTGATGGTTGTCCTGGTGTCAATGGGGGCGGCCA 4503

Db   1284 CGTCCTGAGGAGAAAATCTGGGAGGAGCTGGGTGTGATGAAGGTGTATGTGGGAGGA 1343
           ||||||||| ||||||||| |||||||||| |||||||||||||||| ||||||||
Qy   4504 TGCTCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGTATGATGGGGAGGA 4563

Db   1344 GCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGAGATTTGGTCGCAGGAAAACTA 1403
           |||| |||||||||||||| ||||||||||||| ||||| |||| ||| |||||||
Qy   —

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Qy  4564  GCACAGTGCCTATGGGAGCCCAGCAGTGCCCAGCAGTGATCCCAAGAAGCTGTCACCCAGATTTGGTGTCGAGGAAAAGTA  4623
          |||||||  ||  |||||||||||||||||||||||||||||||||||||||||||||
Db  1404  CCTGGAGTACCGGCAGTGCCGGACGTGCCGGATCCGACGCTATGATGCGTATGTCCTGTGGGGTCCA  1463
          ||||||||| |||||||||  ||||||  |||||||||| | |||||||| |||||||||||
Qy  4624  CCTGGAGTACCGGCAGTGCCGGACAGTGATCCGACGCTATGAGTTCCTGTGGGGTCCA  4683

Db  1464  AGGGCACTGCCTG  1476
          ||||| ||| ||||
Qy  4684  AGGGCCCTCGCTG  4696
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RESULT   7
LOCUS   I36926   1640 bp   DNA   PAT   21-APR-1997
DEFINITION Sequence 11 from patent US 5612201.
ACCESSION   I36926
NID   g2084886
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 1640)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
            Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 11 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..1640
                     /organism="unknown"
BASE COUNT   380 a   402 c   457 g   401 t
ORIGIN

Query Match   60.4%; Score 502; DB 25; Length 1640;
Best Local Similarity   81.8%; Pred. No. 0.00e+00;
Matches 652; Conservative   0; Mismatches 144; Indels   1; Gaps   1;

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Db   276  GCAGGAGGCTGCCTCCTCCTCCTTCTACTCCTAGTTGAAGTCACCCTGGGGAGGTGCCTGC  335
          |||||||||||||  ||||||||||||||  |||  ||  |||||||||| ||||||||||
Qy  3964  GCAGGAGGCTGCCACCCTCCTCCTCCTGGCTCCTGGCCACCCTGGGAGGTGCCCAC  4023

Db   336  GCCGAGTCACCAGATCCTCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCAT  395
          ||| |||||||||||||||||||||||||||||||||||||||  ||| ||||||||||
Qy  4024  TGCTGGGTCAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCAT  4083

Db   396  GAACTACCCCTCTCTGGAGCCAATCCTATGGAGGACTCCAGCAACCAAGAGGAGGGGCC  455
          ||||| |||||| |||||| ||||  ||  ||| ||||||| |||  |||||||||||| |
Qy  4084  CAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCGCCGTGAGAGGAGGGGGC  4143

Db   456  AAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGA  515
          |||||||| | |||||||||||||| ||||||| ||||| | |||||| ||||||||| ||
Qy  4144  AAGCACCTCTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGA  4203

Db   516  GTTGGTTCATTTCTGCTCCTCAAGTATCGAGCCAGGGAGCCCGGTCACAAAGGCAGAAAT  575
          ||||||| |||||||||||||||| ||||||||||||||||| ||||||||||||||||||
Qy  4204  TTTGGTTGGTTTTCGTCTCCTCAAATATCGAGCCAGGGAGCCCAGTCACAAAGGCAGAAAT  4263

Db   576  GCTCGGGGAGTGCGTCGGAAATTGCAGTATTTCTTCCTGTGATCTTCAGCAAAGCTTC  635
          ||| |  ||||| | |||||||||| |||||| ||||||| |||||| |||||||| ||
Qy  4264  GCTGGAGAGTGTCATCAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTC  4323

Db   636  CAGTTCCTTGCAGCTGGTCTTGCAGCTGATCGAGCTGATGGAAGTGGACCCCATCGGCACTT  695
          |||||||||||||||||||||| |  ||||| |||   || |||||| ||||| |||||||
Qy  4324  TGAGTCCTTGCAGCTGGTCTTTGACGTGAAGGAAGCAGAACCCCACCGGCCACTC  4383

Db   696  GTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGAT  755
          || ||| |||||| |||| |||||||| |||||||| |||||||||||||| |||||||||
Qy  4384  CTATGTCCTTGCACGTGCTCTTCCTATGATGCGGCCTGCTGGGTGATAATCAGAT  4443

Db   756  CATGCCCAAGGCAGGCAGGCCTCCTGATAATCGTCCGCCATAATCCGCCATAATGGCGACTG  815
          |||||||||| || | ||||  ||||||||||| |  |||| |||||| | | ||  ||||
Qy  4444  CATGCCCAAGACAGCAGGCTTCCTGATAATTGTGGTCATTGATTGCAATGGAGGCGGCCA  4503
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RESULT   8
LOCUS   I36931   2226 bp   DNA   PAT   21-APR-1997
DEFINITION Sequence 16 from patent US 5612201.
ACCESSION   I36931
NID   g2084891
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 2226)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
            Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 16 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..2226
                     /organism="unknown"
BASE COUNT   539 a   542 c   582 g   563 t
ORIGIN

Query Match   60.2%; Score 500; DB 25; Length 2226;
Best Local Similarity   85.8%; Pred. No. 0.00e+00;
Matches 611; Conservative   0; Mismatches 99; Indels   2; Gaps   2;

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Db   816  TGCCCCTGAGGAGAAATCTGGGAGGAGCTGAGTCGTGTTAGAGGTGTTGAGGGGAGGGGA  875
          ||| |||||||||||||||||||||||||||||||| ||  | |||||| |||||||||| ||
Qy  4504  TGCTCCTGAGGAGAAATCTGGGAGGAGCTGAGTCGTGATGGAGGTGTATGGAGGGGAGGGGA  4563

Db   876  AGACAGTATGTTGGGGATCCCAGAAGCTGTCACCCAACCATTTCGTCGCAGGAAAACTA  935
          | ||||| | |  ||| | |||||| ||||||||||| ||||| ||| ||| ||||| |||
Qy  4564  GCACAGTGCCTATGGGAGCCCAGCAGTGCTGCTCACCCAAGATTTGGTGTCGAGGAAAAGTA  4623

Db   936  CCTGGAGTACCGGCAGGTCCCGCGGCCAGTGATCCTGTGATCTGTATGAATCCTGTGGGGTC  995
          ||||||||| |||||||| ||| ||  ||||||| | |  | | ||||| |||||||||||
Qy  4624  CCTGGAGTAC-GGCAGGTGCCGGACAGTGATCCCGCACGCCTATGAGTTCCTGTGGGGTCC  4682

Db   996  AAGGGCCCCTCGTTGAAACCAGCTATGTGAAAGCTATGGAGAAGTCCTGCACCATTGTAAAGATCAGTGG  1055
          |||||||| |||  ||||||||||||||||||||||||| | | || |  || |||| |||||||||||
Qy  4683  AAGGGCCCTCGCGTCAAACCAGCTATGTGAAAGCTATGTGATGCATCAAGGTCAGTGC  4742

Db  1056  AGGACCTCACATTTCCT  1072
          | |  | || |||| |||
Qy  4743  AAGAGTTCGCTTTTTCT  4759
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Db   687  CTCCTCTGGTCCCAGGCACCCTGGGGAGGTGCCTGCTCGCTGGGGTCCTGGGTCCTCTCA  746
          |||||||||||| ||||||||||| ||| | |||| |||| |||||||| |||| |||||
Qy  3987  CTCCTCTGGTCCTGGGCACCCTGGAGGAGTGCCACCTGCTGGGTCAACAGATCCTCCCC  4046

Db   747  AGAGTCCTCAGGGAGCCTCCAGCCTCCCACTGCCATCTCATGGAGGCAT  806
          ||||||||||||||||||||  |||| ||||| || ||  | | | |||||
Qy  4047  AGAGTCCTCAGGGAGCCTCCGCCTTCCCACTACCAATCAACTCACTCGACAGAGGCAAC  4106

Db   807  CCATTAAGGGCTCCAGCAACCAAGCAGCAGGAGGGGCCAAGCACCTCCCCTGACCCCAGAGT  866
          |||   ||||| |||||||||  |||| |  ||||||||||||||| |    |||| |||||
Qy  4107  CCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTGTATCCTGGGAGT  4166

Db   867  CTGTGTTCCGAGCAGCACTCAGTGAAGTCTAAGAAGCTGGCTGACTTGATTCATTTCTGCTCCTCA  926
          | |||||||||||||| | |||| |||| ||||||||| ||||| ||||| |  ||| |||||||||
Qy  4167  CCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCGTCTCCTCA  4226

Db   927  AGTATTAAGTCAAGGAGCTGGTCACAAAGGCCGTCATCAAAATT  986
          | |||  || |  |||||| |||||||||||| ||||||||| |||
Qy  4227  AATATCGAGCCAGGGAGCCGTCACAAAGGCAGAATGCTGGAGAGTGTCATCAAAAATT  4286

Db   987  ACAAGGCGCTGTTCCTGAGATCTTCGGCAAAGCCTCGGAGATCTTCGAGTCCTGGTCTTTG  1046
          ||||| | ||||| |||||||||||||||||||||| |||| || | |||| ||||||||||
Qy  4287  ACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCGAGTCCTTGGTCTTTG  4346

Db  1047  GCATTGACGTGAAGGAAGCCGACCCCACCGGCCAACACCTACACCCCTTGTCACCTGCTGG  1106
          ||||||||||||||||||||  || |||| |||||| || |||||||||||||||||| |||
Qy  4347  GCATTGACGTGAAGGAAGCAGACGCCCACCTCGGCCACTCTATGTCCTTGTCACCTGCCTAG  4406
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Db 1107 GACTCCTATGATGGCCGCTGCTGGTGTTGATAATAATCAGATCATGCCCAAGACGGGCCTCCTG 1166
          ||| ||| ||| | | - | |-||||||||||||||||| ||| |||||
Qy 4407 GTCTCTCCT-ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTG 4465

Db 1167 ATAATCGTCTTGGGCATGATTGCAATGAGGGCAAATGCGTCCTGGCCAATGCGTCCTG 1226
          ||||| ||| ||| |||||||||||||||||| |||||||
Qy 4466 ATAATTGTCCTGGTCATGATTGCAATGAGGGCGGCCATGCCTG 4525

Db 1227 GAGGAGCTGAGTGTGATGAAGCGTGTATGTTGGGAGGAGCACAGTGTCTGTGGGGAGCCC 1286
          |||||||||||| |||||| ||||||||| ||||||||||||||||| ||
Qy 4526 GAGGAGCTGAGTGTGATGGGAGGTGTATGGGCTGATGGGAGGAGCACAGTGGGGAGCCC 4585

Db 1287 AGGAAGCTGCTCACCCAAGATTTGGTGCAGAAAAACTACCTGGAGTACCGGCCAGGTCCC 1346
          |||||||||||||||||||||||||||||||| |||||||| ||||||||
Qy 4586 AGGAAGCTGAGTTGGTGCAGGAAAAGTACCTGGAGTAC--GGCCAGGTGCCG 4644

Db 1347 AGCAGTGATCCCATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTG 1398
          ||||||||| | ||||||||||||||| ||||||||||||||||||||||||
Qy 4645 GACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCCTCGCTG 4696

RESULT 9
LOCUS I36924 4157 bp DNA PAT 21-APR-1997
DEFINITION Sequence 9 from patent US 5612201.
ACCESSION I36924
NID g2084884
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4157)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 9 18-MAR-1997;
FEATURES Location/Qualifiers
   source 1..4157
           /organism="unknown"
BASE COUNT 953 a 1134 c 1185 g 885 t
ORIGIN

Query Match 58.7%; Score 488; DB 25; Length 4157;
Best Local Similarity 81.2%; Pred. No. 0.00e+00;
Matches 641; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

Db 2710 CCGCTTCTTCCTCTTCTTACTCTAGTGGAAGTTACCCTGGGGGAGGTGCCTGCTGCCGACT 2769
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Qy 3972 CCACCTCCTCCTCCTCCTCTGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGT 4031

Db 2770 CACCGAGCTGCTCCCCCAGAGTCCTCAGGGAGCCTCAGCTTCTGACTACCAACTACA 2829
          || - ||||||||| ||||||||||||||||| ||| ||||||||||||||| |
Qy 4032 CAACAGATCCTCCCAGAGTCCTCAGGGAGCCTCAGGGAGCCTCCCACTACCAACTTCA 4091

Db 2830 CTCTTGGACAATCCGATGAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGAATGT 2889
          || ||| |||||||||||||| |||||||||||||||||||||||||||||||
Qy 4092 CTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCGCCGTGAAGAGGAGGGGCCAAGCACCT 4151

Db 2890 TTCCCGACCTGGAGTCCGAGTTCCAAGCAGCAATCAGTAGGAGAGATGGTTGGTTC 2949
          ||||| ||||| ||| |||||||||| ||||||||| |||| ||||||||
Qy 4152 CTTGTATCCTGGAGTCCTGTTCCGAGCAGTAATCACTAAGAGGTGGCTGATTGGTG 4211

Db 2950 ATTTTCTCTCCTCAAGTATCGAGCCAGGAGCGGCCGGTCACAAGGCAGAAATGCTGGAGA 3009
          |||||||| ||| | |||||||||| |||||||||||||||||||||||||||
Qy 4212 GTTTTCTGCTCCTCCAAATATACAAGCACTGTTTCCTGAGATCTTTCGGCAAAGGCCTCTGAGTCCT 4271

Db 3010 GTGTCCTCAGAATTGCCAGGACTTCTTCCCGTGATCTTCAGCAAAGCCTCCAGTACT 3059
          |||| ||| |||||||||||||||| | ||||||| | |||||||| ||||||
Qy 4272 GTGTCATCAAAAATTACAAGCACTGTTTCCTGAGATCTGTTTCGGCAAAGCCTCTGAGTCCT 4331

Db 3070 TGCAGCTGGTCTTTGGCATCGAGGTGTGGGAAGTGGTCCCATCAGCCACTTGTACATCC 3129
          |||||||||||||||||| || ||||| ||| | |||||| | |||||| || |||
Qy   —

Db 4332 TGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGCACCCACCGGCCACTCCTATGTCC 4391
          |||||||||||||||| || | ||| |||| |||| |||||||| |||||||| |
Qy 3130 TTGTCACCTGCCTGCCTGGGCCTCCTCCTACGATGGCCTGGCCGACAAATCAGTCATGCCCA 3189

Db 4392 TTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCA 4451
          ||||||||||| ||||| || |||||||||||||||||||| || | | |||||||||
Qy 3190 AGACAGGCCCTCCTGATAATCGTCCTGGCCAATCCAATAGAGGGCGACTGTGCCCCTG 3249

Db 4452 AGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGAGGGCGGCCATGCCTG 4511
          ||||||||| ||||||||||||||| |||| | ||||||||| |||||||||||||||
Qy 3250 AGGAGAAATCTGGAGGAGCTGAGTATGTTGGAGTGTTTGAGGGAGGAGGAGCACAGTG 3309

Db 4512 AGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGGAGGTGTATGATGGGAGGAGCACAGTG 4571
          ||||||||| ||| |||||| |||||||| ||||| | | ||| |||||||||||||||
Qy 3310 TCTTCGCACATCCGCAGAAGCTGCTCATGCAAGATCTGGTCAGGAAGATCTACCTGGAGT 3369

Db 4572 CCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGT 4631
          || | || |||||||||||||||||||||||||||||||||||| ||||| |||||||||
Qy 3370 ACCGGCAGGTGCCCGGCAGTGATCCTGCATGCTACCAGAGTTCCTGTGGGGTCCAAGGGCCC 3429

Db 4632 AC-GGCAGTGTGCCGGACAGTGATCCCGCACCGTATGAGTTCCTGTGGGGTCCAAGGGCCC 4690
          || |||| |||||| ||||||||||| || | || |||||||||||||||||||||||||
Qy 3430 TCAATTGAAACCAGCTATGTGAAAGTCCTGCACCATACACTAAAGATCGGTGGAGAACCTC 3489

Db 4691 TCGCTGAAACCAGCTATGTGAAAGTCCTTGAAGTCTTGATATCGATCAAGGTCAGTGCAAGAGTTC 4750
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Qy 3490 ACATTTCCT 3498

Db 4751 GCTTTTTCT 4759

RESULT 10
LOCUS I36935 1810 bp DNA PAT 21-APR-1997
DEFINITION Sequence 20 from patent US 5612201.
ACCESSION I36935
NID g2084895
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1810)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 20 18-MAR-1997;
FEATURES Location/Qualifiers
   source 1..1810
           /organism="unknown"
BASE COUNT 402 a 463 c 508 g 437 t
ORIGIN

Query Match 55.8%; Score 464; DB 25; Length 1810;
Best Local Similarity 82.2%; Pred. No. 0.00e+00;
Matches 663; Conservative 0; Mismatches 133; Indels 11; Gaps 6;

Db 556 GCAGAAGCTGCATCCTCCTCTACTCTGATCATGGGAACCCTTGAGGAGGTGACTGA 615
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Qy 3964 GCAGGTGCCGCCACCCGTGGCTCCTCCTCCTGGCCACCCTGGAGGAGGTGCCCAC 4023

Db 616 TTCTGGGTCACCAGTCCTCCCCAGAGTCCTGAGGGTGCCTCCTCCTGAGACTGTCAC 675
         || |||||||| ||| |||||||||||||||||||||| |||||||||||||||
Qy 4024 TGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCCGCCTTTCCCACTACCAT 4083

Db 676 CGACAGCACTCTGTGGAGCCAATCCGATGAGGGTTCCAGCAGCAGGTTCCAGCAGCAGGGGGC 735
         || | || |||||||||||||||| ||||||||||| |||||||||||||||||||
Qy 4084 CAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCAGCAGGTTCCAGCAGCAGGGGGC 4143

Db 736 AAGCACCTCCCCGGACCACCCAGTCACCTGGAGTCCCTGTTCCGGAAGCACTTGATGAGAA 795
         ||||||| || | ||| | | | | -TC---A--TC--CTGGAGTCCTGTTCCGGAAGCACTTGATGAGAA
Qy 4144 AAGCACCTCTT--GT---A--TC--CTGGAGTCCTGTTCCGAGCAGTAATCACTAAGA 4194

Db 796 AGTGGCTGAGTTAGTTCGTTTCTGCTCCGCCCAAATATCAAATTAAGGAGCGGTCACAAA 855
         ||||||||| | ||| || | ||| | | ||||| ||| | | |||| | || ||
Qy   —

Qy   4195 |||||||| || |||| |||| ||||||||| ||||||| | |||||| ||||||||| 4254
           GGTGGCTGATTTGGTTGGTTTCTGCTCCTCAAAAATTACAAGGCCAGGGAGCCAGTCACAAA

Db   856 GGCAGAAATGCTTGAGAGTGTCATCAAAAATTACAAGGACACTTTCCTGATATCTTCAG 915
           ||||||||||| ||||||||||||||| | ||||||| | ||||||| ||||| |
Qy   4255 GGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTTCCTGAGATCTTCGG 4314

Db   916 CAAAGCCTCTGAGTGCATGCAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCCTGC 975
           |||| |||||||||| ||||||||||| || ||||||||||| |||||||||||| ||
Qy   4315 CAAAGCCTCTGAGTGCCTGGTCTTTGCAGTCGTGAAGGAAGCAGACCCCAC 4374

Db   976 CGGCCACTCCTACACATCCTTGTCACCTGCCTGGGCCTTCCTATGATGGCCTGCTGGGTGA 1035
           ||||||||||| |||||||||| || |||||||||| ||||||||||||||||||
Qy   4375 CGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTTCCTGATGGCCTGCTGGGGTGA 4434

Db   1036 TGATCAGAGTACGCGCCAAGACCGCCTCCTGATAATCGTCCTGGGCATGATCCTTAATGGA 1095
           | ||||| |||||||||| || ||||||| ||||| ||||||| |||||
Qy   4435 TAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGTGTCATGGCAATGGA 4494

Db   1096 GGGGAGCCGCGCCCCGGAGGAGGCAATCTGGAAGCATTGAGTGTGATGGGGGCTGTATG 1155
           ||||||||| || |||||||||||| ||| || |||||||||||||||||||||
Qy   4495 GGCGGGCCATGCTCCTGAGGAGGAAATCTGGGAGAGCT-GAGTGTGATGGAG-TGTATG 4553

Db   1156 ATGGGAGGCACAGTGTCTATTGGAAGCTGCTCAGGAGGAAGCTGCTCACCCAAGAGTGGGTGC 1215
           |||||||||||| |||| || ||| |||||||||||| |||||||| ||||||||
Qy   4554 ATGGGAGGCACAGTGCCTATGGGGAGCCCAGGAGCCTGCTCACCCAAGAGTTGGTGC 4613

Db   1216 AGGAGAACTACCTGGAGTACGGCCCAGGGCGCCCCGGCAGTCGTGCGCCTACGAGTTC 1275
           ||| |||||||||||||| ||| |||||| ||| | |||| |||| |||||||||
Qy   4614 AGGAAAAGTACCTGGAGTACGGC-AGGTGCCGGACAGTGATCCCGCCACCCTATGAGTTCC 4672

Db   1276 TGTGGGGTCCAAGGGCCCTTGCTGAAACCAGCTATGTGAAAGTTCCTGGAGCATGTGGGTCA 1335
           |||||| |||||||||| |||||||||||||||||||||||| |||||||
Qy   4673 TGTGTGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTTCCTTGAGTATGTGATCA 4732

Db   1336 GGGTCAATGCAAGAGTTCGCATTTCCT 1362
           ||||| ||||||||||||||||| || |
Qy   4733 AGGTCAGTGCAAGAGTTCGCTTTTTCT 4759

I36930   1068 bp   DNA   PAT   21-APR-1997

Query Match   54.4%; Score 452; DB 25; Length 1068;
Best Local Similarity   86.9%;
Matches   538; Conservative   0; Mismatches 80; Indels   1; Gaps   1;

Db   1 GGGGCCAAGCACCTCGCCTCGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGT 60
           ||||||||||||||||| | | ||||||||||||||||||||||
Qy   4138 GGGGCCCAGCACCTCCTTGTATCCTGAGTCCGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGT 4197

Db   61 GGATGAGTTGGCTCATTTCTGCTCCCAAGTATCGACCAAGGAGCTGGTCACAAGGC 120
           ||| ||| ||||| || || || |||||||||||||||||||||| ||||||||||
Qy   4198 GGCTGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCCAGGGAGCCAGTCACAAAGGC 4257

Db   121 AGAAATGCTGGAGAGTCATCAAAAATTACAAGGCGCTGCTTCCTGTGATCTTCGGCAA 180
           ||||||||||||||||| |||||||||||||||||| ||| ||||||||||||||||
Qy   4258 AGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTCCTGAGATCTTCGGCAA 4317

Db   181 AGCCTCGAGTCCTCAAGATGATCTTGGCATTGACGTGAAGGAAGTTGACCCCGCCAG 240
           ||||||| ||||||||||| | |||||||||||| ||||||||||| |||||||||
Qy   4318 AGCCTCTGAGTCTTGCAGCTGCTGTCTTGGCATTGACGTGAAGGAAGCAGACCCCACCCG 4377

Db   241 CAACACTACACCTTGTCACCTGCCCTTCCTATGATGGCCTGCTGGTAAТAA 300
           | ||| |||||||||||||||| | || |||||||||||| || |||
Qy   4378 CCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTTCCTGATGGCCTGCTGATAA 4437

Db   301 TCAGATCTTTCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATGCAATGGAGG 360
           ||||| | |||||||||||||| ||||||||||||||||||| |||||||||||||
Qy   4438 TCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTGTCATGATGCAATGGAGG 4497

Db   361 CGACAGCGCCTCGAGGAGGAAATCTGGAGGAGCCAGGAAACTGCTCACCCGCGCCCTGTG 420
           || | |||||||||||||||||||||||||||||||||||||| ||||||||||| |||
Qy   4498 CGGCCATGCTCCTGAGGAGGAAATCTGGGAGAGCTGAGTGTGATGGAGTGTGTATGAGTG 4557

Db   421 GAGGGAGCACACTGTCTATGGGGAGCCCAGGAAACGCTCACCCAAGATTGGTGCAGGA 480
           |||||||||||| |||||||||||||||||||||||||| |||||||| |||||||||
Qy   4558 GAGGGAGCACAGTGCCTATGGGGAGCCCAGGAGCCTGCTCACCCAAGAGTTGGTGCAGGA 4617

Db   481 AAACTACCTGGAGTACCGGCAGTAATCCTGCCGCGCTATGAGTTCCTGTG 540
           ||| ||||||||||| || ||||||||||| | ||||||||||||||
Qy   4618 AAAGTACCTGGAGTAC-GGCAGGTGCCGGACAGTGATCCCGCCACCCTATGAGTTCCTGTG 4676

Db   541 GGGTCCAAGGGCTCGGCTGAAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGT 600
           |||||||||||| | |||||||||||||||||||||| | ||||| | |||| | ||||
Qy   4677 GGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTTCCTTGAGTATGTGATCAAGGT 4736

Db   601 CAATGCAAGAGTTCGCATT 619
           ||||||||||||||| |||
Qy   4737 CAGTGCAAGAGTTCGCTTT 4755

I36934   1947 bp   DNA   PAT   21-APR-1997

Query Match   47.1%; Score 391; DB 25; Length 1947;
Best Local Similarity   78.4%;   Pred. No. 0.00e+00;
Matches   615; Conservative   0; Mismatches 158; Indels 11; Gaps   7;

Db   479 CCTCCTCCTTCACTCTGATTGAAGGCACCCTGGAGGAGGTGCCTGCTGGGTCCCCA 538
           |||||||| |||||| | |||||||||||||||||||||| ||||||||
Qy   3978 CCTCCTCCTCCTCCTCCTGGCTCCTCTGGGCACCCTGGAGGAGGTGCCACTGTCGGTCAACAG 4037

Db   539 GTCCTCCCCTGAGTC-TCAGGGTTCCTCCATTCAGCCACATCAGCAACAACACTCTAT 597
           || ||||||| | |||||||||||| | |||||||||||||
Qy   4038 ATCCTCCCCAGAGTCTCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCTCCAC 4097

Db   598 GGAGCCAATCCAGTGAGGGCACCAGCACCCGGAAGAGAGGGGCCAACCACTAGACAC 657
           ||| ||||||| |||||||| || ||||| | |||||||||||||| |||||
Qy   4098 AGAGGCAACCAGTGAGGGGGTCCAGCAGCCGTGAAGAGAGGGGCCAGCCACCTCTGTA 4157

```
Db   658  ACCCCGTCACCTGG--CGTCCTTGTTCCAATGGGAAGGTTGGCTGAGTTGGTTCGCTTCC  715
          ||  ||  |||||  |  | ||||||  | |||||||||  | ||||||| |||||| ||
Qy  4158  TCCTGGAGTCCTTGCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTTTTC  4217

Db   716  TGCTGCACAAGTATCGAGTCAAGGAGAGCTGGTCACAAGGCAGAAATGCTGGACAGTGTCA  775
          ||||||  ||  |||  |||  |||||| |||| |||| |||||||||||  ||||||||||
Qy  4218  TGCTTCCCAAATATCGAGCCAGGAGCCAGTCACAAGGCAGAAATGCTGGACAGTGTCA     4277

Db   776  TCAAAAATTACAAGCACTAGTTTCCTTGTGATCTATGGCAAAGCCTCAGAGTGTCATGCAG  835
          | |||||||||||| || |||  | || ||  ||||||  |||||| ||| ||  ||||||
Qy  4278  TCAAAAATTACAAGCACTGTTTTCCT-GAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAG   4336

Db   836  GTGATGTTTGGCATTGACATGAACGAAGTGGACCCCGC-GGCCACTCCTACGTCCTTGTC  894
          ||||||||||||||||  ||||| ||||  |||||||  |||||  ||||| ||| ||||
Qy  4337  CTGGTCTTTGGCATTGACGTGAAGCAGAGCCCACCGCCC-CACTCCTATGTCCTTGTC    4396

Db   895  ACCTTGCTGGGCCTCCTCCTACAATGGCCCTGCTGGGTGATGATCAGAGCATGCCCGAGACC  954
          |||| || | |||||| |||  |||||||||| ||||  |||||  || || |||| || |
Qy  4397  ACCTGCCTAGGTCTCCTCCTATGATGGGCCTGCTGGGTGATAATCAGAGCATTGACGTGACA  4456

Db   955  GGCCTTCGATTATGTGTCTTGACCATGATCTTAATGAGGGCCACTGTGCCCCTGAGGAG  1014
          |||  | ||  |  |  || |||  |||  ||||  ||||||  ||| |||  |||||||
Qy  4457  GGCTTCCTGATAATTGTCCTGGTCATGATTGATTGCAATGGCGGCCATGTGCGGGCGGCGGAG  4516

Db  1015  GCAATCTGGGAAGCGTTGAGTGTAATGG---TGTATGATGGGATGGGAGCA--GTTTCTTT  1069
          | ||||||| | ||||  |  ||| |||     |||| ||  |||||  | |   |||||||
Qy  4517  GAAATCTGGGGAGGAGCTGAGTGTGTATGATGGGAGGGCACAGTGCGAT   4576

Db  1070  GGGCAGCTGAGGAAGCTGCTCACCCCAAGATTGGGTGCAGGAGGTGCAATACCTGCAATACCGC  1129
          |||||| ||  || || || || ||| |||  |||  | |||  |  |||  |||||| ||||
Qy  4577  GGGGAGCCCAGGAAGCTGCTCACCCCAAGATTTGGTGCAGGAAAGTACCTGGAGTACGGC     4636

Db  1130  CAGGTGCCCAGCAGTGATGATCCCCGTGCTACCAGTTCCTGTGGGTCCAAGGGCCCTCATT  1189
          ||||||  |||| | ||  |||  ||| |||  |||||||||||||| |||||||| |
Qy  4637  -AGGTGCCGACAGTGATGATCCCCGCACGTATGAGTTCCGTGTGGGTCCAAGGGCCCTTCGCT  4695

Db  1190  GAAACCAGCTACTGTGAAAGTCCTGAGTATGCAGCCCAGGCTGCTAAAGAGAGCATT  1249
          |||| | |||| ||  |||||| ||||| |  |  ||| ||||| |||||||| ||
Qy  4696  GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT   4755

Db  1250  TCCT  1253
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Qy  4756  TTCT  4759
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RESULT 13
LOCUS   I36936   1412 bp   DNA   PAT   21-APR-1997
DEFINITION   Sequence 21 from patent US 5612201.
ACCESSION   I36936
NID   g2084896
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1412)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 21 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..1412
                     /organism="unknown"
BASE COUNT   324 a   402 c   393 g   293 t
ORIGIN

Query Match   46.3%; Score 385; DB 25; Length 1412;
Best Local Similarity   79.0%; Pred. No. 5.56e-298;
Matches 592; Conservative   0; Mismatches 147; Indels 10; Gaps 6;

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Db   565  GGAGGAGGTGTGCTGCTGGGTCATCAAGTCCTCCCCAGAGTCCTCAGGGAGGCGCTTC  624
          ||||||||| |  |||||||| |||| || ||||||||||||||||||||||||||||
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Qy  4009  GGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCTCCAGGGAGGCTCCGC  4068

Db   625  CTCCTCCATTCCGTCTACTACACTTATGGAGCAGTTATCGATGAGGCTCCAGCAGTCA   684
          ||  | ||  ||  |  ||  |||  |  ||  || ||| ||||  | || ||||||||
Qy  4069  CTTTCCCACTACCATCAACTTCACTCGACAGAGCAACCCAGTGAGGGTCCAGCAGCCG   4128

Db   685  AGAAGAGGAAGAGGCAAGCTCCTCGGTCGCCTCAGCTCAGCTGGAGTTCATGTCCAAGA  744
          |||||||||||| ||||| ||||  || |  | || | || ||  ||||| |||  |||
Qy  4129  TGAAGAGGAGGGCCAAGCACCTCT-T-GT--A--TC--CTGGAGTCCTTGTTCCGAGC  4179

Db   745  AGCACTGAAATTGAAGGTGGCTGAGTTGGTTCATTTCTGCTCCACAAATATCGAGTCAA  804
          || |  ||| | |  | | |||| | |||||| || |||| ||||||| | ||| |||
Qy  4180  AGTAATCACTAAGAAGGTGGCTGATTTGGTTTTTCTGCTTCCTCCTCCAAATATCGAGCAGC  4239

Db   805  GGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGAATGCTCATCAACAAAAATTACAGGCTACTT  864
          ||||| ||| || ||| |||||||||||| |||  |||| |||||| ||||||||||| | ||
Qy  4240  GGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAACAAAAATTACAAGCACTGTTT   4299

Db   865  TCCTGATCTTCGGCAAAGCCTTCATGCAGGTGATCTTGGCACTGATGTGAA  924
          ||| | ||| ||||||||||| |||| |||   ||   ||   || ||||
Qy  4300  TCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAA   4359

Db   925  GGAGGTGGACCCCGCCGGTGCCCACTCCTACAATCCTGTCACTGCTTGCCTCTCGTGCGA  984
          |||||||| |||  ||| ||| ||| ||| |  ||||| || |  |||  | || ||
Qy  4360  GGAGCAGAGCCCACCGCCCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCCTCCTATGA  4419

Db   985  TAGCATGCTGGGTGATGGTCATAGCATGCCGCCCCTCTGATCATTGTCCTGGG  1044
          | ||  |||| ||| || |||  |||||| | |||| | ||||| ||| |||
Qy  4420  TGGCCTGCTGGGTGATAATCAGAGCATGGACAGGCTTCCTGATAATTGTCCTGGT  4479

Db  1045  TGTGATCCTAACCAAAGACAACTCGCCCCCTGAAGAGGTTATCTGGAAGCGTTGAGTGT  1104
          |||  |||  |   ||| |  |||  | |||||||| | ||  |||||  || || |||
Qy  4480  CATGATTGCAATGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGT   4539

Db  1105  GATGGGGGTGTATGTTGGGAAGGAGCACAATGTTCTACGGGGAGGTGCCCAGGAAGCTGCTCAC  1164
          ||||||||| ||||| | ||  || |||  ||| |  | |||| | ||||||||||| ||||||
Qy  4540  GATGGAGGGTGTATGATGGGGAGGGCACAGTGCGATCCTATGGGGAGGCCCAGGAAGCTGCTCAC  4599

Db  1165  CCAAGATTGGGTGCAGGAGGTGCCCAGTACCGGCCCAGTCAGTGCCCGGCCAGTGCTCAC  1224
          ||||| ||||| |||||  | || |||||||  | ||  ||||| | | ||||| ||||
Qy  4600  CCAAGATTTGGTGCAGGAAAAGTACCTGGAGTAC--GGCAGGTGCCGACAGTGATGATCCCCGC  4658

Db  1225  GCACTACGAGTTCCTGTGGGGTTCCAAGGCCACCCTGAAACCAGCTATGAGAAGGTCAT  1284
          || || |||||||| || | || |||||| | |||||| |  |||| ||  |||||| |
Qy  4659  ACGTATGAGTTCCGTGTGGGTCCAAGGGCCCTTCGCTGAAACCAGCTATGTGAAAGTCCT  4718

Db  1285  AATTATTTGGTCATGCTCAATGCAAGAG  1313
          | ||  ||| || || ||  ||||| ||
Qy  4719  TGAGTATGTGATCAAGGTCAGTGCGCAGAG  4747
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RESULT 14
LOCUS   I36938   1107 bp   DNA   PAT   21-APR-1997
DEFINITION   Sequence 23 from patent US 5612201.
ACCESSION   I36938
NID   g2084898
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1107)
  AUTHORS   De Plaen,E., Boon-Falleur,T., Lethe ,B., Szikora,J., De Smet,C. and
             Chomez,P.
  TITLE   Isolated nucleic acid molecules useful in determining expression of
             a tumor rejection antigen precursor
  JOURNAL   Patent: US 5612201-A 23 18-MAR-1997;
FEATURES   Location/Qualifiers
     source   1..1107
                     /organism="unknown"
BASE COUNT   269 a   283 c   295 g   260 t
ORIGIN

Query Match   41.2%; Score 342; DB 25; Length 1107;

US-08-190-411A-1.rge

Left column:

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Best Local Similarity 74.9%;  Pred. No. 1.32e-260;
Matches     597; Conservative   0;   Mismatches 189;   Indels  11;   Gaps   6;

Db   311  GCAGGAGGCTGCCTTCTTCTCCTCTACTCTGAATGTGGCACTCTAGAGGAGTTGCCTGC  370
          ||||| || ||| ||| |||||||||| ||||  |||||| || ||||||| |||| |
Qy  3964  GCAGGCTGCCACCTCCTCCTCCTCCTGCTGCTGTCTGGGCACCCTGGAGGAGGTGCCCAC  4023

Db   371  TGCTGAGTCACCAAGTCCTCCCCAGAGTCCTTCAGGAAGAGTCCTTCTCTCCCACTGCCAT  430
          || |||| || || ||||||||||||||| || |||| |||||| || |||||| |||||
Qy  4024  TGCTGGGTCAACAGATCCTCCCCCAGAGTCCTCCAGGGAGTCCTTCAGGGAGGTCCCACTACCAT  4083

Db   431  GGATGCCATCTTTGGGAGCCTATCTGATGAGGGCTCTGGCAGCCAAGAAAAGGAGGGGGCC  490
          |  ||  |||| | |     || ||  || || |||||  |||  | |||||||
Qy  4084  CAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGGCC  4143

Db   491  AAGTACCTCGCCTGACCTGATAGACCCTGAGTCCTTTCCCAAGATATACTACATGACAA  550
          ||||||||| |  ||  || | |   |   ||||||||||| | || || || | |||
Qy  4144  AAGCACCTCT--TG---T-AT---CCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAA  4194

Db   551  GATAATTGATTTGGTTCATTTATT-CTCCCGAAGTATCGAGTCAAGGGGTGATCACAAA  609
          |  |  ||||| || |     | | ||   ||||||||| |||||| ||||||||||||
Qy  4195  GGTGGCTGATTTGGTTGGTTTTCTGCTCCTCTCAAATATCGAGCCAGGGAGCCCAGTCACAAA  4254

Db   610  GGCAGAAATGCTGGGGAGTGTCATCAAAAATTATGAGGACTACTTTCCTGAGATATTTAG  669
          ||||||||||||||||| ||||||| || | |  || ||| || || || ||| || |
Qy  4255  GGCAGAAATGCTGGGAGTGTCATCAAAAATTACAGAGTGTTTTCCTGAGATCTTCGG  4314

Db   670  GGAAGCCTCTGTATGCAACTGCTCTTGGCATTGATGTGAAGGAAGTGGACCCCAC  729
          |||||||||| | ||  |  ||||| ||||||||| |  || ||| ||||||||||
Qy  4315  CAAAGCCTCTGAGTCCTTGCTGGTCTTTGCATTGGCTGTGTTTGGCATTGACCAGCCCAC  4374

Db   730  TAGCCACTCCTATGTCCTTGTCACCTCTCCTCAACCTCTCTATGATAGTGCATACAGTGTAA  789
          |||  || ||||| || || |  |||| ||   |    | ||| | ||| | | |  |
Qy  4375  CGGCGCACTCCTATGTCCTTGTCACCTCTCCTAGGTCTCTCCCCATGATGGCCGTTGCCTGCGGTGA  4434

Db   790  TGAGCAGGAGCCAAGTCTGGCCTTCTGATAATAGTCTGGGTGTAATCTTCATGGA  849
          | ||  ||||||||| | || | ||||  |  || ||||||| | ||| |||||
Qy  4435  TAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGA  4494

Db   850  GGGGAACTGCATCCTCTGAAGAGGTTATGTGGGAAGTTCCTGAGCATTATGGGGTGTATGC  909
          |||    |||||| | |||||||    | ||||| |  ||  ||| | | |||||||||||
Qy  4495  GGGGCGCCATGGCCATGCCCTCCCAAGGGGGCCTCGTGGTGTCCTGAGGTGTGATGA  4554

Db   910  TGGAAGGGAGCACTTCCTCTTTGGGGAGCCCAAGAGGCCTCCTTACCCAAAATTGGGTGCA  969
          |||  |||||||||||||| || |||||||  || |||||  || || |||||||| |||
Qy  4555  TGGGAGGGAGCACAGTGCCATGGGAGCCCAGTGCCTATGGGTTGGTGCA  4614

Db   970  GGAAAAGTACCTGGTGTACCCGGCAGTGCCCGGCACTGACTCCTGCATGCTATGAGTTCCT  1029
          ||||||||||||||||  | || ||  ||||||||||  ||||| || |||| |||||||
Qy  4615  GGAAAAGTACCTGGAGTAC-GGCAGTGCCCGGCACTGACTCCTGCATGCTATGAGTTCCT  4673

Db  1030  GTGGGGTCCAAGGGCCCACGTGAGACCTGAGACCGCAAGATGAAAGTTCTTGAGTACATAGCCAA  1089
          |||||||| ||||||  ||||||| |||||||| | |||||  |||||| ||||| |||| |
Qy  4674  GTGGGGTCCAAGGGCCCCTGCTGAGACCTATGTGAAACCAGCTATGTGAATGTGATCAA  4733

Db  1090  TGCCAATGGGAGGGATC  1106
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Qy  4734  GGTCAGTGCCAAGAGTTC  4750
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RESULT   15
LOCUS   I32295   1866 bp   DNA   PAT   07-JAN-1997
DEFINITION   Sequence 1 from patent US 5587289.
ACCESSION   I32295
NID   g1823086
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 1866)
AUTHORS   Lurquin,C. and Boon-Falleur,T.
TITLE   Isolated nucleic acid molecules which are members of the MAGE-Xp
              family and uses thereof

Right column:

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JOURNAL       Patent: US 5587289-A 1 24-DEC-1996;
FEATURES      Location/Qualifiers
    source    1..1866
              /organism="unknown"
BASE COUNT    504 a    424 c    457 g    481 t
ORIGIN

Query Match       22.1%;   Score 184;  DB 25;  Length 1866;
Best Local Similarity  68.7%;  Pred. No. 5.95e-125;
Matches       347;  Conservative   0;  Mismatches 157;  Indels  1;  Gaps  1;

Db   699  AGAGAGCCCATTATGGAGCCAGATATGCTGAAGGTGTTGATGAATGTACAAGGATCAC  758
          || ||||| |||| ||| || ||||||||||||| ||  ||  |||| |||||||||
Qy  4238  AGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAATTACAAGCACTGT  4297

Db   759  TTCACTGAGATCCTCAATGGAGCCTCCGCCGGCCTCTTGGAGCTCGTCTTGAGTTG  818
          || ||||| |  || || ||||||  |  || ||| || ||| | ||| ||||||
Qy  4298  TTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGTCTTTGGCATTGACGTG  4357

Db   819  AAGGAAGACAACCCTAGTAGCCACACTGAGTCAAGGGGCTGATCACCAT  878
          ||||||||  | |   |  || ||| |  ||||| || ||| || |||
Qy  4358  AAGGAAGCAGCACCCCACCGGCCGCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTAT  4417

Db   879  GATGGAAACCTGAGCAATGATTGGGACTTTCCCAGGAATGGCTTCCTGATGCCTCCTG  938
          ||||| | | ||| || | | |   |   |||||||| || || ||||| ||| |||
Qy  4418  GATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAATTGTCCTG  4477

Db   939  GGTGTGATCTTCTTAAAGGCAACTCTGCCACCGAGGAAGAGATCTGGAAATTCATGAAT  998
          ||||||||  |  |   |||  | | | ||| |   ||||| || ||| || |||||
Qy  4478  GTCATGATTGCAATGGAGGGGCGGCCATGGCCATGCCCTCCCAAGGGGGCCTCGTGGAGT  4537

Db   999  GTGTTGGAGCCTATGATGGAGGAGCACTTAATCTATGGGAACCCCGTAAGTTCATC  1058
          || || |||| |||| ||||| |||||| | |||||||||||||| |  || | ||
Qy  4538  GTGATGGAGGTGTATGGGGTGGAGGGCACAGTGCCTATGGGTTGGTGCAGGAAGCTGCTC  4597

Db  1059  ACCCAAGATCTGGTGCAGGAAAAAATCTGAGTACGAGCAGGTGCCCAACAGTGATCCC  1118
          ||||||||||| |||| |||||||| | || | || || || ||||| ||||||||||
Qy  4598  ACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACG-GCAGGTGCCGGACAGTGATCCC  4656

Db  1119  CCACGCTATCAATTCCTATGGGGTCCGAGGCCTATGCTGAAAAACCAAGATGAAAGTC  1178
          ||||| ||||||| |  |  ||| |||   |  | ||| | || | ||||  ||||||
Qy  4657  GCACGCTATGAGTTCCTGTGTGGGGTCCAAGGGCCCCTGCTGAGACCAGCTATGTGAAAGTC  4716

Db  1179  CTCGAGTTTTGGCCAAGATGAATG  1203
          || |||| | |||| | | |||
Qy  4717  CTTGAGTATGTGATCAAGGTCAGTG  4741
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Search completed: Tue Apr 7 22:16:22 1998
Job time : 682 secs.

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|  \| || |_) |\___ \| |_) | |   | |_| |
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****

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 22:18:14 1998; MasPar time 75.03 Seconds
                                           1271.809 Million cell updates/sec

Tabular output not generated.

Title: >US-08-190-411A-1
Description: (3931-4761) from 5541104.seq
Perfect Score: 831
N.A. Sequence: 3931 GGCCCAACAAGAGGCCCTGG..........CAAGAGTTCGCTTTTTCTTC 4761
Comp: CCGGGTTGTTCTCCCGGGACC..........GTTCTCAAGCGAAAAGAAG

Scoring table: TABLE default
               Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159649 seqs, 57412152 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-geneseq30
               1:n-geneseq1

Statistics: Mean 8.982; Variance 5.045; scale 1.780

               Pred. No. is the number of results predicted by chance to have a
               score greater than or equal to the score of the result being printed,
               and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	831	100.0	2419	1	Q72476	Tumour rejection antig	0.00e+00
2	831	100.0	2419	1	Q32351	Antigen E gene.	0.00e+00
3	831	100.0	5674	1	Q72477	Tumour rejection antig	0.00e+00
4	831	100.0	5724	1	Q98902	Tumour rejection antig	0.00e+00
5	829	99.8	5674	1	Q32352	MAGE-1 nucleic acid.	0.00e+00
6	827	99.5	2419	1	T05086	MZ2-MEL antigen E prec	0.00e+00
7	825	99.3	2420	1	Q72472	Tumour rejection antig	0.00e+00
8	825	99.3	2420	1	Q85435	Human melanoma antigen	0.00e+00
9	781	94.0	1084	1	Q67866	H6/MAGE-1 expression c	0.00e+00
10	781	94.0	1094	1	Q67865	H6/MAGE-1 expression c	0.00e+00
11	584	70.3	2531	1	Q72482	Tumour rejection antig	0.00e+00
12	582	70.0	2531	1	Q72483	Tumour rejection antig	0.00e+00
13	580	69.8	2531	1	Q32358	MAGE-41 gene.	0.00e+00
14	580	69.8	2531	1	Q32357	MAGE-4 gene.	0.00e+00
15	513	61.7	2305	1	Q32361	MAGE-51 genomic DNA.	0.00e+00
16	513	61.7	2305	1	T01165	MAGE-51 gene.	0.00e+00
17	513	61.7	2305	1	Q72486	Tumour rejection antig	0.00e+00
18	502	60.4	1640	1	Q72480	Tumour rejection antig	0.00e+00
19	500	60.2	2226	1	Q32360	MAGE-5 cDNA.	0.00e+00
20	500	60.2	2226	1	Q72485	Tumour rejection antig	0.00e+00
21	490	59.0	1640	1	Q32355	MAGE-3 cDNA.	0.00e+00
22	488	58.7	4157	1	Q72478	Tumour rejection antig	0.00e+00
23	486	58.5	4157	1	Q32353	MAGE-2 gene.	0.00e+00
24	464	55.8	1810	1	T01168	MAGE-8 gene.	0.00e+00
25	464	55.8	1810	1	Q32364	MAGE-8 genomic DNA.	0.00e+00
26	464	55.8	1810	1	Q72489	Tumour rejection antig	0.00e+00
27	452	54.4	1068	1	Q72484	Tumour rejection antig	0.00e+00
28	450	54.2	1068	1	Q32359	MAGE-4 cDNA.	0.00e+00
29	391	47.1	1947	1	T01167	MAGE-7 gene.	5.23e-267
30	391	47.1	1947	1	Q32363	MAGE-7 genomic DNA.	5.23e-267
31	391	47.1	1947	1	Q72488	Tumour rejection antig	5.23e-267
32	385	46.3	1412	1	Q72490	Tumour rejection antig	1.81e-262
33	385	46.3	1412	1	T01169	MAGE-9 gene.	1.81e-262
34	381	45.8	1412	1	Q32365	MAGE-9 genomic DNA.	1.91e-259
35	342	41.2	1107	1	T01171	MAGE-11 gene.	5.40e-230
36	342	41.2	1107	1	Q72492	Tumour rejection antig	5.40e-230
37	342	41.2	1107	1	Q32367	MAGE-11 genomic DNA.	5.40e-230
38	264	31.8	379	1	T63349	Human MAGE-3 DNA.	2.27e-171
39	255	30.7	386	1	T63349	Baboon MAGE-3 homologu	1.23e-164
40	248	29.8	384	1	T63346	Baboon MAGE-3 homologu	2.09e-159
41	184	22.1	279	1	T63350	Baboon MAGE-3 homologu	7.31e-112
42	184	22.1	1866	1	T41492	DNA encoding MAGE-Xp1	7.31e-112
43	181	21.8	271	1	T63348	Baboon MAGE-3 homologu	1.19e-109
44	165	19.9	276	1	T63347	Baboon MAGE-3 homologu	7.03e-98
45	149	17.9	225	1	Q72487	Tumour rejection antig	3.60e-86

ALIGNMENTS

RESULT   1
ID   Q72476 standard; DNA; 2419 BP.
AC   Q72476;
DT   21-JUN-1995 (first entry)
DE   Tumour rejection antigen E encoding DNA.
KW   Tumour rejection antigen E; melanoma antigen-3; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
OS   Homo sapiens.
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Disclosure; Page 58; 105pp; English.
CC   Q72476 encodes tumour rejection antigen E, another sequence
CC   Q72470 encodes melanoma antigen-3 (MAGE-3) a tumour rejection
CC   antigen precursor. Melanomas characterised by the expression of
CC   MAGE-3 can be detected, or monitored, by contacting a test sample
CC   with an agent that can recognise MAGE-3. The melanoma can be treated
CC   by the administration of cytolytic T cells specific for the complex of
CC   antigen D (the mature rejection antigen derived from MAGE-3) and a human
CC   leucocyte antigen (esp. HLA-A1).
SQ   Sequence   2419 BP;   562 A;   581 C;   677 G;   599 T;

Query Match   100.0%;   Score 831; DB 1; Length 2419;
Best Local Similarity   100.0%;   Pred. No. 0.00e+00;
Matches   831; Conservative   0; Mismatches   0; Indels   0; Gaps   0:

Db   676 GGCCCAACAAGAGGCCCTGGGCCTGGTGTGTCGCAGCTGCCACTCCTCCTCCTCCTC 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3931 GGCCCAACAAGAGGCCCTGGGCCTGGTGTGTCGCAGCTGCCACTCCTCCTCCTCCTCC 3990

Db   736 TCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3991 TCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050

Db   796 TCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4051 TCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110
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Db   856  TGAGGGTTCCAGCAGCCGTGAGAGGAGGGCCAAGCACCTCTTGTATCCTGAGTCCTT   915
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4111  TGAGGGTTCCAGCAGCCGTGAGAGGAGGGCCAAGCACCTCTTGTATCCTGAGTCCTT  4170

Db   916  GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTCGTCCTCAAATA   975
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4171  GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTCGTCCTCAAATA  4230

Db   976  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  1035
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4231  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  4290

Db  1036  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTGGCAT  1095
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4291  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTGGCAT  4350

Db  1096  TGAGGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT  1155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4351  TGAGGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT  4410

Db  1156  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT  1215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4411  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT  4470

Db  1216  TGTCCTGGTCATGATTGGTGTCAATGGAGGGCGGCCCATGCTCCTGAGGAGGAAATCGGGAGGA  1275
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4471  TGTCCTGGTCATGATTGGTGTCAATGGAGGGCGGCCCATGCTCCTGAGGAGGAAATCGGGAGGA  4530

Db  1276  GCTGAGTGTGATGGAGGTGTATGAGTGGGAGGGCACAGTGCCTATGGGAGCCCAGGAA  1335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4531  GCTGAGTGTGATGGAGGTGTATGAGTGGGAGGGCACAGTGCCTATGGGAGCCCAGGAA  4590

Db  1336  GCTGCTCACCCAAGATTGGTGCAGGAAAGTACCTGGAGTACGGCCGTGCCGGACAGT  1395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4591  GCTGCTCACCCAAGATTGGTGCAGGAAAGTACCTGGAGTACGGCCGTGCCGGACAGT  4650

Db  1396  GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGAAACCAGCTATGTG  1455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4651  GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGAAACCAGCTATGTG  4710

Db  1456  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC  1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC  4761
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RESULT  2
ID   Q32351 standard; DNA; 2419 BP.
AC   Q32351;
DT   22-APR-1993  (first entry)
DE   Antigen E gene.
KW   Stable; antigen; E; D; F; A: human; melanoma; cell line; MZ2-MEL;
KW   cytolytic T cell; MEL3.1; open reading frame; homology; MAGE;
KW   melanoma antigen; ss.
OS   Homo sapiens.
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992; U04354.
PR   23-MAY-1991; US-705702.
PR   09-JUL-1991; US-728838.
PR   23-SEP-1991; US-764364.
PR   12-DEC-1991; US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure; Page 69-70; 142pp; English.
CC   This sequence encodes the stable antigen E.  This antigen is expressed
CC   along with antigens "D, F and A" by the human melanoma cell line MZ2-
CC   MEL.,These antigens are all recognised by cytolytic T cells.  A
CC   subline of MZ2-MEL is MEL3.1 which only expresses antigen E.  This
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CC   cell line was chosen as a source for the isolation of this sequence.
CC   This sequence was found to contain three exons. The open reading frame
CC   for antigen E was contained within the first two exons. An ATG is
CC   located at position 66 of exon 3 and is followed by an 828 base pair
CC   reading frame. The three exons contain 65, 73 and 1551 base pairs.
CC   During the isolation of this sequence two different but closely reated
CC   cDNAs were also identified. These cDNAs, when tested, did not
CC   transfer expression of antigen E, but they did show substantial
CC   homology to the antigen E cDNA sequence. These new cDNAs represent a
CC   new family of genes refered to as melanoma antigens (MAGE) (see also
CC   Q32352-69).
SQ   Sequence  2419 BP;  562 A;  581 C;  677 G;  599 T;

Query Match  100.0%;  Score 831;  DB 1;  Length 2419;
Best Local Similarity 100.0%;
Matches  831;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db   676  GGCCCAACAAGAGAGGCCCTGGGCCTGGTGTGGTGCAGGCTGCCACCTCCTCCTCCTCC   735
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3931  GGCCCAACAAGAGAGGCCCTGGGCCTGGTGTGGTGCAGGCTGCCACCTCCTCCTCCTCC  3990

Db   736  TCTGGTCCTGGGCACCCTGGAGGAGTGGCCACTGCTGGGTCAACAGATCCTCCCCAGAG   795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3991  TCTGGTCCTGGGCACCCTGGAGGAGTGGCCACTGCTGGGTCAACAGATCCTCCCCAGAG  4050

Db   796  TCCTCAGGGAGCCTCCGCCTTTCCACTACCATCAACTCACTCGACAGAGCAACCCAG   855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4051  TCCTCAGGGAGCCTCCGCCTTTCCACTACCATCAACTCACTCGACAGAGCAACCCAG  4110

Db   856  TGAGGGTTCCAGCAGCCGTGAGAGGAGGGCCAAGCACCTCTTGTATCCTGAGTCCTT   915
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4111  TGAGGGTTCCAGCAGCCGTGAGAGGAGGGCCAAGCACCTCTTGTATCCTGAGTCCTT  4170

Db   916  GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTCGTCCTCAAATA   975
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4171  GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTCGTCCTCAAATA  4230

Db   976  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  1035
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4231  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  4290

Db  1036  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTGGCAT  1095
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4291  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTGGCAT  4350

Db  1096  TGAGGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT  1155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4351  TGAGGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT  4410

Db  1156  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT  1215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4411  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT  4470

Db  1216  TGTCCTGGTCATGATTGGTGTCAATGGAGGGCGGCCCATGCTCCTGAGGAGGAAATCGGGAGGA  1275
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4471  TGTCCTGGTCATGATTGGTGTCAATGGAGGGCGGCCCATGCTCCTGAGGAGGAAATCGGGAGGA  4530

Db  1276  GCTGAGTGTGATGGAGGTGTATGAGTGGGAGGGCACAGTGCCTATGGGAGCCCAGGAA  1335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4531  GCTGAGTGTGATGGAGGTGTATGAGTGGGAGGGCACAGTGCCTATGGGAGCCCAGGAA  4590

Db  1336  GCTGCTCACCCAAGATTGGTGCAGGAAAGTACCTGGAGTACGGCCGTGCCGGACAGT  1395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4591  GCTGCTCACCCAAGATTGGTGCAGGAAAGTACCTGGAGTACGGCCGTGCCGGACAGT  4650

Db  1396  GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGAAACCAGCTATGTG  1455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4651  GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGAAACCAGCTATGTG  4710

Db  1456  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC  1506
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC  4761
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RESULT 3
ID   Q72477   standard; DNA; 5674 BP.
AC   Q72477;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-1 encoding DNA.
KW   Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   3881..4711
FT   /*tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
CC   Example 26; Page 59; 105pp; English.
CC   Q72477 is the DNA sequence which encodes melanoma antigen-1
CC   (MAGE-1). Another melanoma antigen MAGE-3 is encoded by Q72470,
CC   this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T;

Query Match   100.0%; Score 831; DB 1; Length 5674;
Best Local Similarity   100.0%; Pred. No. 0.00e+00;
Matches   831; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCC 3990
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCC 3990

Db 3991 TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3991 TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050

Db 4051 TCCTCAGGGAGGCCTTCCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4051 TCCTCAGGGAGGCCTTCCCGCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

Db 4111 TGAGGGTTCAGCAGCGCGTGAAGAGAGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4111 TGAGGGTTCAGCAGCGCGTGAAGAGAGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170

Db 4171 GTTCCGAGCAGTAATCACTAAGAAGAGGTGCTGATTTGGTTGGTTTTCTGCTCCTCCAAATA 4230
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4171 GTTCCGAGCAGTAATCACTAAGAAGAGGTGCTGATTTGGTTGGTTTTCTGCTCCTCCAAATA 4230

Db 4231 TCGAGCCAGGGAGGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4231 TCGAGCCAGGGAGGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290

Db 4291 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4291 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350

Db 4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACCTCATGTCCTATGGTCCACCTGCCTAGGTCT 4410
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACCTCATGTCCTATGGTCCACCTGCCTAGGTCT 4410

Db 4411 CTCCTATGATGGCCTGCTCGGTGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4411 CTCCTATGATGGCCTGCTCGGTGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470

Db 4471 TGTCCTGGTCATGATTGCAATGAGGCCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4471 TGTCCTGGTCATGATTGCAATGAGGCCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530

Db 4531 GCTGAGTGTGATGGAGGTGTATGATGGGAGGAGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4531 GCTGAGTGTGATGGAGGTGTATGATGGGAGGAGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590

Db 4591 GCTGCTCACCCAAGATTTGGTGCGAGAAAAGTACCTGGAGTACGGCAGTGCCGGACAGT 4650
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4591 GCTGCTCACCCAAGATTTGGTGCGAGAAAAGTACCTGGAGTACGGCAGTGCCGGACAGT 4650

Db 4651 GATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTGCTGAAACCAGCTATGTG 4710
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4651 GATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTGCTGAAACCAGCTATGTG 4710

Db 4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTCAGTGCCAAGAGTTCGCTTTTCTC 4761
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4711 AAAGTCCTTGAGTATGTGATCAAGGTCAGTCAGTGCCAAGAGTTCGCTTTTCTC 4761

RESULT 4
ID   Q98902   standard; DNA; 5724 BP.
AC   Q98902;
DT   28-FEB-1996 (first entry)
DE   Tumour rejection antigen (MAGE-1) gene.
KW   Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb;
KW   diagnosis; immunoassay; cancer; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   3881..4711
FT   /*tag= a
FT   /product= Tumour rejection antigen MAGE-1.
FT   /note= "The CDS is not indicated in the text of the
FT   specification but is suggested in the layout
FT   of the sequence."
PN   WO9520974-A1.
PD   10-AUG-1995.
PF   05-JAN-1995; U00095.
PR   01-FEB-1994; US-190411.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK) SLOAN KETTERING INST CANCER RES.
PA   (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
PI   Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ,
PI   Stockert E, Van der bruggen P;
DR   WPI; 95-283606/37.
PT   New monoclonal antibody binding specifically to MAGE-1 - useful for
PT   diagnosis and monitoring of cancer, also new hybridomas, recombinant
PT   MAGE-1 and immunogenic peptide(s)
PS   Disclosure; Page 16-19; 33pp; English.
CC   A monoclonal antibody directed against the tumour rejection antigen
CC   (MAGE-1) can be used to detect MAGE-1 in samples by standard
CC   immunoassay methods for diagnosis and monitoring of cancer etc. The
CC   monoclonal antibody is designated MA454 and is produced by the
CC   hybridoma deposited as ATCC HBB11540. The monoclonal antibody is
CC   specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
CC   Peptide fragments of MAGE-1 (See R80618-20) may be useful as
CC   immunogens for production of the monoclonal antibody and antisera.
SQ   Sequence 5724 BP; 1282 A; 1653 C; 1589 G; 1200 T;

Query Match   100.0%; Score 831; DB 1; Length 5724;
Best Local Similarity   100.0%; Pred. No. 0.00e+00;
Matches   831; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCC 3990
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCC 3990

Db 3991 TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 3991 TCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050

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PT     treating and preventing cancers, also useful in diagnosis
PS     Disclosure; Page 71-73; 142pp; English.
CC     The sequences given in Q32352-69 represent a new family of genes
CC     refered to as melanoma antigens (MAGE).  The cDNAs of this gene
CC     family were identified during the isolation of the antigen E gene.
CC     The MAGE cDNAs, when tested, did not transfer expression of antigen
CC     E, but they did show substantial homology to the antigen E cDNA
CC     sequence.  The MAGE DNAs share a certain degree of homology with each
CC     other and are expressed in tumour cells including several types of
CC     human tumor cells as well as in human tumors.  MAGE expression is not
CC     restricted to melanomas.  MAGE refers to a family of tumor rejection
CC     antigen precursors.  The antigens resulting from these genes are
CC     refered to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC     See also Q32351.
SQ     Sequence 5674 BP;  1277 A;  1644 C;  1568 G;  1185 T;

Query Match            99.8%;  Score 829;  DB 1;  Length 5674;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  830;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db  3931  GGCCCAACAAGAGGCCTGGCCTGGTGTGTGCCACCTCCTCCTCCTCCTCC  3990
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3931  GGCCCAACAAGAGGCCTGGCCTGGTGTGTGCCACCTCCTCCTCCTCCTCC  3990

Db  3991  TCTGTCCTGGCACCCTGGAGGAGTGCCACTGCTGGGTCAACAGATCCTCCCCCAGAG  4050
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3991  TCTGTCCTGGCACCCTGGAGGAGTGCCACTGCTGGGTCAACAGATCCTCCCCCAGAG  4050

Db  4051  TCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  4110
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4051  TCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  4110

Db  4111  TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCCTTGTATCCTGGAGTCCTT  4170
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4111  TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCCTTGTATCCTGGAGTCCTT  4170

Db  4171  GTTCCGAGCAGTAATCACTACTAAGAAGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATA  4230
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4171  GTTCCGAGCAGTAATCACTACTAAGAAGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATA  4230

Db  4231  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  4290
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4231  TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA  4290

Db  4291  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGTCACCTGCCTAGGTCT  4350
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4291  GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGTCACCTGCCTAGGTCT  4350

Db  4351  TGACGTGAAGGAAGCAGACAGACCCCACCGGCCACCCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT  4410
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4351  TGACGTGAAGGAAGCAGACAGACCCCACCGGCCACCCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCT  4410

Db  4411  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGAGGCTTCCTGATAAT  4470
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4411  CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT  4470

Db  4471  TGTCCTGGTCATGATTGCAATGCAAGCTCAGTGAGTGTATGATGGGAGGTGTATGGAGGTGCAGGAAATCTGGGAGGA  4530
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4471  TGTCCTGGTCATGATTGCAATGCAAGCTCAGTGAGTGTATGATGGGAGGTGTATGGAGGTGCAGGAAATCTGGGAGGA  4530

Db  4531  GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT  4590
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4531  GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGT  4590

Db  4591  GATCCCGCACCGCTATGTTCCTGTGGGTCCTGGGTCCCAAGGGCCCTCGCTGAAACCAGCTATGTG  4650
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4591  GATCCCGCACCGCTATGTTCCTGTGGGTCCTGGGTCCCAAGGGCCCTCGCTGAAACCAGCTATGTG  4650

Db  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC  4761
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTC  4761
```

Left column:

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Qy   4711  AAGTCCTTGAGTATGTGATCAAGGTCAGTCAGGAGAGTTCGCTTTTTCTTC  4761
           ||||||||||||||||||||||||||||||||||||||

RESULT  6
ID   T05086  standard; DNA; 2419 BP.
AC   T05086;
DT   26-FEB-1996  (first entry)
DE   M22-MEL antigen E precursor gene.
KW   Melanoma; M22-MEL; tumour rejection antigen; cancer; diagnosis; ss.
OS   Homo sapiens.
PN   WO9523874-A1.
PD   08-SEP-1995.
PF   23-FEB-1995; U02203.
PR   01-MAR-1994; US-204727.
PR   10-MAR-1994; US-209172.
PR   01-SEP-1994; US-299849.
PR   30-NOV-1994; US-346774.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI   De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI   Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
DR   WPI; 95-320586/41.
PT   Determn. of cancerous condition(s) - using a nucleic acid as a
PT   primer to determine expression of a MAGE tumour rejection antigen
PT   precursor
PS   Example 20; Page 69-70; 121pp; English.
CC   A gene sequence (T05086) hybridies with a 2.4 kb fragment from
CC   human melanoma cell line M22-MEL but not with E- antigen loss
CC   variants of M22-MEL. This E precursor antigen gene sequence was
CC   obtd. from a cosmid derived from DNA of the E+ subclone M22-MEL 43.
SQ   Sequence  2419 BP;  560 A;  581 C;  677 G;  601 T;

Query Match          99.5%;  Score 827;  DB 1;  Length 2419;
Best Local Similarity  99.8%;  Pred. No. 0.00e+00;
Matches  829;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Db    676  GGCCCAACAAGAGGCCCTGGGCCTGGTCGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC  735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3931  GGCCCAACAAGAGGCCCTGGGCCTGGTCGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC  3990

Db    736  TCTGGTCCTGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG  795
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3991  TCTGGTCCTGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG  4050

Db    796  TCCTCAGGGAGGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4051  TCCTCAGGGAGGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  4110

Db    856  TGAGGGTTCCAGCAGTAATCACTAAGAAGTGGCTGATTGGTTTCTGCTCCTCAAATA  915
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4111  TGAGGGTTCCAGCAGTAATCACTAAGAAGTGGCTGATTGGTTTCTGCTCCTCAAATA  4170

Db    916  GTTCCGAGCAGTAATCACTAAGAAGGCAGAAATGCTGAGAGTGTCATCATTAATTACAA  975
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4171  GTTCCGAGCAGTAATCACTAAGAAGGCAGAAATGCTGAGAGTGTCATCATTAATTACAA  4230

Db    976  TCGAGCCAGGGAGGAGCCAGTCACAAAGGCAGAAATGCTGAGAGTGTCATCAAAAATTACAA  1035
           |||||||||||||||||||||||||||||||||||||||||||||||
Qy   4231  TCGAGCCAGGGAGGAGCCAGTCACAAAGGCAGAAATGCTGAGAGTGTCATCAAAAATTACAA  4290

Db   1036  GCACTGTTTCCTGAGATCTTCGGCAAAGCCTCGAGTCGTCTTGCAGCAT  1095
           |||||||||||||||||||||||||||||||||||||||||||||||
Qy   4291  GCACTGTTTCCTGAGATCTTCGGCAAAGCCTCGAGTCGTCTTGCAGCAT  4350

Db   1096  TGACGTGAAGAAGCAGCAGCAGCCCACCCGAGATAATCAGATCATGCCCAGGTCTCCTGATAAT  1155
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4351  TGACGTGAAGAAGCAGCAGCAGCCCACCCGAGATAATCAGATCATGCCCAGGTCTCCTGATAAT  4410

Db   1156  CTCCTATGATGGCCTGCTCGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT  1215
           ||||||||||||||||||||||||||||||||||||||||||||||
Qy   4411  CTCCTATGATGGCCTGCTCGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT  4470
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Right column:

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Db   1216  TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA  1275
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4471  TGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA  4530

Db   1276  GCTGAGTGTGATGGAGGTGTATGATGGGAGGAGCACAGTGCCTATGGGGAGCCCAGGAA  1335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4531  GCTGAGTGTGATGGAGGTGTATGATGGGAGGAGCACAGTGCCTATGGGGAGCCCAGGAA  4590

Db   1336  GCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACGGCGAGTGCCGGACAGT  1395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4591  GCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACGGCGAGTGCCGGACAGT  4650

Db   1396  GATCCCCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCCAAGGGCCCTCGAAACCAGCTATGTG  1455
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4651  GATCCCCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCCAAGGGCCCTCGAAACCAGCTATGTG  4710

Db   1456  AAAGTCCTTGAGTATGTGATCAAGGTCAGTCAGGAGAGTTCGCTTTTTCTTC  1506
           ||||||||||||||||||||||||||||||||||||||||||
Qy   4711  AAAGTCCTTGAGTATGTGATCAAGGTCAGTCAGGAGAGTTCGCTTTTTCTTC  4761

RESULT  7
ID   Q72472  standard; DNA; 2420 BP.
AC   Q72472;
DT   21-JUN-1995  (first entry)
DE   Tumour rejection antigen E precursor gene DNA.
KW   Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
OS   Homo sapiens.
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Example 20; Page 28; 105pp; English.
CC   Q72472 is the tumour rejection antigen E precursor gene, another
CC   gene Q72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection
CC   antigen precursor. Melanomas characterised by the expression of MAGE-3
CC   can be detected, or monitored, by contacting a test sample with an
CC   agent that can recognise MAGE-3. The melanoma can be treated by the
CC   administration of cytolytic T cells specific for the complex of antigen
CC   D (the mature rejection antigen derived from MAGE-3) and a human
CC   leucocyte antigen (esp. HLA-A1).
SQ   Sequence  2420 BP;  562 A;  582 C;  677 G;  599 T;

Query Match          99.3%;  Score 825;  DB 1;  Length 2420;
Best Local Similarity  99.9%;  Pred. No. 0.00e+00;
Matches  831;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  1;

Db    676  GGCCCAACAAGAGGCCCTGGGCCTGGTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC  735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3931  GGCCCAACAAGAGGCCCTGGGCCTGGTGGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC  3990

Db    736  TCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG  795
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3991  TCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG  4050

Db    796  TCCTCAGGGAGGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  855
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4051  TCCTCAGGGAGGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG  4110

Db    856  TGAGGGTTCCAGCAGCCGTGAATCACTAAGAAGAAGGTGGCTGATTGGTTTCTGCTCCTCAGT  915
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4111  TGAGGGTTCCAGCAGCCGTGAATCACTAAGAAGAAGGTGGCTGATTGGTTTCTGCTCCTCAGT  4170

Db    916  GTTCCAGCAGTAATCACTAAGAAGAAGGTGGCTGATTGGTTTCTGCTCCTCAAATA  975
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4171  GTTCCAGCAGTAATCACTAAGAAGAAGGTGGCTGATTGGTTTCTGCTCCTCAAATA  4230
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Db    976 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAATTACAA 1035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4231 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAATTACAA 4290

Db   1036 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 1095
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4291 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350

Db   1096 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGCACCTGCCTAGGTCT 1155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGCACCTGCCTAGGTCT 4410

Db   1156 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 1215
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470

Db   1216 TGTCCTGGTCATGATTGCAATGGCCGGCCCATGCTCCTGAGGAGGAAATCTGGGAGGA 1275
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4471 TGTCCTGGTCATGATTGCAATGGCCGGCCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530

Db   1276 GCTGAGTGTGATGAGGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 1335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4531 GCTGAGTGTGATGAGGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590

Db   1336 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTAC-GGCAGGTGCCGGACAG 1395
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTAC-GGCAGGTGCCGGACAG 4649

Db   1396 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCCGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGT 1455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4650 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCCGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGT 4709

Db   1456 GAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 1507
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4710 GAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 4761
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RESULT 8

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ID   Q85435   standard; DNA; 2420 BP.
AC   Q85435;
DT   09-OCT-1995  (first entry)
DE   Human melanoma antigen MAGE-1.
KW   Human melanoma antigen MAGE-1; vaccines; MAGE associated tumours;
KW   HLA-restricted cytotoxic T-lymphocyte activity; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             626..1555
FT   /*tag=  a
PN   WO9504542-A.
PD   16-FEB-1995.
PF   02-AUG-1994;  U08721.
PR   06-AUG-1993;  US-103623.
PA   (CYTE-) CYTEL CORP.
PI   Fikes JD, Livingston BD, Sette AD, Sidney JC;
DR   WPI; 95-090681/12.
DR   P-PSDB; R70909.
PT   Human melanoma antigen, MAGE-1, peptide(s) - useful for
PT   stimulating immune response against melanoma
PS   Example 1; Fig 1; 59pp; English.
CC   Q85435 encodes R70909 human melanoma antigen MAGE-1, it was used
CC   to produce the C-terminal MAGE-1 peptides described in R70915 to
CC   R70969. These peptides are useful for defining epitopes that
CC   engender a HLA-restricted cytotoxic lymphocyte activity against
CC   MAGE-1 antigens. Compsns. containing these peptides can be
CC   administered, as a vaccine to patients susceptible to MAGE
CC   associated tumours, e.g. melanomas.
SQ   Sequence   2420 BP;   562 A;   582 C;   677 G;   599 T;
```

Query Match   99.3%; Score 825; DB 1; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 831; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db    676 GGCCCAACAAGAGAGCCCTGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC 735
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Qy   3931 GGCCCAACAAGAGAGCCCTGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCC 3990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 TCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCTCCCCAGAG 795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3991 TCTGGTCCTGGGCACCCTGGAGGAGTGCCCACTGCTGGGTCAACAGATCTCCCCAGAG 4050

Db    796 TCCTCAGGGAGCCTCCGCCTTCCACTACCATCAACTCACTCGACAGAGGCAACCCAG 855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4051 TCCTCAGGGAGCCTCCGCCTTCCACTACCATCAACTCACTCGACAGAGGCAACCCAG 4110

Db    856 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170

Db    916 GTTCCGACCAGTAATCACTAAGAGAGGTGCTGATTTGGTTGGTTTTCTGCTCCTCAAATA 975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4171 GTTCCGACCAGTAATCACTAAGAGAGGTGCTGATTTGGTTGGTTTTCTGCTCCTCAAATA 4230

Db    976 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 1035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4231 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290

Db   1036 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 1095
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4291 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350

Db   1096 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGCACCTGCCTAGGTCT 1155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4351 TGACGTGAAGGAAGCAGACCCCACCGGCCACTCCTATGTCCTTGCACCTGCCTAGGTCT 4410

Db   1156 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT 1215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACACAGGCTTCCTGATAAT 4470

Db   1216 TGTCCTGGTCATGATTGCAATGCAATGGCCGGCCCATGCTCCTGAGGAGGAAATCTGGGAGGA 1275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4471 TGTCCTGGTCATGATTGCAATGCAATGGCCGGCCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530

Db   1276 GCTGAGTGTGATGAGGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 1335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4531 GCTGAGTGTGATGAGGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590

Db   1336 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTAC-GGCAGGTGCCGGACAG 1395
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTAC-GGCAGGTGCCGGACAG 4649

Db   1396 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCCGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGT 1455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4650 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCCGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGT 4709

Db   1456 GAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 1507
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4710 GAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTC 4761
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RESULT 9

```
ID   Q67866   standard; DNA; 1084 BP.
AC   Q67866;
DT   22-MAR-1995  (first entry)
DE   H6/MAGE-1 expression cassette from pMAW037.
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   human; MAGE-1; melanoma-associated antigen; MZ2-E; testis; pTZ18RMAGE1;
KW   primary melanoma tumour cell; melanoma-derived cell line; tumour;
KW   poxvirus; antigenic response; immunological response; pathogen; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   misc_feature    1..51
FT   /*tag=  a
FT   /note= "Flanking sequence"
FT   promoter        52..178
FT   /*tag=  b
FT   /note= "Vaccinia H6 promoter"
```

Left column:

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FT   CDS            179. .1009
FT   /*tag=  c
FT   /product= MAGE-1
FT   misc_feature   1010. .1084
FT   /*tag=  d
FT   /note= "Flanking sequence"
PN   WO9416716-A.
PD   04-AUG-1994.
PF   21-JAN-1994; U00888.
PR   21-JAN-1993; US-007115.
PR   19-JAN-1994; US-184009.
PA   (VIRO-) VIROGENETICS CORP.
PI   Cox WI, Paoletti E, Tartaglia J;
DR   WPI; 94-263767/32.
PT   Attenuated recombinant virus used for cancer therapy - comprises
PT   DNA encoding cytokine and/or tumour associated antigen
PS   Example 16; Fig 20; 232pp; English.
CC   The sequences given in Q67865-66 represent expression cassettes
CC   containing the vaccinia H6 promoter and the human MAGE-1 gene which
CC   encodes human melanoma-associated antigen MZ2-E, in vCP235 and pMAW037,
CC   respectively. These sequences were used in the construction of NYVAC-
CC   and ALVAC-based recombinant viruses containing the MAGE-1 gene. MAGE-1
CC   is expressed in primary melanoma tumour cells, melanoma-derived cell
CC   lines and certain tumours of non-melanoma origins but not in normal
CC   cells except in testis. A first PCR fragment containing the last 18 bp
CC   and the initial 24 nucleotides of the MAGE-1 gene was generated and
CC   ligated to a second PCR fragment amplified from plasmid pTZ18RMAGE1
CC   which contains the initial 546 bp of the MAGE-1 coding sequence. The
CC   terminal sequence of MAGE-1 was amplified and a fusion product was
CC   generated containing the H6 promoter and the full length MAGE-1 sequence.
CC   This construct may be introduced in to the poxvirus derived plasmids,
CC   ALVAC and NYVAC. The resulting viruses may be used in a composition for
CC   inducing an antigenic or immunological response, ie. for immunisation
CC   against pathogens.
SQ   Sequence 1084 BP;    266 A;    256 C;    280 G;    282 T;

Query Match            94.0%;  Score 781; DB 1; Length 1084;
Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
Matches  781; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db    229 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCTCC 288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3931 GGCCCAACAAGAGGCCCTGGCCTGGTGTGTGCAGGCTGCCACCTCCTCCTCTCC 3990

Db    289 TCTGGTCCTGGCACCCTGGAGGAGGTGCCCACTGCTGGTCAACAGATCCTCCCCAGAG 348
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3991 TCTGGTCCTGGCACCCTGGAGGAGGTGCCCACTGCTGGTCAACAGATCCTCCCCAGAG 4050

Db    349 TCCTCAGGGAGGCCCTCGCCTTCCCACTACCATCAACTTCACTGCGAGAGGCAACCCAG 408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4051 TCCTCAGGGAGGCCCTCGCCTTCCCACTACCATCAACTTCACTGCGAGAGGCAACCCAG 4110

Db    409 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 468
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4111 TGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTT 4170

Db    469 GTTCCGAGCAGTAATCACTAAGAAGTGGCCAGTTGGTTGGTTTTCTGCTCCTCAAATA 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4171 GTTCCGAGCAGTAATCACTAAGAAGTGGCCAGTTGGTTGGTTTTCTGCTCCTCAAATA 4230

Db    529 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4231 TCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290

Db    589 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGATCTTCGGCAAAGCCTCTGAGATCTTCGGCAT 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4291 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGATCTTCGGCAAAGCCTCTGAGATCTTCGGCAT 4350

Db    649 TGACGTGAAGGAAGCAGACAGACCCCACCCGGCCACTCCTATGTCCTTGTCACCTGCTAGGTCT 708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4351 TGACGTGAAGGAAGCAGACAGACCCCACCCGGCCACTCCTATGTCCTTGTCACCTGCTAGGTCT 4410

Db    709 CTCCTATGATGGCCGCTGCTGGTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 768
```

Right column:

```
Qy   4411 CTCCTATGATGGCCGCTGCTGGTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 TGTCCTGGTCATGATTGCAATGGGCCATGTCGCTGGCCATGTCCTGAGGAGGAAATCTGGGAGGA 828
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4471 TGTCCTGGTCATGATTGCAATGGGCCATGTCGCTGGCCATGTCCTGAGGAGGAAATCTGGGAGGA 4530
          
Db    829 GCTGAGTGTGATGGAGTGTATGATGGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 888
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4531 GCTGAGTGTGATGGAGTGTATGATGGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590

Db    889 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCCAGGTGCCGGACAGT 948
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCCAGGTGCCGGACAGT 4650

Db    949 GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 1008
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4651 GATCCCGCACGCTATGAGTTCCTGTGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710

Db   1009 A 1009
          |
Qy   4711 A 4711


RESULT  10
ID   Q67865 standard; DNA; 1094 BP.
AC   Q67865;
DT   22-MAR-1995  (first entry)
DE   H6/MAGE-1 expression cassette from vCP235.
KW   Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW   human; MAGE-1; melanoma-associated antigen; MZ2-E; testis; pTZ18RMAGE1;
KW   primary melanoma tumour cell; melanoma-derived cell line; tumour;
KW   poxvirus; antigenic response; immunological response; pathogen; ss.
OS   Synthetic.
FH   Key            Location/Qualifiers
FT   promoter       74. .200
FT   /*tag=  a
FT   /note= "Vaccinia H6 promoter"
FT   CDS            201. .1031
FT   /*tag=  b
FT   /product= MAGE-1
FT   misc_feature   1032. .1094
FT   /*tag=  c
FT   /note= "Flanking sequence"
PN   WO9416716-A.
PD   04-AUG-1994.
PF   21-JAN-1994; U00888.
PR   21-JAN-1993; US-007115.
PR   19-JAN-1994; US-184009.
PA   (VIRO-) VIROGENETICS CORP.
PI   Cox WI, Paoletti E, Tartaglia J;
DR   WPI; 94-263767/32.
PT   Attenuated recombinant virus used for cancer therapy - comprises
PT   DNA encoding cytokine and/or tumour associated antigen
PS   Example 16; Fig 19; 232pp; English.
CC   The sequences given in Q67865-66 represent expression cassettes
CC   containing the vaccinia H6 promoter and the human MAGE-1 gene which
CC   encodes human melanoma-associated antigen MZ2-E, in vCP235 and pMAW037,
CC   respectively. These sequences were used in the construction of NYVAC-
CC   and ALVAC-based recombinant viruses containing the MAGE-1 gene. MAGE-1
CC   is expressed in primary melanoma tumour cells, melanoma-derived cell
CC   lines and certian tumours of non-melanoma origins but not in normal
CC   cells except in testis. A first PCR fragment containing the last 18 bp
CC   and the initial 24 nucleotides of the MAGE-1 gene was generated and
CC   ligated to a second PCR fragment amplified from plasmid pTZ18RMAGE1
CC   which contains the initial 546 bp of the MAGE-1 coding sequence. The
CC   terminal sequence of MAGE-1 was amplified and a fusion product was
CC   generated containing the H6 promoter and the full length MAGE-1 sequence.
CC   This construct may be introduced in to the poxvirus derived plasmids,
CC   ALVAC and NYVAC. The resulting viruses may be used in a composition for
CC   inducing an antigenic or immunological response, ie. for immunisation
CC   against pathogens.
SQ   Sequence 1094 BP;    269 A;    259 C;    293 G;    273 T;
```

```
Query Match          94.0%;    Score 781;   DB 1;    Length 1094;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;   Indels   0;    Gaps   0;
Matches   781;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   251 GGCCCAACAAGAGGCCCTGGGCCTGGTGTGCAGGCTGCCACCTCCTCCTCCTCC 310
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3931 GGCCCAACAAGAGAGGGCCCTGGGCGTGTGCAGGCTGCCACCTCCTCCTCCTCC 3990

Db   311 TCTGGTCCTGGGCCACCTGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 370
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3991 TCTGGTCCTGGGCCACCTGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAG 4050

Db   371 TCCTCAGGGAGGCCCTCCGCCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 430
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4051 TCCTCAGGGAGGCCCTCCGCCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAG 4110

Db   431 TGAGGGTTCCAGCAGCCGGTGAAGAGGGCCAAGCACCTTCGTATCCTGGAGTCCTT 490
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4111 TGAGGGTTCCAGCAGCCGTGAAGAGGGCCAAGCACCTTCGTATCCTGGAGTCCTT 4170

Db   491 GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATA 550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4171 GTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATA 4230

Db   551 TCGAGCCAGGGAGGCAGTCACAAAGTGCTGGAGAGTGTCATCAAAAATTACAA 610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4231 TCGAGCCAGGGAGGCCAGTGCAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAA 4290

Db   611 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4291 GCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCAT 4350

Db   671 TGACCTGAAGGAAGCAGAGCCCACCACCGGCACTTCCTATGTCCTTGTCACCTGCCTAGGTCT 730
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4351 TGACCTGAAGGAAGCAGAGCCCACCACCGGCACTTCCTATGTCCTTGTCACCTGCCTAGGTCT 4410

Db   731 CTCCTATGATGGCCTGCTCGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 790
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4411 CTCCTATGATGGCCTGCTCGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470

Db   791 TGTCCTGGTCATGATGGAGGGCGGCCATGCTCCTGAGGAGAATCTGGGAGGA 850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4471 TGTCCTGGTCATGATGGAGGGCGGCCATGCTCCTGAGGAGAATCTGGGAGGA 4530

Db   851 GCTGAGTGTGTGATGGAGGTGTATGATGGGGAGGCACAGTGCCTATGGGGAGGCCCAGGAA 910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4531 GCTGAGTGTGTGATGGAGGTGTATGATGGGGAGGCACAGTGCCTATGGGGAGCCCCAGGAA 4590

Db   911 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGTGCCGGACAGT 970
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGTGCCGGACAGT 4650

Db   971 GATCCCGCAGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 1030
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4651 GATCCCGCAGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTG 4710

Db  1031 A 1031
           |
Qy  4711 A 4711
```

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FT   /*tag=   a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02483.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI: 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Disclosure; Page 68; 105pp; English.
CC   Q72483 is the gene which contains the coding sequence for melanoma
CC   antigen-41 (MAGE-41). Another melanoma antigen MAGE-3 is encoded by
CC   Q72470, this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-Al).
SQ   Sequence  2531 BP;    607 A;    593 C;    701 G;    630 T;
```

```
Query Match           70.3%;     Score 584;    DB 1;    Length 2531;
Best Local Similarity 87.2%;     Pred. No. 0.00e+00;
Matches   690;    Conservative   0;    Mismatches 100;    Indels   1;    Gaps   1;

Db   734 AGGCTGCTGCTCTCCTCCTCCTCGGTCCCTGCCACCCTGGAGGAGTGCCTGCTG 793
             ||||||||||||||||||||||| |||||| ||||||||||||||||||||||||
Qy  3966 AGGCTGCCACCTCCTCCTCCTCCTCTGGTCCTGGGCCACCCTGGAGGAGTGCCCACTG 4025

Db   794 CTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCCTTGCCTTACCCACTACCATCA 853
             ||| ||| |||   ||||||||||||| |||||||||||| || |||||||||||||||
Qy  4026 CTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCCTTCCCACTACCATCA 4085

Db   854 GCTTCACTTGCTGAGGCAACCCAATGAGGGTTCAGCAGCCAAGAAGAGAGGGGCCAA 913
             ||||||| | |||||||||||||| |||||| |||||||| || ||||||||||||
Qy  4086 ACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGGGCCAA 4145

Db   914 GCACCTCGCCTGACCGACCAGAGTCCTTGTTCCCGAGAAGCACTCAGTAACAAGGTGGATGAGT 973
             ||||||||  | |  ||||| |||||| ||| ||| || | || | ||||||||| || |||
Qy  4146 GCACCTTCGTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATT 4205

Db   974 TGGCTCATTTTCTGCTCCGCAAGTATCCAGAGTCGTCACAAAGGCCAGAAATGC 1033
             ||| ||  ||| |||| ||  | || ||| ||| | ||| |||||||| ||||||
Qy  4206 TGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGTGCAGGCCAGAAATGC 4265

Db  1034 TGGAGAGAGTCATCAAAAATTACAAGCACGGCTGCTTCCTGTGATCTTCGGCAAAGCCTCCG 1093
             ||||||||||||||||||||||| |||| | |||| |||| |||| | ||||||| ||| |
Qy  4266 TGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTG 4325

Db  1094 AGTCCTTGCAGATGATCTTTGGCATTGACGTGAAGGAAGTGGAACCCCACCAGCAACACCT 1153
             |||||||||||| || || |||||||||| |||||||| || ||||  |||||||| |||
Qy  4326 AGTCCTTGCAGCTGGTCTTTGGCATTGACCTGAAGGAAGCAGAGCCCACCACCGGCACTCCT 4385

Db  1154 ACACCCTTGCTACCTGGCCTGGCCCTTCCTATGATGGCCTGGGTAATAATCAGATCT 1213
             |||||||||| ||| |  ||||| ||||| ||||||||| || |||| ||||||||
Qy  4386 ATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTCGGGTGATAATCAGATCA 4445

Db  1214 TTCCCAAGACAGGCCTTCTGATAATCGTCTCGGGCACAATTGCAATGGAGGGCGACACGCG 1273
             | |||||||||||| ||||||||||| | ||||  || ||| ||||  ||||||| |||
Qy  4446 TGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATGGAGGGCGGCCATG 4505

Db  1274 CCTCTGAGGAGAATCTGGGAGGAGCTGGGTGTATGATGGGGTGTATGATGGGGAGGAGC 1333
             | |||||||||||||||||||||||||||| ||||| |||||  |||||||||||||||
Qy  4506 CTCCTGAGGAGAATCTGGGAGGAGCTGAGTGTGTGATGGAGGTGTATGATGGGGAGGAGC 4565

Db  1334 ACACTGTCATGGGAGGCCCAGGAAGCCCCAGGAAAACTGCTCACCCAAGAAAAACTACC 1393
             ||||| |||| |||||| || || ||| |||||| ||| ||||||||| ||||||||||
Qy  4566 ACAGTGCCTATGGGGAGCCCCAGGAGCCCCAGGAAGCCCCAGGAAAAGTACC 4625

Db  1394 TGGAGTACCGGCAGTGACCGGTACCCGCAGTAATCCTCGCGCCTATGAGTTCCTGTGGGGTCCAA 1453
             ||||||||| |||  |    || ||| || | |||  | ||| |||||||||||||||||||||
Qy  4626 TGGAGTAC-GGCAGTGCCGGACAGTGATCCCGCAGCTATGAGTTCCTGTGGGGTCCAA 4684
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Db  1454 GGGCCTCGCTGAAACCAGCTATGTGGTCAGGTCAATGCAA 1513
         ||||| || |||||||||||||||| |||||| ||| |||||
Qy  4685 GGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGTGTCAGTGCAA 4744

Db  1514 GAGTTCGCATT 1524
         |||||||| ||
Qy  4745 GAGTTCGCTTT 4755
```

RESULT 12
ID   Q72482 standard: DNA; 2531 BP.
AC   Q72482;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-4 gene.
KW   Tumour rejection antigen; melanoma antigen-4; MAGE-4; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   625. .1578
FT   /*tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-failleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI: 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
CC   Example 30: Page 66; 105pp; English.
CC   Q72482 is the gene which contains the coding sequence for melanoma
CC   antigen-4 (MAGE-4). Another melanoma antigen MAGE-3 is encoded by
CC   Q72470, this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-Al).
SQ   Sequence 2531 BP;   608 A;   593 C;   700 G;   630 T;

Query Match   70.0%; Score 582; DB 1; Length 2531;
Best Local Similarity 87.1%; Pred. No. 0.00e+00;
Matches 689; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

```
Db   734 AGGCTGCGTGTCTCCTCCTCCTCCTCCTCCTGGTCCCTGGCACCCTGGAGGAAGTGCCTGCTG 793
         |||||||   ||||||||||||||||||||| |||| |||||||||||||||||| |||| |||
Qy  3966 AGGCTGCCACCTCCTCCTCCTCCTCCTCGTCCTGTCCTCTGGCACCCTGGAGGAGTGCCCACTG 4025

Db   794 CTGAGTCAGGTGCCTCCCCCAGAGTCCTCCAGAGGCCTCTGCGTTACCCACTACCATCA 853
         ||| |||||   ||||||||||||||||| ||  ||||||| ||| ||||||||||||||
Qy  4026 CTGGGTCAACAGATCCTCCCCCAGAGTCCTCAGGGAGTCCTCCAGGGAGCCTTCGCGTTTCCCACTACCATCA 4085

Db   854 GCTTCACTTGCTGGAGGCAACCCATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAA 913
         ||||||||  | |||||||||||| | |||||||||||||||  |||||||||||||||
Qy  4086 ACTTCACTCGACGAGGCAACCCAGGAGGGTTCCAGCAGCCCGTGAAGAGGAGGAGGGGCCAA 4145

Db   914 GCACCTCGCCTGACGCAGATCCTTGTTCCGAGAAGCACTCAGTAGCAACAAGGTGATGAGT 973
         ||||||||  ||  | ||| ||| |||||| | ||||||| |||| |||| |||||| |||
Qy  4146 GCACCTCGTTGTATCCTGGATCCTGTTCCGGAGTCCGGAGCAGTAATCACTAAGAAGGTGGCTGATT 4205

Db   974 TGGCTCATTTCTGTTCTGCTCCGGAAGATGCAGGATCGGAGCAGGAGGCGATCAGGAGGCAGAAATGC 1033
         ||| | |||| |||||| ||||| ||| |||||| |||||||||||||||| |||||||||||
Qy  4206 TGGTTGGTTTTCTGCTCCTCAAATATCAGAGCAGGATCGGAGCAGGAGGCAGAAATGC 4265

Db  1034 TGGAGAGTCATCAAAAATTACAAGGCGCTGCTTTCCTGTGATCTTCGGCAAAGGCTCCG 1093
         ||||||||||||||||||||||||||| ||| |||||| |||||||||||||||||| |
Qy  4266 TGGAGAGTCATCAAAAATTACAAGGCACTGTTTTCCTGAGATCTTCGGCAAAGGCTCTG 4325

Db  1094 AGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCAACACCT 1153
         ||||| ||| || || |||||||||| ||||||||||||  |  || |||||| |||| ||
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Qy  4326 AGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGAGCCCACCGGCCACTCCT 4385

Db  1154 ACACCCTGTCACCTGCCTGGGCCTTCCTATGATGGCCGTGGTAATAATCAGATCT 1213
Qy  4386 ATGTCCTTGTCACCTGCCTAGGTCTCTCTATGATGGCCTGGGTGATAATCAGATCA 4445

Db  1214 TTCCCAAGACAGGCCTTCTGATAATCGTCCTGGGCACAATTGCAATGAGGGGCGACAGCG 1273
Qy  4446 TGCCCAAGACAGGCCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGGCGGCCATG 4505

Db  1274 CCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGTGTATGATGGGGGAGC 1333
Qy  4506 CTCCTGAGGAGGAAATCTGGGAGGAGCTGGGAGTGTGATGGGTGTATGATGGGGGAGC 4565

Db  1334 ACACTGCTATGGGAGCCCAGGAAAACTGCTCACCCAGAGATTGGGTGCAGGAAAACTACC 1393
Qy  4566 ACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGAGTTGCAGGAAAAGTACC 4625

Db  1394 TGGAGTACCGGCAGCAGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGTCCAA 1453
Qy  4626 TGGAGTAC-GGCAGGTGCCGGACAGTGATCCCCGCACCTATGAGTTCCTGTGGGTCCAA 4684

Db  1454 GGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGCAGGGTCAATGCAA 1513
Qy  4685 GGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTGAAAGTCCTGAGTATGTGATCAAGTGTCAGTGCAA 4744

Db  1514 GAGTTCGCATT 1524
Qy  4745 GAGTTCGCTTT 4755
```

RESULT 13
ID   Q33258 standard: cDNA; 2531 BP.
AC   Q33258;
DT   22-APR-1993 (first entry)
DE   MAGE-41 gene.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   625. .1578
FT   /*tag= a
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992; U04354.
PR   23-MAY-1991; US-705702.
PR   09-JUL-1991; US-728838.
PR   23-SEP-1991; US-764364.
PR   12-DEC-1991; US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure: Page 81-82; 142pp; English.
CC   The sequences given in Q33352-59 represent a new family of genes
CC   refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence. The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors. MAGE expression is not
CC   restricted to melanomas. MAGE refers to a family of tumor rejection
CC   antigen precursors. The antigens resulting from these genes are
CC   referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence 2531 BP;   607 A;   593 C;   701 G;   630 T;

Query Match   69.8%; Score 580; DB 1; Length 2531;
Best Local Similarity 87.0%; Pred. No. 0.00e+00;

PR   23-MAY-1991; US-705702.
PR   09-JUL-1991; US-728838.
PR   23-SEP-1991; US-764364.
PA   12-DEC-1991; US-807043.
PI   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
DR   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
PT   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PS   precursor - useful as an immunostimulant in a vaccine for
CC   treating and preventing cancers, also useful in diagnosis
CC   Disclosure; Page 79-80; 142pp; English.
CC   The sequences given in Q32352-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence. The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors. MAGE expression is not
CC   restricted to melanomas. MAGE refers to a family of tumor rejection
CC   antigen precursors. The antigens resulting from these genes are
CC   referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence 2531 BP;   608 A;   592 C;   701 G;   630 T;

Query Match   69.8%; Score 580; DB 1; Length 2531;
Best Local Similarity   87.0%; Pred. No. 0.00e+00;
Matches 688; Conservative   0; Mismatches 102; Indels   1; Gaps   1;

Db   734 AGGCTGCTGTCTCCTCCTCCTCCTCCTGGTCCTCCTGGCACCCTGGGAAGTGCCTGCTG 793
            |||||| |||||||||||||||||||||||||| ||||||||| |||||| |||
Qy   3966 AGGCTGCCACCTCCTCCTCCTCCTCCTCCTGGTCCTGGCACCCTGGGAGGAGTGCCCACTG 4025

Db   794 CTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGTCCTCAGGGAGCCTCGGCCTTTCCCACTACCATCA 853
            || |||| ||| ||||||||||||||||||||||| |||| ||||||||||||| |||||||||||||||
Qy   4026 CTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGTCCTCAGGGAGCCTTTCCCACTACCATCA 4085

Db   854 GCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGGCCAA 913
            ||||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||
Qy   4086 ACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGGCCAA 4145

Db   914 GCACCCTCGCCGCCAGAGTCCTTGTCCGAGAAGCACTCAGTAACAAGGTGGATGAGT 973
            ||||||| | | |||||||||||||||||||| ||||||||| ||||||| |||
Qy   4146 GCACCCTCGTATCCTGAGTCCTTGTCCGAGCAGTAATACTAAGGAAGGTGGCTGATT 4205

Db   974 TGGGTCATTTTCTGCTCCGCAAGATATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGC 1033
            ||| ||||||| ||||| ||||| |||||||||||||||||||| ||||||||||||||
Qy   4206 TGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGCCAGCAGCCAGTCACAAAGGCAGAAATGC 4265

Db   1034 TGGAGAGTCATCAAAAATTACAAGCCGCTGCTTTCCTGTGATCTTCCGGCAAAGCCTCCG 1093
            ||||||||||||||||||||||||||||||||| | | |||| ||||||||||||||||
Qy   4266 TGGAGAGTGTCATCAAAAATTACAAGCCACTGTTTTCCTGAGATCTTCCGGCAAAGCCTCTG 4325

Db   1094 AGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGACCCCGCCAGCAACACCT 1153
            || ||||| |||||||| || ||| || ||||||||||| | |||||||||||||
Qy   4326 AGTCCTTGCAGCTGGTCTTTGGCATTGACGTGACGTGAAGGAAGCAGACCCGCCACTCCT 4385

Db   1154 ACACCCTTGTCACCTGGCCTTCTCCTATGATGGCCTGCTGGGTAATAATCAGATCT 1213
            | ||||||||||||| | ||||| || |||||||||||||||||||||||||||||
Qy   4386 ATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGGGTGATAATCAGATCA 4445

Db   1214 TTCCCAAGACAGGCCTTCTCGATAATCGTCTGCGCCACAATTGCAATGGAGGGCGACAGCG 1273
            | |||||||||||||||||||||||||||||| |||||| |||||||||||||||||
Qy   4446 TGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTGATAATTGCAATGGAGGGCGGCCATG 4505

Db   1274 CCTCTGAGGAGGAAATCTCGGGAGGAGCTCGGGTGTGTGATGGGAGGAGC 1333
            ||||||||||||||||||||||||||||||| |||||||||||||||||||
Qy   4506 CCTCTGAGGAGGAAATCTCGGGAGGAGCTCGAGTGTGTGATGGGAGGAGC 4565

Db   1334 ACACTGTCTATGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAACTACC 1393
            ||| ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Qy   4566 ACAGTGCCTATGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACC 4625

Db   1394 TGGAGTACCGGCCAGGTACCCGGCAGTAATCCTGCGCCGCCAGTAGTTCCTGTGGGGTCCAA 1453
            ||| |||||||||| | | | |||||||| | | ||| |||||||| |||| |||||||
Qy   4626 TGGAGTAC-GGCCAGGTGCCGGACAGTGATCCCGGACCACCCGTAGTTCCTGTGGGGTCCAA 4684

Db   1454 GGGCCCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGAAGGTTCAATGCAA 1513
            ||| ||||||| ||||| ||||||||| |||||| |||||||| |||| || |||||||
Qy   4685 GGGCCCTGGCTGAAACCAGCTATGTGAAAGTCCTGAGTTCGGTTATGTGCAGTGCAA 4744

Db   1514 GAGTTCGCCATT 1524
            |||||||||||
Qy   4745 GAGTTCGCTTT 4755

RESULT 14
ID   Q32357 standard; cDNA; 2531 BP.
AC   Q32357;
DT   22-APR-1993 (first entry)
DE   MAGE-4 gene.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   625..1578
FT   /*tag=   a
PN.,   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992; U04354.

```
Db   988 CTTGAGTTCATTTCTGCTCCTCAGTATTAAGTCAAGGAGCCGGTCACAAAGGCAGAAAT 1047
          ||| ||  ||||||||||||||| |||  |||||| |||||||||||||||||||||||
Qy  4204 TTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGAAAT 4263

Db  1048 GCTGGAGAGCGTCATCAAAT ... 1107
          |||||||||| |||||||||
Qy  4264 GCTGGAGAGTGTCATCAACACTGTTTCCTGAGATCTTCGGCAAAGCCTC 4323

Db  1108 CGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCACCAGCAACAC 1167
          ||||||||||||||||||||||||||||||||||||||| || |  ||
Qy  4324 TGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCCGGCCACTC 4383

Db  1168 CTACACCCTTGTCACCTGCCTGGGACTC--CTATGATGGCCTGGTGGTT--TAATCAGAT 1223
          |||  ||||||||||||||||  |  |    |||||||||||||  |   ||||||||||
Qy  4384 CTATGTCCTTGTCACCTGCCTGCTAGGTCTCTCCTATGATGGCCTGCCTGCGGGTGATAATCAGAT 4443

Db  1224 CATGCCCAAGACGGGCCTTCCTGATAATCGTCTTGGCAATGATTGCAATGG ... 1283
          ||||||||||||||| ||||||||||| ||| ||| ||||||||||||||
Qy  4444 CATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGCGGCGGCCA 4503

Db  1284 CGTCCCTGAGGAGAAAATCTGGGAGGAGCTGGGTGTGATGAAGGTGTATGTGGGAGGGA 1343
          | ||||||||||||| ||||||||||||||| |||||||  |||||||||  ||||||
Qy  4504 TGCTCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGA 4563

Db  1344 GCACAGTGTCTGTGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTCGCAGGAAAACTA 1403
          |||||||| |||||| ||||| ||||||||||||||||||||||||| ||||||||| ||
Qy  4564 GCACAGTGCCTATGGGAGCCCCAGGAAGCTGCTCACCCAAGATTTGGTGCGCAGGAAAGTA 4623

Db  1404 CCTGGAGTACCGGCCAGGTGCGCCCAGGTGTCGATCCCATATGCTATGAGTTACTGTGGGTCCA 1463
          ||||||||| |||| ||||||  ||||||||  ||||| || ||||||||||| |||||||||||
Qy  4624 CCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGACAGTGATGAGTTCCTGTGGGTCCA 4683

Db  1464 AGGGCACTCGCTG 1476
          ||||| |||||||
Qy  4684 AGGGCCCCGCTG 4696
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Search completed: Tue Apr 7 22:19:33 1998
Job time : 79 secs.

```
RESULT  15
ID   Q32361 standard; DNA; 2305 BP.
AC   Q32361;
DT   22-APR-1993 (first entry)
DE   MAGE-51 genomic DNA.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key              Location/Qualifiers
FT   CDS              645..992
FT   /*tag=           a
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992; U04354.
PR   22-MAY-1991; US-705702.
PR   23-MAY-1991; US-728838.
PR   09-JUL-1991; US-764364.
PR   23-SEP-1991; US-764364.
PR   12-DEC-1991; US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure: Page 86-87; 142pp; English.
CC   The sequences given in Q32352-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE). The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence. The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors.  MAGE expression is not
CC   restricted to melanomas.  MAGE refers to a family of tumor rejection
CC   antigen precursors.  The antigens resulting from these genes are
CC   referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence 2305 BP;   549 A;   568 C;   611 G;   577 T;
```

Query Match   61.7%; Score 513; DB 1; Length 2305;
Best Local Similarity   86.4%;
Matches 633; Conservative   0; Mismatches 96; Indels   4; Gaps   2;
                        Pred. No. 0.00e+00;

```
Db   748 GCAGGAGGCTGTGTCCTCCTCCTCCTCCTCGTCCCAGGCACCCTGGGGAGGTGCCTGC 807
          |||||  ||||  |||||||||||||||||||||||  |||||| ||||| ||||||
Qy  3964 GCAGGCTGCCACCTCCTCCTCCTCCTCCTCGTCCTGGTCCTGGGCACCCTGGGAGGTGCCCAC 4023

Db   808 TGCTGGGTCACCAGGTCCTCTCAGAGTCCTCAGGGAGCCTCATCCCCACTGCCAT 867
          ||||||||||| ||| ||||| |||||||||||||||||||        ||| ||
Qy  4024 TGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCAGGGAGCCTTTCCCACTACCAT 4083

Db   868 CGATTTCACTCATGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGAGGGCC 927
          | |||||||||  |||||||  ||| | |||||  ||||| || ||||||||||| ||
Qy  4084 CAACTTCACTCGACAGAGGCAACCACCCAGTGAGGGTTCCAGCAGCAGCCGTGAAGAGAGGGGCC 4143

Db   928 AAGCACCTCCCTGACCCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGGTGGCTGA 987
          |||||||||  |  |||||||||  |||  |||||||||||  ||||||||||||||||
Qy  4144 AAGCACCTCTTGTATCCGGAGTCCTTGGTCCCGACAGTAATCACTCAAGAAGGTGGCTGA 4203

Db  1394 TGGAGTACCGGCAGGCAGTAATCCTGGCGCGCAGTAATCCTGGCGCTATGAGTTCCTGTGGGTCCAA 1453
          |||||||| |||||| || ||  | |   |  ||| |  |   |  |||||||||||||||||||||
Qy  4626 TGGAGTAC-GGCAGGTGCCGGACGACGTGCCGGACGTCCTGTGGGTCCAA 4684

Db  1454 GGGCTCCTGCTGAAACCACCAGCTATGTGAAAGTCCTGAGACATGTGGTCAGGGTCAATGCAA 1513
          ||||  ||||| | ||||||||||||||||||||||| || ||||||| | |||||| ||||
Qy  4685 GGGCCCTGCTTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAA 4744

Db  1514 GAGTTGGCATT 1524
          ||||| || ||
Qy  4745 GAGTTCGCTTT 4755
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M P S R C H (TM)
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          Distribution rights by IntelliGenetics, Inc.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 7 22:00:50 1998; MasPar time 18.26 Seconds
                 1024.763 Million cell updates/sec

Tabular output not generated.

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Title:          >US-08-190-411A-1
Description:    (57-219) from 5541104.seq
Perfect Score:  163
N.A. Sequence:  57 ACCATCCAAACATCTTCAC..........TCGGTCTGAGGGGCGGCTTG 219
      Comp:        TGGGTAGGTTTGTAGAAGTG..........AGCCAGACTCCCGCCGAAC
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Scoring table: TABLE default
                Gap 6

Nmatch   STD : Dbase 0: Query 0

Searched: 159649 seqs, 57412152 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-geneseq30
                1:n-geneseq1

Statistics: Mean 7.397; Variance 4.240; scale 1.745

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description	Pred. No.
1		163	100.0	5674	1	Q32352	MAGE-1 nucleic acid.	4.43e-98
2		163	100.0	5674	1	Q72477	Tumour rejection antig	4.43e-98
3		163	100.0	5724	1	Q98902	Tumour rejection antig	4.43e-98
4		71	43.6	4157	1	Q72478	Tumour rejection antig	1.23e-32
5		71	43.6	4157	1	Q32353	MAGE-2 gene.	1.23e-32
6		70	42.9	662	1	Q32354	MAGE-21 gene.	5.95e-32
7		70	42.9	662	1	Q72479	Tumour rejection antig	5.95e-32
8		44	27.0	99	1	Q51746	Oligonucleotide probe	1.27e-14
9	c	36	22.1	99	1	Q51746	Oligonucleotide probe	1.40e-09
10	c	33	20.2	204	1	N81164	Base substituted E.col	9.49e-08
11	c	32	19.6	186	1	T76405	Human endothelin-1 ant	3.80e-07
12	c	31	19.0	122	1	Q70468	Generic DNA sequence t	1.50e-06
13	c	30	18.4	122	1	Q70467	Generic DNA sequence t	5.87e-06
14		30	18.4	204	1	N81164	Base substituted E.col	5.87e-06
15	c	30	18.4	1055	1	Q10572	Human Natriuretic Pept	5.87e-06
16		29	17.8	122	1	Q70467	Generic DNA sequence t	2.27e-05
17		29	17.8	122	1	Q70468	Generic DNA sequence t	2.27e-05
18	c	29	17.8	122	1	Q70465	Generic DNA sequence t	2.27e-05
19	c	28	17.2	122	1	Q70470	Generic DNA sequence t	8.63e-05
20	c	28	17.2	122	1	Q70469	Generic DNA sequence t	8.63e-05
21		28	17.2	1055	1	Q10572	Human Natriuretic Pept	8.63e-05
22		26	16.0	122	1	Q70465	Generic DNA sequence t	1.20e-03
23		26	16.0	122	1	Q70466	Generic DNA sequence t	1.20e-03
24	c	25	15.3	122	1	Q70472	Generic DNA sequence t	4.36e-03
25		25	15.3	198	1	T76452	Chymase antisense olig	4.36e-03
26	c	24	14.7	122	1	Q70469	Generic DNA sequence t	1.56e-02
27		24	14.7	122	1	Q70470	Generic DNA sequence t	1.56e-02
28	c	24	14.7	122	1	Q70473	Generic DNA sequence t	1.56e-02
29		23	14.1	122	1	Q70471	Generic DNA sequence t	5.45e-02
30		23	14.1	122	1	Q70473	Generic DNA sequence t	5.45e-02
31	c	23	14.1	136	1	T76233	Human IL6 antisense ol	5.45e-02
32	c	23	14.1	180	1	T76363	Human interleukin 8 an	5.45e-02
33	c	22	13.5	83	1	T13612	DC43 TSAR library gene	1.87e-01
34	c	22	13.5	90	1	T13610	DC43 TSAR library gene	1.87e-01
35	c	22	13.5	258	1	T76438	Substance P antisense	1.87e-01
36		22	13.5	456	1	T84598	CC288_9 cDNA clone.	1.87e-01
37		22	13.5	573	1	Q35072	HCV envelope region nu	1.87e-01
38	c	21	12.9	64	1	T13598	R26 library generating	6.28e-01
39		21	12.9	74	1	T13585	TSAR-9 library generat	6.28e-01
40		21	12.9	82	1	T13613	DC43 TSAR library gene	6.28e-01
41		21	12.9	154	1	T13624	ME#2b library generati	6.28e-01
42	c	21	12.9	155	1	T76294	Human defensin 1 antis	6.28e-01
43	c	21	12.9	573	1	Q35072	HCV envelope region nu	6.28e-01
44		21	12.9	1442	1	N70696	Sequence encoding a ca	6.28e-01
45		21	12.9	3879	1	N71302	HSV-1 gB and surroundi	6.28e-01

ALIGNMENTS

```
RESULT  1
ID   Q32352 standard; DNA; 5674 BP.
AC   Q32352;
DT   22-APR-1993 (first entry)
DE   MAGE-1 nucleic acid.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             3881..4711
FT   /*tag=  a
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992; U04354.
PR   23-MAY-1991; US-705702.
PR   09-JUL-1991; US-728838.
PR   23-SEP-1991; US-764364.
PR   12-DEC-1991; US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure; Page 71-73; 142pp; English.
CC   The sequences given in Q32352-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE).  The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence.  The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors.  MAGE expression is not
CC   restricted to melanomas.  MAGE refers to a family of tumor rejection
CC   antigen precursors.  The antigens resulting from these genes are
CC   referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence 5674 BP;     1277 A;     1644 C;     1568 G;     1185 T;

Query Match             100.0%;    Score 163;   DB 1;   Length 5674;
Best Local Similarity 100.0%;                   Pred. No. 4.43e-98;
Matches  163;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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FT   /*tag= a
FT   /product= Tumour rejection antigen MAGE-1.
FT   /note= "The CDS is not indicated in the text of the
FT   specification but is suggested in the layout
FT   of the sequence."
PN   WO9520974-A1
PD   10-AUG-1995.
PF   05-JAN-1995; U00095.
PR   01-FEB-1994; US-190411.
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK) SLOAN KETTERING INST CANCER RES.
PA   (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.
PI   Boon-falleur T, Chen Y, Garin-chesa P, Old LJ, Rettig WJ;
PI   Stockert E, Van der bruggen P;
DR   WPI; 95-283606/37.
PT   New monoclonal antibody binding specifically to MAGE-1 - useful for
PT   diagnosis and monitoring of cancer, also new hybridomas, recombinant
PT   MAGE-1 and immunogenic peptide(s)
PS   Disclosure; Page 16-19; 33pp; English.
CC   A monoclonal antibody directed against the tumour rejection antigen
CC   (MAGE-1) can be used to detect MAGE-1 in samples by standard
CC   immunoassay methods for diagnosis and monitoring of cancer etc. The
CC   monoclonal antibody is designated MA454 and is produced by the
CC   hybridoma deposited as ATCC HB11540. The monoclonal antibody is
CC   specific for MAGE-1, having no reactivity for MAGE-2 or MAGE-3.
CC   Peptide fragments of MAGE-1 (See R80618-20) may be useful as
CC   immunogens for production of the monoclonal antibody and antisera.
SQ   Sequence 5724 BP; 1282 A; 1653 C; 1589 G; 1200 T;

Query Match   100.0%; Score 163; DB 1; Length 5724;
Best Local Similarity   100.0%; Pred. No. 4.43e-98;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   57 ACCATCCAAACATCTTCACGCTCACCCCCAGCCCAGCCAGAATCCGGTTCCACC 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   57 ACCATCCAAACATCTTCACGCTCACCCCCAGCCCAGCCAGAATCCGGTTCCACC 116

Db   117 CCTGCTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGGCCCACTGACTTGAGCATTA 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   117 CCTGCTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGGCCCACTGACTTGAGCATTA 176

Db   177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219
              ||||||||||||||||||||||||||||||||||||||||||
Qy   177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219

RESULT 4
ID   Q72478 standard; DNA; 4157 BP.
AC   Q72478;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-2 gene.
KW   Tumour rejection antigen; melanoma antigen-2; MAGE-2; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   2598..3542
FT   /*tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Example 32; Page 61; 105pp; English.
CC   Q72478 is the gene which contains the coding sequence for melanoma
CC   antigen-2 (MAGE-2). Another melanoma antigen MAGE-3 is encoded by
CC   Q72470, this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can

Db   57 ACCATCCAAACATCTTCACGCTCACCCCCAGCCCAGCCAGAATCCGGTTCCACC 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   57 ACCATCCAAACATCTTCACGCTCACCCCCAGCCCAGCCAGAATCCGGTTCCACC 116

Db   117 CCTGCTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGGCCCACTGACTTGAGCATTA 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   117 CCTGCTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGGCCCACTGACTTGAGCATTA 176

Db   177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219
              ||||||||||||||||||||||||||||||||||||||||||
Qy   177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219

RESULT 2
ID   Q72477 standard; DNA; 5674 BP.
AC   Q72477;
DT   22-JUN-1995 (first entry)
DE   Tumour rejection antigen MAGE-1 encoding DNA.
KW   Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   3881..4711
FT   /*tag= a
PN   WO9423031-A.
PD   13-OCT-1994.
PF   17-MAR-1994; U02877.
PR   26-MAR-1993; US-037230.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR   WPI; 94-333192/41.
PT   New tumour rejection antigen precursor MAGE3 - useful in
PT   treatment and diagnosis of cancer
PS   Example 26; Page 59; 105pp; English.
CC   Q72477 is the DNA sequence which encodes melanoma antigen-1
CC   (MAGE-1). Another melanoma antigen MAGE-3 is encoded by Q72470,
CC   this is a tumour rejection antigen precursor. Melanomas
CC   characterised by the expression of MAGE-3 can be detected, or
CC   monitored, by contacting a test sample with an agent that can
CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T;

Query Match   100.0%; Score 163; DB 1; Length 5674;
Best Local Similarity   100.0%; Pred. No. 4.43e-98;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   57 ACCATCCAAACATCTTCACGCTCACCCCCAGCCCAGCCAGAATCCGGTTCCACC 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   57 ACCATCCAAACATCTTCACGCTCACCCCCAGCCCAGCCAGAATCCGGTTCCACC 116

Db   117 CCTGCTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGGCCCACTGACTTGAGCATTA 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   117 CCTGCTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGGCCCACTGACTTGAGCATTA 176

Db   177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219
              ||||||||||||||||||||||||||||||||||||||||||
Qy   177 GTGGTTAGAGAGAAGCGAGGTTTCGGTCTGAGGGGCGGCTTG 219

RESULT 3
ID   Q98902 standard; DNA; 5724 BP.
AC   Q98902;
DT   28-FEB-1996 (first entry)
DE   Tumour rejection antigen (MAGE-1) gene.
KW   Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb;
KW   diagnosis; immunoassay; cancer; ss.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   CDS   3881..4711

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CC   recognise MAGE-3. The melanoma can be treated by the administration
CC   of cytolytic T cells specific for the complex of antigen D (the
CC   mature rejection antigen derived from MAGE-3) and a human leucocyte
CC   antigen (esp. HLA-A1).
SQ   Sequence  4157 BP;  953 A;  1134 C;  1185 G;  885 T;

Query Match  43.6%;  Score 71;  DB 1;  Length 4157;
Best Local Similarity 77.1%;  Pred. No. 1.23e-32;
Matches  108;  Conservative  0;  Mismatches 31;  Indels 1;  Gaps  1;

Db     3 CATCCAGATCCCATCCGGGCAGAATCCGGTTCCACCCTTGCCGTGAACCCAGGGAAGTC  62
         |||-| |||| || |||||||||||||||||||||||| ||| | ||||||||||||||
Qy    80 CACCCCCAGCCCAAGCCAGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGCC  139

Db    63 ACGG-GCCCGGATGTGACGCCACTGACTTGCACATTGGAGGTCAGAGGACGAGGATTC  121
         || |||||||||||||||||||||||| |||| ||| |||||| ||||| |||||| ||
Qy   140 CAGGTGCCCAGATGTGACGCCCACTGACTTGAGCATTAGTTGGTTAGAGAAGCGAGGTTT  199

Db   122 TCGCCCTGAGCAACGGCCTG  141
         ||| ||||| ||
Qy   200 TCGGTCTGAGGGGCCGGCTTG  219


RESULT 5
ID   Q32353  standard; DNA; 4157 BP.
AC   Q32353;
DT   22-APR-1993  (first entry)
DE   MAGE-2 gene.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   CDS            2958..3542
FT   /*tag~  a
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992;  U04354.
PR   23-MAY-1991;  US-705702.
PR   09-JUL-1991;  US-728838.
PR   23-SEP-1991;  US-764364.
PR   12-DEC-1991;  US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure: Page 74-75; 142pp; English.
CC   The sequences given in Q32352-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE).  The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors.  MAGE expression is not
CC   restricted to melanomas.  MAGE refers to a family of tumor rejection
CC   antigen precursors.  The antigens resulting from these genes are
CC   referred to as MAGE TRAS or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence  4157 BP;  953 A;  1135 C;  1134 G;  885 T;

Query Match  43.6%;  Score 71;  DB 1;  Length 4157;
Best Local Similarity 77.1%;  Pred. No. 1.23e-32;
Matches  108;  Conservative  0;  Mismatches 31;  Indels 1;  Gaps  1;

Db     3 CATCCAGATCCCATCCGGGCAGAATCCGGTTCCACCCTTGCCGTGAACCCAGGGAAGTC  62
         |||-| |||| || |||||||||||||||||||||||| ||| | ||||||||||||||
Qy    80 CACCCCCAGCCCAAGCCAGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGCC  139

Db    63 ACGG-GCCCGGATGTGACGCCACTGACTTGCACATTGGAGGTCAGAGGACGAGGATTC  121
         || |||||||||||||||||||||||| |||| ||| |||||| ||||| |||||| ||
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Qy   140 CAGTGCCCAGATGTGACGCCCACTGACTTGAGCATTAGTTGGTTAGAGAGAGGCGAGGTT  199

Db   122 TCGCCCTGAGCAACGGCCTG  141
         || ||||| |||| ||
Qy   200 TCGGTCTGAGGGGCCGGCTTG  219


RESULT 6
ID   Q32354  standard; DNA; 662 BP.
AC   Q32354;
DT   22-APR-1993  (first entry)
DE   MAGE-21 gene.
KW   melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW   tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
OS   Homo sapiens.
PN   WO9220356-A.
PD   26-NOV-1992.
PF   22-MAY-1992;  U04354.
PR   23-MAY-1991;  US-705702.
PR   09-JUL-1991;  US-728838.
PR   23-SEP-1991;  US-764364.
PR   12-DEC-1991;  US-807043.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI   Van Den Eynde B, Van Der Bruggen P, Van Pel A;
DR   WPI; 92-415460/50.
PT   Nucleic acid mol. encoding a human tumour rejection antigen
PT   precursor - useful as an immunostimulant in a vaccine for
PT   treating and preventing cancers, also useful in diagnosis
PS   Disclosure: Page 76; 142pp; English.
CC   The sequences given in Q32355-69 represent a new family of genes
CC   refered to as melanoma antigens (MAGE).  The cDNAs of this gene
CC   family were identified during the isolation of the antigen E gene.
CC   The MAGE cDNAs, when tested, did not transfer expression of antigen
CC   E, but they did show substantial homology to the antigen E cDNA
CC   sequence.  The MAGE DNAs share a certain degree of homology with each
CC   other and are expressed in tumour cells including several types of
CC   human tumor cells as well as in human tumors.  MAGE expression is not
CC   restricted to melanomas.  MAGE refers to a family of tumor rejection
CC   antigen precursors.  The antigens resulting from these genes are
CC   referred to as MAGE TRAS or melanoma antigen tumor rejection antigens.
CC   See also Q32351.
SQ   Sequence  662 BP;  155 A;  244 C;  176 G;  87 T;

Query Match  42.9%;  Score 70;  DB 1;  Length 662;
Best Local Similarity 80.0%;  Pred. No. 5.95e-32;
Matches  100;  Conservative  0;  Mismatches 24;  Indels 1;  Gaps  1;

Db    15 CCAGGAAGAATCCAGTTCCACCCCTGCTGTGAACCCAGGGAAGTCACGGGGCCG-GATGT  73
         |||| ||||| ||||||| ||||||||| |||||||||||||| | ||| |||||
Qy    95 CCAGGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGCCCAGATGT  154

Db    74 GACGCCACTGACTTGCGCGTTGCGGTTGGAGGTCAGAGAACAGCGAGATTCTCGCCCTGAGCCAACG  133
         ||||||| |||||||| | || || |||||||| ||||||||| ||||| ||||||| |||||
Qy   155 GACGCCCACTGACTTGAGCATTAGTTGGTTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCCG  214

Db   134 GCCTG  138
         |||||
Qy   215 GCCTG  219


RESULT 7
ID   Q72479  standard; DNA; 662 BP.
AC   Q72479;
DT   22-JUN-1995  (first entry)
DE   Tumour rejection antigen MAGE-21 gene.
KW   Tumour rejection antigen; melanoma antigen-21; MAGE-21; MAGE-3;
KW   cancer; cytolytic T cells; antigen D; human leucocyte antigen;
KW   ss.
OS   Homo sapiens.
PN   WO9423301-A.
PD   13-OCT-1994.
PF   17-MAR-1994;  U02877.
```

PR 26-MAR-1993; US-037230.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
DR WPI; 94-333192/41.
PT New tumour rejection antigen precursor MAGE3 - useful in
PT treatment and diagnosis of cancer
PS Disclosure: Page 63; 105pp; English.
CC Q72479 is the gene which contains the coding sequence for melanoma
CC antigen-21 (MAGE-21). Another melanoma antigen precursor MAGE-3 is encoded by
CC Q72470, this is a tumour rejection antigen precursor. Melanomas
CC characterised by the expression of MAGE-3 can be detected, or
CC monitored, by contacting a test sample with an agent that can
CC recognise MAGE-3. The melanoma can be treated by the administration
CC of cytolytic T cells specific for the complex of antigen D (the
CC mature rejection antigen derived from MAGE-3) and a human leucocyte
CC antigen (esp. HLA-A1).
SQ Sequence 662 BP; 155 A; 244 C; 176 G; 87 T;

Query Match 42.9%; Score 70; DB 1; Length 662;
Best Local Similarity 80.0%; Pred. No. 5.95e-32;
Matches 100; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

Db 15 CCAGGAAGAATCCAGTTCCACCCCTGCTGTGAACCCAGGGAGTCACGGGGCCG-GATGT 73
        ||||| ||||||||| ||||||||||||||||||||| || |||| |||||
Qy 95 CCAGGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGAGCCCCAGGTGCCCAGATGT 154

Db 74 GACGGCCACTGACTTGCCGCGTTGGAGGTCAGAGAACAGCGAGATTCTCGCCCTGAGCAACG 133
        |||||||||||||||| || || ||||| ||||||| |||| || |||| |
Qy 155 GACGGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTTTCGGTCGAGGGGGCG 214

Db 134 GCCTG 138
        |||
Qy 215 GCTTG 219

RESULT 8
ID Q51746 standard; cDNA; 91 BP.
AC Q51746;
DT 31-MAY-1994 (first entry)
DE Oligonucleotide probe MK14-A
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW ss.
OS Synthetic.
PN EP-571911-A.
PD 01-DEC-1993.
PF 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PA (BECT) BECTON DICKINSON CO.
PI Shank DD, Spears PA;
DR WPI; 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for
PT detection and amplification of Mycobacteria nucleic acid in
PT samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
CC cross reacted to a few non-mycobacterial infection. The probe may
CC be useful as an initial screen for mycobacterial infection.
CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 27.0%; Score 44; DB 1; Length 99;
Best Local Similarity 8.9%; Pred. No. 1.27e-14;
Matches 5; Conservative 45; Mismatches 6; Indels 0; Gaps 0;

Db 17 CGSSVHSYYVHVVSHHHSVHHVHVHVSVVVVHHVHVHVHVYVSVCTCA 72
        || |||||||||||||||||||| ||||| ||||| : || |
Qy 76 CGCTCACCCCCAGCCCCAGCCAGCAGAATCCGGTTCCACCCCTGCTCTCAACCCA 131

RESULT 9
ID Q51746 standard; cDNA; 91 BP.
AC Q51746;

DT 31-MAY-1994 (first entry)
DE Oligonucleotide probe MK14-A
KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW ss.
OS Synthetic.
PN EP-571911-A.
PD 01-DEC-1993.
PF 24-MAY-1993; 108325.
PR 26-MAY-1992; US-889651.
PA (BECT) BECTON DICKINSON CO.
PI Shank DD, Spears PA;
DR WPI; 93-378844/48.
PT New oligo:nucleotide probes specific for Mycobacteria - used for
PT detection and amplification of Mycobacteria nucleic acid in
PT samples
PS Claim 3; Page 14; 23pp; English.
CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC (Q51735). It hybridized to all spp. of mycobacteria tested, but
CC cross reacted to a few non-mycobacterial spp. The probe may
CC be useful as an initial screen for mycobacterial infection.
CC See also Q51735-45 and Q51747-59.
SQ Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 22.1%; Score 36; DB 1; Length 99;
Best Local Similarity 4.2%; Pred. No. 1.40e-09;
Matches 2; Conservative 40; Mismatches 6; Indels 0; Gaps 0;

Db 17 CGSSVHSYYVHVVSHHHSVHHVHVHVSVVVVHHVHVHVHV 64
        || |||||||||||| ::::::: : ::::::::
Cp 214 CGCCCCTCAGACCGAAAACCTCGCTTCTCTCTAACCACTAATGCTCAA 167

RESULT 10
ID N81164 standard: DNA; 204 BP.
AC N81164;
DT 08-NOV-1990 (first entry)
DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS Escherichia coli.
FH Key Location/Qualifiers
FT misc_feature 19..69
FT /*tag= a
FT /function=multiple cloning site
FT primer_bind 187..204
FT /*tag= b
PN EP-285123-A.
PD 05-MAY-1988.
PF 30-MAR-1988; 105163.
PR 03-APR-1987; US-034819.
PA (SUSO) SUOMEN SOKERI OY.
PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
DR WPI; 88-279927/40.
PT Introducing random point mutations into nucleic acods -
PT by prepn of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PS Disclosure: p; English.
CC Random point mutations were introduced into the alpha fragment of
CC E.coli beta-galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC transcriptase and the molecules are completed to forms that can be
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 diff base substitutions, most of which
CC occurred singularly in any given mutant.
CC See also P80575.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 20.2%; Score 33; DB 1; Length 204;
Best Local Similarity 7.2%; Pred. No. 9.49e-08;
Matches 7; Conservative 51; Mismatches 39; Indels 0; Gaps 0;

Db   92 HHYRRMRBNVYRDYNRSDAAAWTCCYRRSVKYDCCYNACHHDDHYVYBBBVYNVHNHNNC 151
                 :::::::   :: :   :: ::   :: |::   ::| : |:: :|
Cp   204 ACCGAAAACCTCGCTTCTCTCTAACCACTAATGCTCAAGTCAGTGGCGTCACATCTGGGC 145

Db   152 NCCCBNNHVCHNVHBNNHRNWAYVRHDARRDDVHCCV 188
                 || :| : : | ::::: :| :::|
Cp   144 ACTGGGCTTCCCTGGGTGAGAGCAGGGGTGGAACC 108

RESULT 11
ID   T76405 standard; DNA; 178 BP.
AC   T76405;
DT   15-SEP-1997 (first entry)
DE   Human endothelin-1 antisense oligonucleotide.
KW   Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW   chronic obstructive pulmonary disease; bronchitis; ss.
OS   Synthetic.
PN   WO964162-A1.
PD   19-DEC-1996.
PF   06-JUN-1996; U09306.
PR   07-JUN-1995; US-474497.
PA   (UYEC-) UNIV EAST CAROLINA.
PI   Metzger WJ, Nyce JW;
DR   WPI; 97-051871/05.
PT   Treatment of airway diseases such as asthma - by topically applying
PT   adenosine-free antisense oligo:nucleotide to airway epithelium of
PT   subject
PS   Claim 5; Page 38; 71pp; English.
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide specific
CC   for the human endothelin-1, targeted at the initiation codon. The
CC   method can be used to treat airway diseases such as cystic fibrosis,
CC   asthma, chronic obstructive pulmonary disease, bronchitis and other
CC   airway diseases characterised by an inflammatory response. By
CC   eliminating adenosine from the antisense ON, its liberation upon
CC   antisense degradation is prevented, thereby preventing adenosine-
CC   induced bronchoconstriction in patients with hyper-reactive airways.
SQ   Sequence   178 BP;   0 A;   52 C;   46 G;   32 T;

Query Match   19.6%;   Score 32; DB 1; Length 186;
Best Local Similarity   27.3%;   Pred. No. 3.80e-07;
Matches   18; Conservative   31; Mismatches 17; Indels   0; Gaps   0;

Db   113 CBBGCCCBCBBCCBCGBCGBGBGBBBTCBTGBGCBBBTBBTCCBTTCTGBBBBBBBGGBT 172
                |::| | :: :: : | |:::::| |: :::| | : |||||::: :::|||::|
Cp   195 CTCGCTTCTCTCTAACCACTAATGCTCAAGTCAGTGGCGTCACATCTGGGCACCTGGGCT 136

Db   173 CBBBBB 178
             ::::::
Cp   135 TCCCTG 130

RESULT 12
ID   Q70468 standard; DNA; 114 BP.
AC   Q70468;
DT   05-APR-1995 (first entry)
DE   Generic DNA sequence to generate a random TSAR petide library.
KW   TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW   effector domain; concatenated heterofunctional protein; linker;
KW   direct; rapid; detection; screening; treatment; generic; ss.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   misc_feature   55. .60
FT   /*tag=   a
FT   /note= "this sequence represents 'z'; z can be a
FT   sequence of 6, 9 or 12 nucleotides (see
FT   comments)"
PN   WO941818-A.
PD   18-AUG-1994.
PF   01-FEB-1994; U00977.

PT   Identifying proteins or peptides(s) which bind a ligand - by
PT   screening a recombinant vector library expressing fusion proteins
PT   comprising a binding domain and an effector domain
PS   Disclosure; Page 35; 255pp; English.
CC   Q70468 is a generic DNA sequence used to generate random TSAR (Totally
CC   Synthetic Affinity Reagents) peptides.This generic formula can also be
CC   represented as follows: X(NNB)11(TGC)(NNB)62(NNB)7(TGC)(NNB)10Y. X
CC   and Y are flanking restriction sites (X is not the same as Y) that are
CC   not specified further. Other generic sequences are shown in Q70466-68.
CC   Other specific peptides generated by these generic sequences are shown in
CC   R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC   comprising at least two functional regions - a binding domain with
CC   affinity for a ligand and a second effector peptide portion that is
CC   chemically or biologically active.They may further comprise a linker
CC   peptide between the 2 domains.The oligonucleotides are also designed so
CC   that the expressed peptide contains 2 or 4 cysteine residues positioned
CC   in, or flanking, the unpredicted or variant residues. These residues
CC   confer some degree of conformational rigidity to the peptides. The TSARs
CC   or compsns. comprising a TSAR binding domain can be used in vivo to
CC   deliver a chemically or biologically active moiety, eg. metal ion,
CC   radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC   cell. They can also replace the function of macromolecules, eg.
CC   monoclonal or polyclonal antibodies and therefore circumvent the need
CC   for complex methods of hybridoma formation or in vivo antibody
CC   production. The TSARs are easily characterised and have designed activity
CC   allowing direct and rapid detection in a screening process.
SQ   Sequence   114 BP;   0 A;   2 C;   2 G;   2 T;

Query Match   19.0%;   Score 31; DB 1; Length 122;
Best Local Similarity   3.3%;   Pred. No. 1.50e-06;
Matches   4; Conservative   34; Mismatches 84; Indels   0; Gaps   0;

Db   1 SQOthersNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBTGCNNBNNBNNBNNBNNBNNBNNBN 60
                                                             :   :   : .   :
Cp   186 CTCTAACCACTAATGCTCAAGTCAGTGCGTCACATCTGGGCACCTGGGCTTCCCTGGGT 127

Db   61 NBNNNNNNNBNNBNNBNNBNNBNNBNNBTGCNNBNNBNNBNNBNNBNNBNNBNNBN 120
                      . : : :: : :   : :: |||
Cp   126 TGAGAGCAGGGTGGAACCAGGGGATTCTGCCTGCCTGGGCTGGGTGGGTGAGCGTGAAGATGT 67

Db   121 NB 122
             ::
Cp   66 TT 65

RESULT 13
ID   Q70467 standard; DNA; 114 BP.
AC   Q70467;
DT   05-APR-1995 (first entry)
DE   Generic DNA sequence to generate a random TSAR petide library.
KW   TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW   effector domain; concatenated heterofunctional protein; linker;
KW   direct; rapid; detection; screening; treatment; generic; ss.
OS   Synthetic.
FH   Key   Location/Qualifiers
FT   misc_feature   55. .60
FT   /*tag=   a
FT   /note= "this sequence represents 'z'; z can be a
FT   sequence of 6, 9 or 12 nucleotides (see
FT   comments)"
PN   WO941818-A.
PD   18-AUG-1994.
PF   01-FEB-1994; U00977.

PA   (UYNC-) UNIV NORTH CAROLINA.
PI   Fowlkes DM, Kay BK;
DR   WPI: 94-279739/34.
DR   P-PSDB: R65153.
PT   Identifying proteins or peptide(s) which bind a ligand - by
PT   screening a recombinant vector library expressing fusion proteins
PT   comprising a binding domain and an effector domain
PS   Disclosure: Page 35; 255pp; English.
CC   Q70467 is a generic DNA sequence used to generate random TSAR (Totally
CC   Synthetic Affinity Reagents) peptides.This generic formula can also be
CC   represented as follows: X(NNB)16(TGC)(NNB)12(TGC)(NNB)16(TGC)(NNB)1Y. X
CC   and Y are flanking restriction sites (X is not the same as Y)that are
CC   not specified further. Other generic sequences are shown in Q70466-68.
CC   Other specific peptides generated by these generic sequences are shown in
CC   R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC   comprising at least two functional regions - a binding domain with
CC   affinity for a ligand and a second effector peptide portion that is
CC   chemically or biologically active.They may further comprise a linker
CC   peptide between the 2 domains.The oligonucleotides are also designed so
CC   that the expressed peptide contains 2 or 4 cysteine residues positioned
CC   in, or flanking, the unpredicted or variant residues. These residues
CC   confer some degree of conformational rigidity to the peptides. The TSARs
CC   or compsns. comprising a TSAR binding domain can be used in vivo to
CC   deliver a chemically or biologically active moiety, eg. metal ion,
CC   radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC   cell. They can also replace the function of macromolecules, eg.
CC   monoclonal or polyclonal antibodies and therefore circumvent the need for
CC   complex methods of hybridoma formation or in vivo antibody production.
CC   The TSARs are easily characterised and have designed activity allowing
CC   direct and rapid detection in a screening process.
SQ   Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match   18.4%; Score 30; DB 1; Length 122;
Best Local Similarity 0.9%; Pred. No. 5.87e-06;
Matches   1; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

```
Db       5 hersNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBTGCNNBNN 64
             : ::   : ::   : ::   : ::   : ::   : ::    : |    : :
Cp     165 TCAGTGGCGTCACATCTGGGCACCTGGGCTTCCCTGCGTTGAGAGCAGGAGGGGGTGGAACCGG 106

Db      65 NNNNNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNB 113
Cp     105 ATTCTCCTGGCTCTTGGGCTGGGGGTGAGCGTGAAGATGTTTGGATGGGT 57
```

RESULT   14
ID   N81164 standard; DNA; 204 BP.
AC   N81164;
DT   08-NOV-1990 (first entry)
DE   Base substituted E.coli beta-galactosidase alpha-fragment.
KW   E.coli beta galactosidase alpha fragment; base substitutions; ss.
OS   Escherichia coli.
FH   Key   Location/Qualifiers
FT   misc_feature   19..69
FT   /*tag= a
FT   /function=multiple cloning site
FT   primer_bind   187..204
FT   /*tag= b
PN   EP-285123-A.
PD   05-MAY-1988.
PF   30-MAR-1988; 105163.
PR   03-APR-1987; US-034819.
PA   (SUSO) SUOMEN SOKERI OY.
PI   Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
DR   WPI; 88-279927/40.
PT   Introducing random point mutations into nucleic acds -
PT   by prepn of single stranded template, annealing a primer, elongation,
PT   misincorporation, completion of molecules and screening.
PS   Disclosure; p; English.
CC   Random point mutations were introduced into the alpha fragment of
CC   E.coli beta galactosidase. The wild type sequence was obtained as a
CC   single stranded template and an oligonucleotide was hybridised to
CC   it to generate a popn of DNA molecules which terminate at all

CC   possible nucleotide positions within a specified region. The
CC   variable 3' ends generated in this way are used as primers for
CC   reverse transcriptase. Nucleotides are misincorporated by the
CC   transcriptase and the molecules are completed to forms that can be
CC   amplified and then expressed in a suitable host-vector system.
CC   The sequence covers all 176 difft base substitutions, most of which
CC   occurred singularly in any given mutant.
CC   See also P80575.
SQ   Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match   18.4%; Score 30; DB 1; Length 204;
Best Local Similarity 12.1%; Pred. No. 5.87e-06;
Matches   8; Conservative 34; Mismatches 24; Indels 0; Gaps 0;

```
Db     126 CYNACHHDDHYVYBBBVYNVHNHNCNCCCBNNHVCHNVHBNNHRNWAYVRHDARRDDVH 185
             |: |   :|:::::::|:: |  : ||  |  | .| .: .: ::| :: : ::
Qy      58 CCCATCCAAACATCTTCACGCTCACCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCC 117

Db     186 CCVCHC 191
             | :|:|
Qy     118 CTGCTC 123
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RESULT   15
ID   Q10572 standard; DNA; 1047 BP.
AC   Q10572;
DT   09-APR-1991 (first entry)
DE   Human Natriuretic Peptide Receptor B.
KW   NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
KW   hyperaldosteronism; glaucoma; guanyl cyclase.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   Peptide   1..22
FT   /label= signal sequence
FT   Protein   12
FT   /label= mature NPBR
FT   Domain   23..455
FT   /label= extracellular domain
FT   /note= "binds natriuretic peptides A,B and C]"
FT   Domain   456..456
FT   /label= transmembrane domain
FT   Domain   479..1047
FT   /label= cytoplasmic domain
FT   /note= "GC and protien kinase activity"
FT   Modified-site   24..26
FT   /label= N-glycos_site
FT   Modified-site   35..37
FT   /label= N-glycos_site
FT   Modified-site   161..163
FT   /label= N-glycos_site
FT   Modified-site   195..197
FT   /label= N-glycos_site
FT   Modified-site   244..246
FT   /label= N-glycos_site
FT   Modified-site   277..279
FT   /label= N-glycos_site
FT   Modified-site   349..351
FT   /label= N-glycos_site
FT   Modified-site   600..602
FT   /label= N-glycos_site
PN   WO9100292-A.
PD   10-JAN-1991.
PF   22-JUN-1990; U03586.
PR   23-JUN-1989; US-370673.
PA   (GETH) GENENTECH INC.
PI   Chang M, Goeddel D, Lowe D;
DR   WPI: 91-036711/05.
DR   N-PSDB: Q10324.
PT   Natriuretic protein receptor B - for diagnosis and treatment of
PT   kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
PS   Claim 3; Fig 1; 49pp; English.
CC   The sequence was derived from the DNA encoding natriuretic peptide
CC   receptor B, NPRB, having guanyl cyclase (GC) activity and protein

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```
CC   kinase activity.  The DNA can be inserted into expression vectors
CC   for the prodn. of the protein, opt. after being mutated to produce
CC   NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
CC   114,952).  The protein (or variants) can be used in treatment of
CC   natriuretic peptide disorders, and also to isolate peptides using
CC   affinity chromatography.  Antibodies with affinity for NPRB can
CC   also be prepd.
SQ   Sequence   1047 BP;    87 A;    15 C;    83 G;    51 T;

Query Match          18.4%;  Score 30;  DB 1; Length 1055;
Best Local Similarity 13.3%;  Pred. No. 5.87e-06;
Matches    19; Conservative    40; Mismatches   83;  Indels    1;  Gaps    1;

Db     295 RNANNTVNVNTYRNNNNNNYNNNNNRNNNNRARNDNGVNNGNSNMNNNAGCNYDGNNNYAN 354
           : |::::|:    |::       |||       | ::  :|  :|   |  :|
Cp     199 AAACCTCGCTCTCTCTCTCTCAACCACTAATGCTCAAGTCAGTGCGTCACATCTGGGCACCTG 140

Db     355 VNNNTNNNGTRNDGNRNVNKMNGRRYHGVTGNVVMDKNNDRNTDNVNWAMGDNDSGDNN 414
           :   |  ||||||:  :|:::||  :  ||:::: |: :: |: : : ::|:  ::|:
Cp     139 GGCTTCCCTGGGTGAGAGC-AGGGGTGGAACCGGATTCTGCCTGCCTTGGGCTGGGGGT 81

Db     415 NAAHYSGANKNNWWTGRNNNNWVK 437
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Cp      80 GAGCGTGAAGAATGTTTGGATGGG 58
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Search completed: Tue Apr 7 22:01:11 1998
Job time : 21 secs.